Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences.

SEQ ID NO.	Nucleotide sequence[a]	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Bacterial species:	***Chlamydia pneumoniae***		
2091	5'-CGC GAC TTG AGA TGG AAC TTA GTG AGC TTC TTG GTC GCG	20	157-183
2092	5'-CGC GAC GAA AGA ACT TCC TGA AGG TCG TGC AGG TCC AG	20	491-516
Bacterial species:	***Chlamydia trachomatis***		
2213	5'-CGT GCC ATT GAC ATG ATT TCC GAA GAA GAC GCT GAA GGC ACG	1739[b]	412-441
Bacterial species:	***Enterococcus faecalis***		
1236	5'-GCG AGC CGT GGT GAA GTT CGC GTT GGT GGC TCG C	883	370-391
Bacterial species:	***Enterococcus faecium***		
1235	5'-GCG AGC CGA AGT TGA AGT TGT TGG TAT TGC TGG CTC GC	64	412-437
Bacterial species:	***Legionella pneumophila***		
2084[c]	5'-CAC GCG TCA ACA CCC GTA CAA GTC GTC TTT TGC GCG TG	112	461-486
Bacterial species:	***Mycoplasma pneumoniae***		
2096[c]	5'-CGC GAC CGG TAC CAC GGC CAG TAA TCG TGT CGC G	2097[b]	658-679
Bacterial species:	***Neisseria gonorrhoeae***		
2177	5'-GGC ACG GAC AAA CCA TTC CTG CTG CCT ATC GAA ACG TGT TCC CGT GCC	126	323-357
2178	5'-GGC ACG ACA AAC CAT TCC TGC TGC CTA TCG AAC GTG CC	126	323-348
2179	5'-GGC AGC TCT ACT TCC GTA CCA CTG ACG TAA CCG GCT GCC	126	692-718

[a] Underlined nucleotides indicate the molecular beacon's stem.
[b] Sequence from databases.
[c] This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequenc s (continued).

SEQ ID NO.	Nucleotide sequence[a]	Originating DNA fragment: SEQ ID NO.	Originating DNA fragment: Nucleotide position
Bacterial species:	***Pseudomonas aeruginosa***		
2122	5'-CCG AGC GAA TGT AGG AGT CCA GGG TCT CTG CTC GG	153,880,2138[b,c]	280-302[d]
Bacterial species:	***Staphylococcus aureus***		
2186	5'-ACG CGC TCA AAG CAG AAG TAT ACG TAT TAT CAA AAG ACG CGC GT	1728	615-646
Bacterial group:	***Staphylococcus* sp. other than *S. aureus***		
1233	5'-GCG AGC GTT ACT GGT GTA GAA ATG TTC CGG CTC GC	878	372-394
Fungal species:	***Candida albicans***		
2073	5'-CCG AGC AAC ATG ATT GAA CCA TCC ACC AAC TGG CTC GG	408	404-429
Fungal species:	***Candida dubliniensis***		
2074	5'-CCG AGC AAC ATG ATT GAA GCT TCC ACC AAC TGG CTC GG	414	416-441
Fungal species:	***Candida glabrata***		
2110[b]	5'-GCG GGC CCT TAA CGA TTT CAG CGA ATC TGG ATT CAG CCC GC	417	307-335
2111	5'-GCG GGC ATG TTG AAG CCA CCA CCA ACG CTT CCT GGC CCG C	417	419-447
Fungal species:	***Candida krusei***		
2112[b]	5'-GCG GGC TTG ATG AAG TTT GGG TTT CCT TGA CAA TTG CCC GC	422	318-347
2113	5'-GCG GGC ACA AGG GTT GGA CTA AGG AAA CCA AGG CAG CCC GC	422	419-447
2114	5'-GCG GGC ATC GAT GCT ATT GAA CCA CCT GTC AGA CCG CCC GC	422	505-533

[a] Underlined nucleotides indicate the molecular beacon's stem.
[b] Sequence from databases.
[c] These sequences were aligned to derive the corresponding primer.
[d] The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences (continued).

SEQ ID NO.	Nucleotide sequence[a]	Originating DNA fragment: SEQ ID NO.	Originating DNA fragment: Nucleotide position
Fungal species:	***Candida lusitaniae***		
2115[b]	5'-GCG GGC GGT AAG TCC ACC GGT AAG ACC TTG TTG GCC CGC	424	304-330
2116	5'-GCG GGC GTA AGT CAC CGG TAA GAC CTT GTT GGC CCG C	424	476-502
2117	5'-GCG GGC GAC GCC ATT GAG CCA CCT TCG AGA GCC CGC	424	512-535
Fungal species:	***Candida parapsilosis***		
2118[b]	5'-GCG GGC TCC TTG ACA ATT TCT TCG TAT CTG TTC TTG GCC CGC	426	301-330
Fungal species:	***Candida tropicalis***		
2119	5'-GCG GGC TTA CAA CCC TAA GGC TGT TCC ATT CGT TGC CCG C	429	357-384
2120	5'-GCG GGC AGA AAC CAA GGC TGG TAA GGT TAC CGG AGC CCG C	429	459-487
Fungal species:	***Cryptococcus neoformans***		
2106	5'-GCG AGC AGA GCA CGC CCT CCT CGC CGC TCG C	623,1985,1986[c]	226-244[d]
2107	5'-GCG AGC TCC CCA TCT CTG GTT GGC ACG CTC GC	623,1985,1986[c]	390-408[d]
Bacterial genus:	***Legionella sp.***		
2083	5'-CCG CCG ATG TTC CGT AAA TTA CTT GAI GAA GGT CGA GCC GGC GG	111-112[a]	488-519[e]

[a] Underlined nucleotides indicate the molecular beacon's stem.
[b] This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
[c] These sequences were aligned to derive the corresponding primer.
[d] The nucleotide positions refer to the *C. neoformans tuf* (EF-1) sequence fragment (SEQ ID NO. 623).
[e] The nucleotide positions refer to the *L. pneumophila tuf* (EF-1) sequence fragment (SEQ ID NO. 112).

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences (continued).

SEQ ID NO.	Nucleotide sequence[a]	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Fungal genus:	***Candida sp.***		
2108	5'-GCG GGC AAC TTC RTC AAG AAG GTT GGT TAC AAC CCG CCC GC	414,417, 422,424, 426,429,624[b]	52-80[c]
2109	5'-GCG GGC CCA ATC TCT GGT TGG AAY GGT GAC AAG CCC GC	Same as SEQ ID NO. 2108	100-125[c]
Bacterial group:	**Pseudomonads**		
2121	5'-CGA CCG CIA GCC GCA CAC CAA GTT CCG GTC G	153-155, 205,880,2137[d], 2138[d,b]	598-616[e]

[a] Underlined nucleotides indicate the molecular beacon's stem.
[b] These sequences were aligned to derive the corresponding primer.
[c] The nucleotide positions refer to the *C. albicans tuf* (EF-1) sequence fragment (SEQ ID NO. 624).
[d] Sequence from databases.
[e] The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).

Annex XLVIII: Molecular beacon internal hybridization probes for specific detection of *ddl* and *mtl* gene sequences.

SEQ ID NO.	Nucleotide sequence[a]	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Bacterial species:	***E. faecium (ddl)***		
1237	5'-GCG AGC CGC GAA ATC GAA GTT GCT GTA TTA GGG CTC GC	1242[b]	334-359
Bacterial species:	***E. faecalis (mtl)***		
1238	5'-GCG AGC GGC GTT AAT TTT GGC ACC GAA GAA GAG CTC GC	1243[b]	631-656

[a] Underlined nucleotides indicate the molecular beacon's stem.
[b] Sequence from databases.

Annex XLIX: Internal hybridization probe for specific detection of *S. aureus* sequences of unknown coding potential.

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Bacterial species:	***Staphylococcus aureus***		
1234	5'-ACT AAA TAA ACG CTC ATT CG	1244	35-54

Annex L: Specific and ubiquitous primers for nucl ic acid amplification (antimicrobial agents resistance genes sequences).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***aac(2')-Ia***		
1344	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1348[a]	163-186
1345[b]	5'-CCC GCC GAG CAT TTC AAC TAT TG	1348[a]	392-414
1346	5'-GAT GTT ACG CAG CAG GGC AGT C	1348[a]	172-193
1347[b]	5'-ACC AAG CAG GTT CGC AGT CAA GTA	1348[a]	467-490
Resistance gene:	***aac(3')-Ib***		
1349	5'-CAG CCG ACC AAT GAG TAT CTT GCC	1351[a]	178-201
1350[b]	5'-TAA TCA GGG CAG TTG CGA CTC CTA	1351[a]	356-379
Resistance gene:	***aac(3')-IIb***		
1352	5'-CCA CGC TGA CAG AGC CGC ACC G	1356[a]	383-404
1353[b]	5'-GGC CAG CTC CCA TCG GAC CCT G	1356[a]	585-606
1354	5'-CAC GCT GAC AGA GCC GCA CCG	1356[a]	384-404
1355[b]	5'-ATG CCG TTG CTG TCG AAA TCC TCG	1356[a]	606-629
Resistance gene:	***aac(3')-IVa***		
1357	5'-GCC CAT CCA TTT GCC TTT GC	1361[a]	295-314
1358[b]	5'-GCG TAC CAA CTT GCC ATC CTG AAG	1361[a]	517-540
1359	5'-TGC CCC TGC CAC CTC ACT C	1361[a]	356-374
1360[b]	5'-CGT ACC AAC TTG CCA TCC TGA AGA	1361[a]	516-539
Resistance gene:	***aac(3')-VIa***		
1362	5'-CGC CGC CAT CGC CCA AAG CTG G	1366[a]	285-306
1363[b]	5'-CGG CAT AAT GGA GCG CGG TGA CTG	1366[a]	551-574
1364	5'-TTT CTC GCC CAC GCA GGA AAA ATC	1366[a]	502-525
1365[b]	5'-CAT CCT CGA CGA ATA TGC CGC G	1366[a]	681-702
Resistance gene:	***aac(6')-Ia***		
1367	5'-CAA ATA TAC TAA CAG AAG CGT TCA	1371[a]	56-79
1368[b]	5'-AGG ATC TTG CCA ATA CCT TTA T	1371[a]	269-290
1379	5'-AAA CCT TTG TTT CGG TCT GCT AAT	1371[a]	153-176
1380[b]	5'-AAG CGA TTC CAA TAA TAC CTT GCT	1371[a]	320-343

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Ann x L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***aac(6')-Ic***		
1372	5'-GCT TTC GTT GCC TTT GCC GAG GTC	1376[a]	157-180
1373[b]	5'-CAC CCC TGT TGC TTC GCC CAC TC	1376[a]	304-326
1374	5'-AGA TAT TGG CTT CGC CGC ACC ACA	1376[a]	104-127
1375[b]	5'-CCC TGT TGC TTC GCC CAC TCC TG	1376[a]	301-323
Resistance gene:	***ant(3')-Ia***		
1377	5'-GCC GTG GGT CGA TGT TTG ATG TTA	1381[a]	100-123
1378[b]	5'-GCT CGA TGA CGC CAA CTA CCT CTG	1381[a]	221-244
1379	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1381[a]	127-150
1380[b]	5'-CGC TCG ATG ACG CCA ACT ACC TCT	1381[a]	222-245
Resistance gene:	***ant(4')-Ia***		
1382	5'-TAG ATA TGA TAG GCG GTA AAA AGC	1386[a]	149-172
1383[b]	5'-CCC AAA TTC GAG TAA GAG GTA TT	1386[a]	386-408
1384	5'-GAT ATG ATA GGC GGT AAA AAG C	1386[a]	151-172
1385[b]	5'-TCC CAA ATT CGA GTA AGA GGT A	1386[a]	388-409
Resistance gene:	***aph(3')-Ia***		
1387	5'-TTA TGC CTC TTC CGA CCA TCA AGC	1391[a]	233-256
1338[b]	5'-TAC GCT CGT CAT CAA AAT CAC TCG	1391[a]	488-511
1389	5'-GAA TAA CGG TTT GGT TGA TGC GAG	1391[a]	468-491
1390[b]	5'-ATG GCA AGA TCC TGG TAT CGG TCT	1391[a]	669-692
Resistance gene:	***aph(3')-IIa***		
1392	5'-TGG GTG GAG AGG CTA TTC GGC TAT	1396[a]	43-66
1393[b]	5'-CAG TCC CTT CCC GCT TCA GTG AC	1396[a]	250-272
1394	5'-GAC GTT GTC ACT GAA GCG GGA AGG	1396[a]	244-267
1395[b]	5'-CTT GGT GGT CGA ATG GGC AGG TAG	1396[a]	386-409

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance g nes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***aph(3')-IIIa***		
1397	5'-GTG GGA GAA AAT GAA AAC CTA T	1401[a]	103-124
1398[b]	5'-ATG GAG TGA AAG AGC CTG AT	1401[a]	355-374
1399	5'-ACC TAT GAT GTG GAA CGG GAA AAG	1401[a]	160-183
1400[b]	5'-CGA TGG AGT GAA AGA GCC TGA TG	1401[a]	354-376
Resistance gene:	***aph(3')-VIa***		
1402	5'-TAT TCA ACA ATT TAT CGG AAA CAG	1406[a]	18-41
1403[b]	5'-TCA GAG AGC CAA CTC AAC ATT TT	1406[a]	175-197
1404	5'-AAA CAG CGT TTT AGA GCC AAA TAA	1406[a]	36-59
1405[b]	5'-TTC TCA GAG AGC CAA CTC AAC ATT	1406[a]	177-200
Resistance gene:	***blaCARB***		
1407	5'-CCC TGT AAT AGA AAA GCA AGT AGG	1411[a]	351-374
1408[b]	5'-TTG TCG TAT CCC TCA AAT CAC C	1411[a]	556-577
1409	5'-TGG GAT TAC AAT GGC AAT CAG CG	1411[a]	205-227
1410[b]	5'-GGG GAA TAG GTC ACA AGA TCT GCT T	1411[a]	329-353
Resistance gene:	***blaCMY-2***		
1412	5'-GAG AAA ACG CTC CAG CAG GGC	1416[a]	793-813
1413[b]	5'-CAT GAG GCT TTC ACT GCG GGG	1416[a]	975-995
1414	5'-TAT CGT TAA TCG CAC CAT CAC	1416[a]	90-110
1415[b]	5'-ATG CAG TAA TGC GGC TTT ATC	1416[a]	439-459
Resistance genes:	***blaCTX-M-1, blaCTX-M-2***		
1417	5'-TGG TTA ACT AYA ATC CSA TTG CGG A	1423[a]	314-338
1418[b]	5'-ATG CTT TAC CCA GCG TCA GAT T	1423[a]	583-604
Resistance gene:	***blaCTX-M-1***		
1419	5'-CGA TGA ATA AGC TGA TTT CTC ACG	1423[a]	410-433
1420[b]	5'-TGC TTT ACC CAG CGT CAG ATT ACG	1423[a]	580-603
1421	5'-AAT TAG AGC GGC AGT CGG GAG GAA	1423[a]	116-139
1422[b]	5'-GAA ATC AGC TTA TTC ATC GCC ACG	1423[a]	405-428

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents r sistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***blaCTX-M-2***		
1424	5'-GTT AAC GGT GAT GGC GAC GCT AC	1428[a]	30-52
1425[b]	5'-GAA TTA TCG GCG GTG TTA ATC AGC	1428[a]	153-176
1426	5'-CAC GCT CAA TAC CGC CAT TCC A	1428[a]	510-531
1427[b]	5'-TTA TCG CCC ACT ACC CAT GAT TTC	1428[a]	687-710
Resistance gene:	***blaIMP***		
1429	5'-TTT ACG GCT AAA GAT ACT GAA AAG T	1433[a]	205-229
1430[b]	5'-GTT TAA TAA AAC AAC CAC CGA ATA AT	1433[a]	513-538
1431	5'-TAA TTG ACA CTC CAT TTA CGG CTA A	1433[a]	191-215
1432[b]	5'-ACC GAA TAA TAT TTT CCT TTC AGG CA	1433[a]	497-522
Resistance gene:	***blaOXA2***		
1434	5'-CAC AAT CAA GAC CAA GAT TTG CGA T	1438[a]	319-343
1435[b]	5'-GAA AGG GCA GCT CGT TAC GAT AGA G	1438[a]	532-556
Resistance gene:	***blaOXA10***		
1436	5'-CAG CAT CAA CAT TTA AGA TCC CCA	1439[a]	194-217
1437[b]	5'-CTC CAC TTG ATT AAC TGC GGA AAT TC	1439[a]	479-504
Resistance gene:	***blaPER-1***		
1440	5'-AGA CCG TTA TCG TAA ACA GGG CTA AG	1442[a]	281-306
1441[b]	5'-TTT TTT GCT CAA ACT TTT TCA GGA TC	1442[a]	579-604
Resistance gene:	***blaPER-2***		
1443	5'-CTT CTG CTC TGC TGA TGC TTG GC	1445[a]	32-54
1444[b]	5'-GGC GAC CAG GTA TTT TGT AAT ACT GC	1445[a]	304-329
Resistance genes:	***blaPER-1, blaPER-2***		
1446	5'-GGC CTG YGA TTT GTT ATT TGA ACT GGT	1442[a]	414-440
1447[b]	5'-CGC TST GGT CCT GTG GTG GTT TC	1442[a]	652-674
1448	5'-GAT CAG GTG CAR TAT CAA AAC TGG AC	1442[a]	532-557
1449[b]	5'-AGC WGG TAA CAA YCC TTT TAA CCG CT	1442[a]	671-696

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***blaSHV***		
1883	5'-AGC CGC TTG AGC AAA TTA AAC TA	1900[a]	71-93
1884[b]	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900[a]	763-785
1885	5'-AGC GAA AAA CAC CTT GCC GAC	1900[a]	313-333
1884[b]	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900[a]	763-785
Resistance gene:	***blaTEM***		
1906	5'-CCT TAT TCC CTT TTT TGC GG	1927[a]	27-46
1907[b]	5'-CAC CTA TCT CAG CGA TCT GTC T	1927[a]	817-838
1908	5'-AAC AGC GGT AAG ATC CTT GAG AG	1927[a]	148-170
1907[b]	5'-CAC CTA TCT CAG CGA TCT GTC T	1927[a]	817-838
Resistance gene:	***catI***		
2145	5'-GCA AGA TGT GGC GTG TTA CGG T	2147[a]	363-384
2146[b]	5'-GGG GCG AAG AAG TTG TCC ATA TT	2147[a]	484-506
Resistance gene:	***catII***		
2148	5'-CAG ATT AAA TGC GGA TTC AGC C	2150[a]	67-88
2149[b]	5'-ATC AGG TAA ATC ATC AGC GGA TA	2150[a]	151-173
Resistance gene:	***catIII***		
2151	5'-ATA TTT CAG CAT TAC CTT GGG TT	2153[a]	419-441
2152[b]	5'-TAC ACA ACT CTT GTA GCC GAT TA	2153[a]	603-625
Resistance gene:	***catP***		
2154	5'-CGC CAT TCA GAG TTT AGG AC	2156[a]	178-197
2155[b]	5'-TTC CAT ACC GTT GCG TAT CAC TT	2156[a]	339-361
Resistance gene:	***cat***		
2157	5'-CCA CAG AAA TTG ATA TTA GTG TTT TAT	2159[a]	89-115
2158[b]	5'-TCG CTA TTG TAA CCA GTT CTA	2159[a]	201-221
2160	5'-TTT TGA ACA CTA TTT TAA CCA GC	2162[a]	48-70
2161[b]	5'-GAT TTA ACT TAT CCC AAT AAC CT	2162[a]	231-253

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucl ic acid amplification (antimicrobial agents resistanc genes sequenc s) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene: ***dfrA***			
1450	5'-ACC ACT GGG AAT ACA CTT GTA ATG GC	1452[a]	106-131
1451[b]	5'-ATC TAC CTG GTC AAT CAT TGC TTC GT	1452[a]	296-321
Resistance gene: ***dhfrIa***			
1457	5'-CAA AGG TGA ACA GCT CCT GTT T	1461[a]	75-96
1458[b]	5'-TCC GTT ATT TTC TTT AGG TTG GTT AAA	1461[a]	249-275
1459	5'-AAG GTG AAC AGC TCC TGT TT	1461[a]	77-96
1560[b]	5'-GAT CAC TAC GTT CTC ATT GTC A	1461[a]	207-228
Resistance genes: ***dhfrIa, dhfrXV***			
1453	5'-ATC GAA GAA TGG AGT TAT CGG RAA TG	1461[a]	27-52
1454[b]	5'-CCT AAA AYT RCT GGG GAT TTC WGG A	1461[a]	384-408
1455	5'-CAG GTG GTG GGG AGA TAT ACA AAA	1461[a]	290-313
1456[b]	5'-TAT GTT AGA SRC GAA GTC TTG GKT AA	1461[a]	416-441
Resistance gene: ***dhfrIb***			
1466	5'-AAG CAT TGA CCT ACA ATC AGT GT	1470[a]	98-120
1467[b]	5'-AAT ACA ACT ACA TTG TCA TCA TTT GAT	1470[a]	204-230
1468	5'-CGT TAC CCG CTC AGG TTG GAC ATC AA	1470[a]	183-208
1469[b]	5'-CAT CCC CCT CTG GCT CGA TGT CG	1470[a]	354-376
Resistance gene: ***dhfrV***			
1471	5'-GAT AAT GAC AAC GTA ATA GTA TTC CC	1475[a]	208-233
1472[b]	5'-GCT CAA TAT CAA TCG TCG ATA TA	1475[a]	342-364
1473	5'-TTA AAG CCT TGA CGT ACA ACC AGT GG	1475[a]	95-120
1474[b]	5'-TGG GCA ATG TTT CTC TGT AAA TCT CC	1475[a]	300-325
Resistance genes: ***dhfrIb, dhfrV***			
1462	5'-GCA CTC CCY AAT AGG AAA TAC GC	1470[a]	157-179
1463[b]	5'-AGT GTT GCT CAA AAA CAA CTT CG	1470[a]	405-427
1464	5'-ACG TTY GAA TCT ATG GGM GCA CT	1470[a]	139-161
1465[b]	5'-GTC GAT AAG TGG AGC GTA GAG GC	1470[a]	328-350

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene: ***dhfrVI***			
1476	5'-GGC GAG CAG CTC CTA TTC AAA G	1480[a]	79-100
1477[b]	5'-TAG GTA AGC TAA TGC CGA TTC AAC A	1480[a]	237-261
1478	5'-GAG AAT GGA GTA ATT GGC TCT GGA TT	1480[a]	31-56
1479[b]	5'-GCG AAA TAC ACA ACA TCA GGG TCA T	1480[a]	209-233
Resistance gene: ***dhfrVII***			
1485	5'-AAA ATG GCG TAA TCG GTA ATG GC	1489[a]	32-54
1486[b]	5'-CAT TTG AGC TTG AAA TTC CTT TCC TC	1489[a]	189-214
1487	5'-AAT CGA AAA TAT GCA GTA GTG TCG AG	1489[a]	166-191
1488[b]	5'-AGA CTA TTG TAG ATT TGA CCG CCA	1489[a]	294-317
Resistance genes: ***dhfrVII, dhfrXVII***			
1481	5'-RTT ACA GAT CAT KTA TAT GTC TCT	1489[a]	268-291
1482[b]	5'-TAA TTT ATA TTA GAC AWA AAA AAC TG	1489[a]	421-446
1483	5'-CAR YGT CAG AAA ATG GCG TAA TC	1489[a]	23-45
1484[b]	5'-TKC AAA GCR WTT TCT ATT GAA GGA AA	1489[a]	229-254
Resistance gene: ***dhfrVIII***			
1490	5'-GAC CTA TGA GAG CTT GCC CGT CAA A	1494[a]	144-168
1491[b]	5'-TCG CCT TCG TAC AGT CGC TTA ACA AA	1494[a]	376-401
1492	5'-CAT TTT AGC TGC CAC CGC CAA TGG TT	1494[a]	18-43
1493[b]	5'-GCG TCG CTG ACG TTG TTC ACG AAG A	1494[a]	245-269
Resistance gene: ***dhfrIX***			
1495	5'-TCT CTA AAC ATG ATT GTC GCT GTC	1499[a]	7-30
1496[b]	5'-CAG TGA GGC AAA AGT TTT TCT ACC	1499[a]	133-156
1497	5'-CGG ACG ACT TCA TGT GGT AGT CAG T	1499[a]	171-195
1498[b]	5'-TTT GTT TTC AGT AAT GGT CGG GAC CT	1499[a]	446-471

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequ nces) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***dhfrXII***		
1500	5'-ATC GGG TTA TTG GCA ATG GTC CTA	1504[a]	50-73
1501[b]	5'-GCG GTA GTT AGC TTG GCG TGA GAT T	1504[a]	201-225
1502	5'-GCG GGC GGA GCT GAG ATA TAC A	1504[a]	304-325
1503[b]	5'-AAC GGA GTG GGT GTA CGG AAT TAC AG	1504[a]	452-477
Resistance gene:	***dhfrXIII***		
1505	5'-ATT TTT CGC AGG CTC ACC GAG AGC	1507[a]	106-129
1506[b]	5'-CGG ATG AGA CAA CCT CGA ATT CTG CTG	1507[a]	413-439
Resistance gene:	***dhfrXV***		
1508	5'-AGA ATG TAT TGG TAT TTC CAT CTA TCG	1512[a]	215-241
1509[b]	5'-CAA TGT CGA TTG TTG AAA TAT GTA AA	1512[a]	336-361
1510	5'-TGG AGT GCC AAA GGG GAA CAA T	1512[a]	67-88
1511[b]	5'-CAG ACA CAA TCA CAT GAT CCG TTA TCG	1512[a]	266-292
Resistance gene:	***dhfrXVII***		
1513	5'-TTC AAG CTC AAA TGA AAA CGT CC	1517[a]	201-223
1514[b]	5'-GAA ATT CTC AGG CAT TAT AGG GAA T	1517[a]	381-405
1515	5'-GTG GTC AGT AAA AGG TGA GCA AC	1517[a]	66-88
1516[b]	5'-TCT TTC AAA GCA TTT TCT ATT GAA GG	1517[a]	232-257
Resistance gene:	***emhR***		
2102	5'-CAC CTT CAC CCT GAC CGA CG	2105[a]	822-841
2103[b]	5'-CGA ACC AGC GGA AAT AGT TGG AC	2105[a]	948-970
Resistance genes:	***ereA, ereA2***		
1528	5'-AAC TTG AGC GAT TTT CGG ATA CCC TG	1530[a]	80-105
1529[b]	5'-TTG CCG ATG AAA TAA CCG CCG ACT	1530[a]	317-340

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***ereB***		
1531	5'-TCT TTT TGT TAC GAC ATA CGC TTT T	1535[a]	152-176
1532[b]	5'-AGT GCT TCT TTA TCC GCT GTT CTA	1535[a]	456-479
1533	5'-CAG CGG ATA AAG AAG CAC TAC ACA TT	1535[a]	461-486
1534[b]	5'-CCT CCT GAA ATA AAG CCC GAC AT	1535[a]	727-749
Resistance gene:	***gyrA***		
1340	5'-GAA CAA GGT ATG ACA CCG GAT AAA T	1299[a]	163-188
1341[b]	5'-GAT AAC TGA AAT CCT GAG CCA TAC G	1299[a]	274-299
1936	5'-TAC CAC CCG CAC GGC	1954[a]	205-219
1937[b]	5'-CGG AGT CGC CGT CGA TG	1954[a]	309-325
1942	5'-GAC TGG AAC AAA GCC TAT AAA AAA TCA	1954[a]	148-174
1937[b]	5'-CGG AGT CGC CGT CGA TG	1954[a]	309-325
2040	5'-TGT GAC CCC AGA CAA ACC C	2054[a]	33-51
2041[b]	5'-GTT GAG CGG CAG CAC TAT CT	2054[a]	207-226
Resistance gene:	***inhA***		
2098	5'-CTG AGT CAC ACC GAC AAA CGT C	2101[a]	910-931
2099[b]	5'-CCA GGA CTG AAC GGG ATA CGA A	2101[a]	1074-1095
Resistance genes:	***linA, linA'***		
1536	5'-AGA TGT ATT AAC TGG AAA ACA ACA A	1540[a]	99-123
1537[b]	5'-CTT TGT AAT TAG TTT CTG AAA ACC A	1540[a]	352-376
1538	5'-TTA GAA GAT ATA GGA TAC AAA ATA GAA G	1540[a]	187-214
1539[b]	5'-GAA TGA AAA AGA AGT TGA GCT T	1540[a]	404-425
Resistance gene:	***linB***		
1541	5'-TGA TAA TCT TAT ACG TGG GGA ATT T	1545[a]	246-270
1542[b]	5'-ATA ATT TTC TAA TTG CCC TGT TTC AT	1545[a]	359-384
1543	5'-GGG CAA TTA GAA AAT TAT TTA TCA GA	1545[a]	367-392
1544[b]	5'-TTT TAC TCA TGT TTA GCC AAT TAT CA	1545[a]	579-604

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***mefA***		
1546	5'-CAA GAA GGA ATG GCT GTA CTA C	1548[a]	625-646
1547[b]	5'-TAA TTC CCA AAT AAC CCT AAT AAT AGA	1548[a]	816-842
Resistance gene:	***mefE***		
1549	5'-GCT TAT TAT TAG GAA GAT TAG GGG GC	1551[a]	815-840
1550[b]	5'-TAG CAA GTG ACA TGA TAC TTC CGA	1551[a]	1052-1075
Resistance genes:	***mefA, mefE***		
1552	5'-GGC AAG CAG TAT CAT TAA TCA CTA	1548[a]	50-73
1553[b]	5'-CAA TGC TAC GGA TAA ACA ATA CTA TC	1548[a]	318-343
1554	5'-AGA AAA TTA AGC CTG AAT ATT TAG GAC	1548[a]	1010-1035
1555[b]	5'-TAG TAA AAA CCA ATG ATT TAC ACC G	1548[a]	1119-1143
Resistance genes:	***mphA, mphK***		
1556	5'-ACT GTA CGC ACT TGC AGC CCG ACA T	1560[a]	33-57
1557[b]	5'-GAA CGG CAG GCG ATT CTT GAG CAT	1560[a]	214-237
1558	5'-GTG GTG GTG CAT GGC GAT CTC T	1560[a]	583-604
1559[b]	5'-GCC GCA GCG AGG TAC TCT TCG TTA	1560[a]	855-878
Resistance gene:	***mupA***		
2142	5'-GCC TTA ATT TCG GAT AGT GC	2144[a]	1831-1850
2143[b]	5'-GAG AAA GAG CCC AAT TAT CTA ATG T	2144[a]	2002-2026
Resistance gene:	***parC***		
1342	5'-GAT GTT ATT GGT CAA TAT CAT CCA	1321[a]	205-229
1343[b]	5'-AAG AAA CTG TCT CTT TAT TAA TAT CAC GT	1321[a]	396-425
1934	5'-GAA CGC CAG CGC GAA ATT CAA AAA G	1781	67-91
1935[b]	5'-AGC TCG GCA TAC TTC GAC AGG	1781	277-297
2044	5'-ACC GTA AGT CGG CCA AGT CA	2055[a]	176-195
2045[b]	5'-GTT CTT TCT CCG TAT CGT C	2055[a]	436-454

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequenc Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***ppflo*-like**		
2163	5'-ACC TTC ATC CTA CCG ATG TGG GTT	2165[a]	922-945
2164[b]	5'-CAA CGA CAC CAG CAC TGC CAT TG	2165[a]	1136-1158
Resistance gene:	***rpoB***		
2065	5'-CCA GGA CGT GGA GGC GAT CAC A	2072[a]	1218-1239
2066[b]	5'-CAC CGA CAG CGA GCC GAT CAG A	2072[a]	1485-1506
Resistance gene:	***satG***		
1581	5'-AAT TGG GGA CTA CAC CTA TTA TGA TG	1585[a]	93-118
1582[b]	5'-GGC AAA TCA GTC AGT TCA GGA GT	1585[a]	310-332
1583	5'-CGA TTG GCA ACA ATA CAC TCC TG	1585[a]	294-316
1584[b]	5'-TCA CCT ATT TTT ACG CCT GGT AGG AC	1585[a]	388-413
Resistance gene:	***sulII***		
1961	5'-GCT CAA GGC AGA TGG CAT TCC C	1965[a]	222-243
1962[b]	5'-GGA CAA GGC GGT TGC GTT TGA T	1965[a]	496-517
1963	5'-CAT TCC CGT CTC GCT CGA CAG T	1965[a]	237-258
1964[b]	5'-ATC TGC CTG CCC GTC TTG C	1965[a]	393-411
Resistance gene:	***tetB***		
1966	5'-CAT GCC AGT CTT GCC AAC G	1970[a]	66-84
1967[b]	5'-CAG CAA TAA GTA ATC CAG CGA TG	1970[a]	242-264
1968	5'-GGA GAG ATT TCA CCG CAT AG	1970[a]	457-476
1969[b]	5'-AGC CAA CCA TCA TGC TAT TCC A	1970[a]	721-742
Resistance gene:	***tetM***		
1586	5'-ATT CCC ACA ATC TTT TTT ATC AAT AA	1590[a]	361-386
1587[b]	5'-CAT TGT TCA GAT TCG GTA AAG TTC	1590[a]	501-524
1588	5'-GTT TTT GAA GTT AAA TAG TGT TCT T	1590[a]	957-981
1589[b]	5'-CTT CCA TTT GTA CTT TCC CTA	1590[a]	1172-1192

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continu d).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***vatB***		
1609	5'-GCC CTG ATC CAA ATA GCA TAT A	1613[a]	11-32
1610[b]	5'-CCT GGC ATA ACA GTA ACA TTC TG	1613[a]	379-401
1611	5'-TGG GAA AAA GCA ACT CCA TCT C	1613[a]	301-322
1612[b]	5'-ACA ACT GAA TTC GCA GCA ACA AT	1613[a]	424-446
Resistance gene:	***vatC***		
1614	5'-CCA ATC CAG AAG AAA TAT ACC C	1618[a]	26-47
1615[b]	5'-ATT AGT TTA TCC CCA ATC AAT TCA	1618[a]	177-200
1616	5'-ATA ATG AAT GGG GCT AAT CAT CGT AT	1618[a]	241-266
1617[b]	5'-GCC AAC AAC TGA ATA AGG ATC AAC	1618[a]	463-486
Resistance gene:	***vga***		
1619	5'-AAG GCA AAA TAA AAG GAG CAA AGC	1623[a]	641-664
1620[b]	5'-TGT ACC CGA GAC ATC TTC ACC AC	1623[a]	821-843
1621	5'-AAT TGA AGG ACG GGT ATT GTG GAA AG	1623[a]	843-868
1622[b]	5'-CGA TTT TGA CAG ATG GCG ATA ATG AA	1623[a]	975-1000
Resistance gene:	***vgaB***		
1624	5'-TTC TTT AAT GCT CGT AGA TGA ACC TA	1628[a]	354-379
1625[b]	5'-TTT TCG TAT TCT TCT TGT TGC TTT C	1628[a]	578-602
1626	5'-AGG AAT GAT TAA GCC CCC TTC AAA AA	1628[a]	663-688
1627[b]	5'-TTA CAT TGC GAC CAT GAA ATT GCT CT	1628[a]	849-874
Resistance genes:	***vgb, vgh***		
1629	5'-AAG GGG AAA GTT TGG ATT ACA CAA CA	1633[a]	73-98
1630[b]	5'-GAA CCA CAG GGC ATT ATC AGA ACC	1633[a]	445-468
1631	5'-CGA CGA TGC TTT ATG GTT TGT	1633[a]	576-596
1632[b]	5'-GTT AAT TTG CCT ATC TTG TCA CAC TC	1633[a]	850-875

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene: ***vgbB***			
1634	5'-TTA ACT TGT CTA TTC CCG ATT CAG G	1882[a]	23-47
1635[b]	5'-GCT GTG GCA ATG GAT ATT CTG TA	1882[a]	267-289
1636	5'-TTC CTA CCC CTG ATG CTA AAG TGA	1882[a]	155-178
1637[b]	5'-CAA AGT GCG TTA TCC GAA CCT AA	1882[a]	442-464
Sequencing primers			
Resistance gene: ***gyrA***			
1290	5'-GAY TAY GCI ATG ISI GTI ATH GT	1299[a]	70-83
1292[b]	5'-ARI SCY TCI ARI ATR TGI GC	1299[a]	1132-1152
1291	5'-GCI YTI CCI GAY GTI MGI GAY GG	1299[a]	100-123
1292[b]	5'-ARI SCY TCI ARI ATR TGI GC	1299[a]	1132-1152
1293	5'-ATG GCT GAA TTA CCT CAA TC	1299[a]	1-21
1294[b]	5'-ATG ATT GTT GTA TAT CTT CTT CAA C	1299[a]	2626-2651
1295[b]	5'-CAG AAA GTT TGA AGC GTT GT	1299[a]	1255-1275
1296	5'-AAC GAT TCG TGA GTC AGA TA	1299[a]	1188-1208
1297	5'-CGG TCA ACA TTG AGG AAG AGC T	1300[a]	29-51
1298[b]	5'-ACG AAA TCG ACC GTC TCT TTT TC	1300[a]	415-437
Resistance gene: ***gyrB***			
1301	5'-GTI MGI AWI MGI CCI GSI ATG TA	1307[a]	82-105
1302[b]	5'-TAI ADI GGI GGI KKI GCI ATR TA	1307[a]	1600-1623
1303	5'-GGI GAI GAI DYI MGI GAR GG	1307[a]	955-975
1304[b]	5'-CIA RYT TIK YIT TIG TYT G	1307[a]	1024-1043
1305	5'-ATG GTG ACT GCA TTG TCA GAT G	1307[a]	1-23
1306[b]	5'-GTC TAC GGT TTT CTA CAA CGT C	1307[a]	1858-1888

[a] Sequence from databases.
[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
	Sequencing primers (continued)		
Resistance gene:	***parC***		
1308	5'-ATG TAY GTI ATI ATG GAY MGI GC	1320[a]	67-90
1309[b]	5'-ATI ATY TTR TTI CCY TTI CCY TT	1320[a]	1993-2016
1310	5'-ATI ATI TSI ATI ACY TCR TC	1320[a]	1112-1132
1311[b]	5'-GAR ATG AAR ATI MGI GGI GAR CA	1320[a]	1288-1311
1312	5'-AAR TAY ATI ATI CAR GAR MGI GC	1321[a]	67-90
1313[b]	5'-AMI AYI CKR TGI GGI TTI TTY TT	1321[a]	2212-2235
1314	5'-TAI GAI TTY ACI GAI SMI CAR GC	1321[a]	1228-1251
1315[b]	5'-ACI ATI GCI TCI GCY TGI KSY TC	1321[a]	1240-1263
1316	5'-GTG AGT GAA ATA ATT CAA GAT T	1321[a]	1-23
1317[b]	5'-CAC CAA AAT CAT CTG TAT CTA C	1321[a]	2356-2378
1318	5'-ACC TAY TCS ATG TAC GTR ATC ATG GA	1320[a]	58-84
1319[b]	5'-AGR TCG TCI ACC ATC GGY AGY TT	1320[a]	832-855
Resistance gene:	***parE***		
1322	5'-RTI GAI AAY ISI GTI GAY GAR G	1328[a]	133-155
1325[b]	5'-RTT CAT YTC ICC IAR ICC YTT	1328[a]	1732-1752
1323	5'-ACI AWR SAI GGI GGI ACI CAY G	1328[a]	829-850
1324[b]	5'-GCI GCI GCI SWR TCI CCY TC	1328[a]	1280-1302
1326	5'-TGA TTC AAT ACA GGT TTT AGA G	1328[a]	27-49
1327[b]	5'-CTA GAT TTC CTC CTC ATC AAA T	1328[a]	1971-1993

[a] Sequence from databases.

[b] These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex LI: Internal hybridization probes for specific detection of antimicrobial ag nts resistance genes sequences (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***blaTEM* (continued)**		
2007	5'-TGG AGC CAG TGA GCG TGG	2010[a]	699-716
2008	5'-TCT GGA GCC GAT GAG CGT G	1929[a]	697-715
2009	5'-CTG GAG CCA GTA AGC GTG G	2011[a]	698-716
2141	5'-CAC CAG TCA CAG AAA AGC	1927[a]	311-328
Resistance gene:	***dhfrIa***		
2253	5'-CAT TAC CCA ACC GAA AGT A	1461[a]	158-176
Resistance gene:	***embB***		
2104	5'-CTG GGC ATG GCI CGA GTC	2105[a]	910-927
Resistance gene:	***gyrA***		
1333	5'-TCA TGG TGA CTT ATC TAT TTA TG	1299[a]	240-263
1334	5'-CAT CTA TTT ATA AAG CAA TGG TA	1299[a]	251-274
1335	5'-CTA TTT ATG GAG CAA TGG T	1299[a]	254-273
1940	5'-GTA TCG TTG GTG ACG TAA T	1299[a]	206-224
1943	5'-GCT GGT GGA CGG CCA G	1954[a]	279-294
1945	5'-CGG CGA CTA CGC GGT AT	1954[a]	216-232
1946	5'-CGG CGA CTT CGC GGT AT	1954[a]	216-232
1947	5'-CGG TAT ACG GCA CCA TCG T	1954[a]	227-245
1948	5'-GCG GTA TAC AAC ACC ATC G	1954[a]	226-244
1949	5'-CGG TAT ACG CCA CCA TCG T	1954[a]	227-245
2042	5'-CAC GGG GAT TTC TCT ATT TA	2054[a]	103-122
2043	5'-CAC GGG GAT TAC TCT ATT TA	2054[a]	103-122
Resistance gene:	***inhA***		
2100	5'-GCG AGA CGA TAG GTT GTC	2101[a]	1017-1034
Resistance gene:	***parC***		
1336	5'-TGG AGA CTA CTC AGT GT	1321[a]	232-249
1337	5'-TGG AGA CTT CTC AGT GT	1321[a]	232-249
1338	5'-GTG TAC GGA GCA ATG	1321[a]	245-260
1339	5'-CCA GCG GAA ATG CGT	1321[a]	342-357
1941	5'-GCA ATG GTC CGT TTA AGT	1321[a]	253-270
1944	5'-TTT CGC CGC CAT GCG TTA C	1781	247-265
1950	5'-GGC GAC ATC GCC TGC	1781	137-151
1951	5'-GGC GAC AGA GCC TGC TA	1781	137-153

[a] Sequence from databases.

Annex LI: Internal hybridization probes for specific det ction of antimicrobial agents resistance genes sequences.

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***aph3'VIa***		
2252	5'-CCA CAT ACA GTG TCT CTC	1406[a]	149-166
Resistance gene:	***blaSHV***		
1886	5'-GAC GCC CGC GCC ACC ACT	1900[a]	484-501
1887	5'-GAC GCC CGC GAC ACC ACT A	1899[a]	514-532
1888	5'-GAC GCC CGC AAC ACC ACT A	1901[a]	514-532
1889	5'-GTT CGC AAC TGC AGC TGC TG	1899[a]	593-612
1890	5'-TTC GCA ACG GCA GCT GCT G	1899[a]	594-612
1891	5'-CCG GAG CTG CCG AIC GGG	1902[a]	692-709
1892	5'-CGG AGC TGC CAA RCG GGG	1903[a]	693-710
1893	5'-GGA GCT GGC GAR CGG GGT	1899[a]	694-711
1894	5'-GAC CGG AGC TAG CGA RCG	1904[a]	690-707
1895	5'-CGG AGC TAG CAA RCG GGG T	1905[a]	693-711
1896	5'-GAA ACG GAA CTG AAT GAG GCG	1899[a]	484-504
1897	5'-CAT TAC CAT GGG CGA TAA CAG	1899[a]	366-386
1898	5'-CCA TTA CCA TGA GCG ATA ACAG	1899[a]	365-386
Resistance gene:	***blaTEM***		
1909	5'-ATG ACT TGG TTA AGT ACT CAC C	1928[a]	293-314
1910	5'-ATG ACT TGG TTG AGT ACT CAC C	1927[a]	293-314
1911	5'-CCA TAA CCA TGG GTG ATA ACA C	1928[a]	371-392
1912	5'-CCA TAA CCA TGA GTG ATA ACA C	1927[a]	371-392
1913	5'-CGC CTT GAT CAT TGG GAA CC	1928[a]	475-494
1914	5'-CGC CTT GAT CGT TGG GAA CC	1927[a]	475-494
1915	5'-CGC CTT GAT AGT TGG GAA CC	1929[a]	475-494
1916	5'-CGT GGG TCT TGC GGT ATC AT	1927[a]	712-731
1917	5'-CGT GGG TCT GGC GGT ATC AT	1930[a]	712-731
1918	5'-GTG GGT CTC ACG GTA TCA TTG	1927[a]	713-733
1919	5'-CGT GGG TCT CTC GGT ATC ATT	1931[a]	712-732
1920	5'-CGT GGI TCT CGC GGT ATC AT	1927[a]	712-731
1921	5'-CGT GGG TCT AGC GGT ATC ATT	1932[a]	713-733
1922	5'-GTT TTC CAA TGA TTA GCA CTT TTA	1927[a]	188-211
1923	5'-GTT TTC CAA TGA TAA GCA CTT TTA	1927[a]	188-211
1924	5'-GTT TTC CAA TGC TGA GCA CTT TT	1932[a]	188-210
1925	5'-CGT TTT CCA ATG ATG AGC ACT TT	1927[a]	187-209
1926	5'-GTT TTC CAA TGG TGA GCA CTT TT	1933[a]	188-210
2006	5'-TGG AGC CGG TGA GCG TGG	1927[a]	699-716

[a] Sequence from databases.

Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences (continued).

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene:	***parC* (continued)**		
1952	5'-CCT GCT ATG GAG CGA TGG T	1781	147-165
1953	5'-CGC CTG CTA TAA AGC GAT GGT	1781	145-165
2046	5'-ACG GGG ATT TTT CTA TCT AT	2055[a]	227-246
Resistance gene:	***rpoB***		
2067	5'-AGC TGA GCC AAT TCA TGG	2072[a]	1304-1321
2068	5'-ATT CAT GGA CCA GAA CAA C	2072[a]	1314-1332
2069	5'-CGC TGT CGG GGT TGA CCC	2072[a]	1334-1351
2070	5'-GTT GAC CCA CAA GCG CCG	2072[a]	1344-1361
2071	5'-CGA CTG TCG GCG CTG GGG	2072[a]	1360-1377
Resistance gene:	***tetM***		
2254	5'-ACC TGA ACA GAG AGA AAT G	1590[a]	1062-1080

[a] Sequence from databases.

Annex LII: Molecular beacon internal hybridization probes for specific detection of *atpD* sequences.

SEQ ID NO.	Nucleotide sequence[a]	Originating DNA fragment: SEQ ID NO.	Originating DNA fragment: Nucleotide position
Bacterial species:	***Bacteroides fragilis***		
2136	5'-CCA ACG CGT CCT CAA TCA TTT CTA ACT TCT ATG GCC GGC GTT GG	929	353-382
Bacterial species:	***Bordetella pertussis***		
2182	5'-GCG CGC CAA CGA CTT CTA CCA CGA AAT GGA AGA GTC GCG CGC	1672	576-605
Bacterial group:	***Campylobacter jejuni and C. coli***		
2133	5'-CCA CGC ACA WAA ACT TGT TTT AGA AGT AGC AGC WCA GCG TGG	1576, 1600,1849, 1863,2139[b,c]	44-73[d]
Fungal species:	***Candida glabrata***		
2078	5'-CCG AGC CTT GGT CTT CGG CCA AAT GAA CGC TCG G	463	442-463
Fungal species:	***Candida krusei***		
2075	5'-CCG AGC CAG GTT CTG AAG TCT CTG CAT TAT TAG GTG CTC GG	468	720-748
Fungal species:	***Candida lusitaniae***		
2080	5'-CCG AGC CGA AGA GGG CCA AGA TGT CGC TCG G	470	520-538
Fungal species:	***Candida parapsilosis***		
2079	5'-CCG AGC GTT CAG TTA CTT CAG TCC AAG CCG GCT CGG	472	837-860
Fungal species:	***Candida tropicalis***		
2077	5'-CCG AGC AAC CGA TCC AGC TCC AGC TAC GCT CGG	475	877-897
Bacterial species:	***Klebsiella pneumoniae***		
2281	5'-CCC CCA GCT GGG CGG CGG TAT CGA TGG GGG	317	40-59

[a] Underlined nucleotides indicate the molecular beacon's stem.
[b] Sequence from databases.
[c] These sequences were aligned to derive the corresponding primer.
[d] The nucleotide positions refer to the *C. jejuni atpD* sequence fragment (SEQ ID NO. 1576).

Annex LII: Molecular beacon internal hybridization probes for specific detection of *atpD* s quences (continued).

SEQ ID NO.	Nucleotide sequence[a]	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Fungal genus:	***Candida sp.***		
2076	5'-CCG AGC YGA YAA CAT TTT CAG ATT CAC CCA RGC GCT CGG	460-478, 663[b]	697-723[c]

[a] Underlined nucleotides indicate the molecular beacon's stem.
[b] These sequences were aligned to derive the corresponding primer.
[c] The nucleotide positions refer to the *C. albicans atpD* sequence fragment (SEQ ID NO. 460).

Annex LIII: Internal hybridization prob s for specific detection of *atpD* sequences.

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Bacterial species:	***Acinetobacter baumannii***		
2169	5'-CCC GTT TGC GAA AGG TGG	243	304-321
Bacterial species:	***Klebsiella pneumoniae***		
2167	5'-CAG CAG CTG GGC GGC GGT	317	36-53

Annex LIV: Internal hybridization probes for specific d tection of *ddl* and *mtl* sequences.

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Bacterial species:	***Enterococcus faecium (ddl)***		
2286	5'-AGT TGC TGT ATT AGG AAA TG	2288[a]	784-803
2287	5'-TCG AAG TTG CTG TAT TAG GA	2288[a]	780-799
Bacterial species:	***Enterococcus faecalis mtl)***		
2289	5'-CAC CGA AGA AGA TGA AAA AA	1243[a]	264-283
2290	5'-TGG CAC CGA AGA AGA TGA	1243[a]	261-278
2291	5'-ATT TTG GCA CCG AAG AAG A	1243[a]	257-275

[a] Sequence from databases.

What is claimed is:

1. A method for generating a repertory of nucleic acids of *tuf*, *fus*, *atpD* and/or *recA* genes from which are derived probes or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the step of:

- amplifying the nucleic acids of a plurality of determinedalgal, archaeal, bacterial, fungal and parasitical species with any combination of the primer pairs defined in SEQ ID NOs.: 543, 556-574, 636-655, 664, 681-683, 694, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

2. A method for generating a repertory of nucleic acid sequences, which comprises the steps of:

- reproducing the method of claim 1, and
- adding the step of:
  - sequencing said nucleic acids.

3. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae,archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 2, and
- adding the steps of:
  - aligning a subset of nucleic acid sequences of said repertory,
  - locating nucleic acid stretches that are present in the nucleic acids of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and

- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

4. A bank of nucleic acids comprising the repertory of nucleic acids obtained from the method of claim 1.

5. A bank of nucleic acid sequences comprising the repertory of nucleic acid sequences obtained from the method of claim 2.

6. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae,archaea, bacteria, fungi and parasites, which comprises the steps of.

- aligning a subset of nucleic acid sequences of the bank as defined in claim 5,
- locating nucleic acid sequence stretches that are present in the nucleic acid sequences of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and
- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

7. A method for generating probes, or primers or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 3 or 6, and
- adding the step of:
  - synthesising said probes or primers upon the nucleic acid sequences thereof.

8. A nucleic acid used for universal detection of any one of alga, archaeon, bacterium, fungus and parasite which is obtained from the method of claim 7.

9. A nucleic acid used for universal detection as set forth in claim 8, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any one of alga, archaeon, bacterium, fungus and parasite and with any one of SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696, 697, 699, 700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

10. A nucleic acid used for the specific and ubiquitous detection and for identification of any one of a algal, archaeal, bacterial, fungal and parasitital species, genus, family and group, which is obtained from the method of claim 7.

11. A nucleic acid as set forth in claim 10 having any one of the nucleotide sequences which are defined in SEQ ID NOs.:

539, 540	for the detection and/or identification of *Mycobacteriaceae* family
541, 542, 544, 2121	for the detection and/or identification of Pseudomonads group
545, 546	for the detection and/or identification of *Corynebacterium* sp.
547, 548, 1202	for the detection and/or identification of *Streptococcus* sp.
549, 550, 582, 583, 625, 626, 627, 628, 1199	for the detection and/or identification of *Streptococcus agalactiae*
551, 552, 2166, 2173, 2174, 2175, 2176, 2177, 2178, 2179	for the detection and/or identification of *Neisseria gonorrhoeae*
553, 575, 605, 606, 707, 1175, 1176	for the detection and/or identification of *Staphylococcus* sp.
554, 555, 2213	for the detection and/or identification of *Chlamydia trachomatis*

576, 631, 632, 633, 634, 635, 1163, 1164, 1167, 2076, 2108, 2109	for the detection and/or identification of *Candida* sp.
577, 1156, 1160 2073	for the detection and/or identification of *Candida albicans*
578, 1166, 1168, 2074	for the detection and/or identification of*Candida dubliniensis*
579, 2168	for the detection and/or identification of *Escherichia coli*
580, 603, 1174, 1236, 1238, 2289, 2290, 2291	for the detection and/or identification of *Enterococcus faecalis*
581	for the detection and/or identification of *Haemophilus influenzae*
584, 585, 586, 587, 588, 1232, 1234, 2186	for the detection and/or identification of *Staphylococcus aureus*
589, 590, 591, 592, 593	for the detection and/or identification of *Staphylococcus epidermidis*
594, 595	for the detection and/or identification of *Staphylococcus haemolyticus*
596, 597, 598	for the detection and/or identification of *Staphylococcus hominis*
599, 600, 601, 695, 1208, 1209	for the detection and/or identification of *Staphylococcus saprophyticus*
602, 1235, 1237, 1696, 1697, 1698, 1699, 1700, 1701, 2286, 2287	for the detection and/or identification of *Enterococcus faecium*
604	for the detection and/or identification of *Enterococcus gallinarum*
620, 1122	for the detection and/or identification of *Enterococcus casseliflavus, E. flavescens* and *E. gallinarum*
629, 630, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092	for the detection and/or identification of *Chlamydia pneumoniae*

636, 637, 638, 639, 640, 641, 642	for the detection and/or identification of at least the following: *Abiotrophia adiacens, Abiotrophia defectiva, Acinetobacter baumannii, Acinetobacter lwoffi, Aerococcus viridans, Bacillus anthracis, Bacillus cereus, Bacillus subtilis, Brucella abortus, Burkholderia cepacia, Citrobacter diversus, Citrobacter freundii, Enterobacter aerogenes, Enterobacter agglomerans, Enterobacter cloacae, Enterococcus avium, Enterococcus casseliflavus, Enterococcus dispar, Enterococcus durans, Enterococcus faecalis, Enterococcus faecium, Enterococcus flavescens, Enterococcus gallinarum, Enterococcus mundtii, Enterococcus raffinosus, Enterococcus solitarius, Escherichia coli, Gemella morbillorum, Haemophilus ducreyi, Haemophilus haemolyticus, Haemophilus influenzae, Haemophilus parahaemolyticus, Haemophilus parainfluenzae, Hafnia alvei, Kingella kingae, Klebsiella oxytoca, Klebsiella pneumoniae, Legionella pneumophila, Megamonas hypermegale, Moraxella atlantae, Moraxella catarrhalis, Morganella morganii, Neisseria gonorrheae, Neisseria meningitidis, Pasteurella aerogenes, Pasteurella multocida, Peptostreptococcus magnus, Proteus mirabilis, Providencia alcalifaciens, Providencia rettgeri, Providencia rustigianii, Providencia stuartii, Pseudomonas aeruginosa, Pseudomonas fluorescens, Pseudomonas stutzeri, Salmonella bongori, Salmonella choleraesuis, Salmonella enteritidis, Salmonella gallinarum, Salmonella typhimurium, Serratia liquefaciens, Serratia marcescens, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus capitis Staphylococcus epidermidis, Staphylococcus haemolyticus, Staphylococcus hominis, Staphylococcus lugdunensis, Staphylococcus saprophyticus, Staphylococcus simulans, Staphylococcus warneri, Stenotrophomonas maltophilia, Streptococcus acidominimus, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus bovis, Streptococcus constellatus, Streptococcus cricetus, Streptococcus cristatus, Streptococcus dysgalactiae, Streptococcus equi, Streptococcus ferus, Streptococcus gordonii, Streptococcus intermedius, Streptococcus macacae, Streptococcus mitis, Streptococcus mutans, Streptococcus oralis, Streptococcus parasanguinis, Streptococcus parauberis, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus ratti, Streptococcus salivarius, Streptococcus sanguinis, Streptococcus sobrinus, Streptococcus uberis, Streptococcus vestibularis, Vibrio cholerae, Yersinia enterocolitica, Yersinia pestis, Yersinia pseudotuberculosis.*
656, 657, 271, 1136, 1137	for the detection and/or identification of *Enterococcus* sp.
701, 702	for the detection and/or identification of *Leishmania* sp.

703, 704, 705, 706, 793	for the detection and/or identification of *Entamoeba* sp.
794, 795	for the detection and/or identification of *Trypanosoma cruzi*
796, 797, 808, 809, 810, 811	for the detection and/or identification of *Clostridium* sp.
798, 799, 800, 801, 802, 803, 804, 805, 806, 807	for the detection and/or identification of *Cryptosporidium parvum*
816, 817, 818, 819	for the detection and/or identification of *Giardia* sp.
820, 821, 822	for the detection and/or identification of *Trypanosoma brucei*
823, 824	for the detection and/or identification of *Trypanosoma* sp.
825, 826	for the detection and/or identification of *Bordetella* sp.
923, 924, 925, 926, 927, 928	for the detection and/or identification of *Trypanosomatidae* family
933, 934	for the detection and/or identification of *Enterobacteriaceae* group
994, 995, 996, 997, 998, 999, 1000, 1001, 1200, 1210, 1211	for the detection and/or identification of *Streptococcus pyogenes*
1157, 2079, 2118	for the detection and/or identification of *Candida parapsilosis*
1158, 1159, 2078, 2110, 2111	for the detection and/or identification of *Candida glabrata*
1160, 2077, 2119, 2120	for the detection and/or identification of *Candida tropicalis*
1161, 2075, 2112, 2113, 2114	for the detection and/or identification of *Candida krusei*
1162	for the detection and/or identification of *Candida guilliermondii*
1162, 2080, 2115 2116, 2117	for the detection and/or identification of *Candida lusitaniae*
1165	for the detection and/or identification of *Candida zeylanoides*
1201	for the detection and/or identification of *Streptococcus pneumoniae*

1233	for the detection and/or identification of *Staphylococcus* sp. other than *S. aureus*
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of *Klebsiella pneumoniae*
1661, 1665	for the detection and/or identification of *Escherichia coli* and *Shigella* sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of *Acinetobacter baumanii*
1694, 1695, 2122	for the detection and/or identification of *Pseudomonas aeruginosa*
1971, 1972, 1973	for the detection and/or identification of *Cryptococcus sp.*
2081, 2082, 2083	for the detection and/or identification of *Legionella sp.*
2084	for the detection and/or identification of *Legionella pneumophila*
2093, 2094, 2095, 2096	for the detection and/or identification of *Mycoplasma pneumoniae*
2106, 2107	for the detection and/or identification of *Cryptococcus neoformans*
2131, 2132, 2133	for the detection and/or identification of *Campylobacter jejuni and C. coli*
2134, 2135, 2136	for the detection and/or identification of *Bacteroides fragilis*
2170	for the detection and/or identification of *Abiotrophia adiacens*
2171	for the detection and/or identification of *Gemella* sp.
2172	for the detection and/or identification of *Enterococcus* sp., *Gemella* sp., *A. adiacens*
2180, 2181, 2182	for the detection and/or identification of *Bordetella pertussis.*

12. A method for detecting the presence in a test sample of a microorganism that is an alga, archaeum, bacterium, fungus or parasite, which comprises:

a) putting in contact any test sample *tuf* or *atpD* or *recA* nucleic acids and nucleic acid primers and/or probes, said primers and/or probes having

been selected to be sufficiently complementary to hybridize to one or more *tuf* or *atpD* or *recA* nucleic acids that are specific to said group of microorganisms;

b) allowing the primers and/or probes and any test sample *tuf* or *atpD* or *recA* nucleic acids to hybridize under specified conditions such as said primers and/or probes hybridize to the *tuf* or *atpD* or *recA* nucleic acids of said microorganism and does not detectably hybridize to *tuf* or *atpD* or *recA* sequences from other microorganisms; and,

c) testing for hybridization of said primers and/or probes to any test sample *tuf* or *atpD* or *recA* nucleic acids.

13. The method of claim 12 wherein c) is based on a nucleic acid target amplification method.

14. The method of claim 12 wherein c) is based on a signal amplification method.

15. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are perfectly complementary.

16. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are not perfectly complementary.

17. A method for the specific detection and/or identification of a microorganism that is an algal, archaeal, bacterial, fungal or parasitical species, genus, family or group in any sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid which has a nucleotide sequence of at least 12 nucleotides in length capable of hybridizing with the nucleic acids of said microorganism and with a nucleic acid having any one of the nucleotide sequences defined in SEQ ID NOs.:

539, 540	for the detection and/or identification of *Mycobacteriaceae* family
541, 542, 544, 2121	for the detection and/or identification of Pseudomonads group

545, 546	for the detection and/or identification of *Corynebacterium* sp.
547, 548, 1202	for the detection and/or identification of *Streptococcus* sp.
549, 550, 582, 583, 625, 626, 627, 628, 1199	for the detection and/or identification of *Streptococcus agalactiae*
551, 552, 2166, 2173, 2174, 2175, 2176, 2177, 2178, 2179	for the detection and/or identification of *Neisseria gonorrhoeae*
553, 575, 605, 606, 707, 1175, 1176	for the detection and/or identification of *Staphylococcus* sp.
554, 555, 2213	for the detection and/or identification of *Chlamydia trachomatis*
576, 631, 632, 633, 634, 635, 1163, 1164, 1167, 2076, 2108, 2109	for the detection and/or identification of *Candida* sp.
577, 1156, 1160 2073	for the detection and/or identification of *Candida albicans*
578, 1166, 1168, 2074	for the detection and/or identification of *Candida dubliniensis*
579, 2168	for the detection and/or identification of *Escherichia coli*
580, 603, 1174, 1236, 1238, 2289, 2290, 2291	for the detection and/or identification of *Enterococcus faecalis*
581	for the detection and/or identification of *Haemophilus influenzae*
584, 585, 586, 587, 588, 1232, 1234, 2186	for the detection and/or identification of *Staphylococcus aureus*
589, 590, 591, 592, 593	for the detection and/or identification of *Staphylococcus epidermidis*
594, 595	for the detection and/or identification of *Staphylococcus haemolyticus*
596, 597, 598	for the detection and/or identification of *Staphylococcus hominis*

599, 600, 601, 695, 1208, 1209	for the detection and/or identification of *Staphylococcus saprophyticus*
602, 1235, 1237, 1696, 1697, 1698, 1699, 1700, 1701, 2286, 2287	for the detection and/or identification of *Enterococcus faecium*
604	for the detection and/or identification of *Enterococcus gallinarum*
620, 1122	for the detection and/or identification of *Enterococcus casseliflavus, E. flavescens* and *E. gallinarum*
629, 630, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092	for the detection and/or identification of *Chlamydia pneumoniae*
636, 637, 638, 639, 640, 641, 642	for the detection and/or identification of at least the following: *Abiotrophia adiacens, Abiotrophia defectiva, Acinetobacter baumannii, Acinetobacter lwoffi, Aerococcus viridans, Bacillus anthracis, Bacillus cereus, Bacillus subtilis, Brucella abortus, Burkholderia cepacia, Citrobacter diversus, Citrobacter freundii, Enterobacter aerogenes, Enterobacter agglomerans, Enterobacter cloacae, Enterococcus avium, Enterococcus casseliflavus, Enterococcus dispar, Enterococcus durans, Enterococcus faecalis, Enterococcus faecium, Enterococcus flavescens, Enterococcus gallinarum, Enterococcus mundtii, Enterococcus raffinosus, Enterococcus solitarius, Escherichia coli, Gemella morbillorum, Haemophilus ducreyi, Haemophilus haemolyticus, Haemophilus influenzae, Haemophilus parahaemolyticus, Haemophilus parainfluenzae, Hafnia alvei, Kingella kingae, Klebsiella oxytoca, Klebsiella pneumoniae, Legionella pneumophila, Megamonas hypermegale, Moraxella atlantae, Moraxella catarrhalis, Morganella morganii, Neisseria gonorrheae, Neisseria meningitidis, Pasteurella aerogenes, Pasteurella multocida, Peptostreptococcus magnus, Proteus mirabilis, Providencia alcalifaciens, Providencia rettgeri, Providencia rustigianii, Providencia stuartii, Pseudomonas aeruginosa, Pseudomonas fluorescens, Pseudomonas stutzeri, Salmonella bongori, Salmonella choleraesuis, Salmonella enteritidis, Salmonella gallinarum, Salmonella typhimurium, Serratia liquefaciens, Serratia marcescens, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus capitis Staphylococcus epidermidis, Staphylococcus haemolyticus, Staphylococcus hominis, Staphylococcus lugdunensis, Staphylococcus saprophyticus, Staphylococcus simulans, Staphylococcus warneri, Stenotrophomonas*

	maltophilia, Streptococcus acidominimus, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus bovis, Streptococcus constellatus, Streptococcus cricetus, Streptococcus cristatus, Streptococcus dysgalactiae, Streptococcus equi, Streptococcus ferus, Streptococcus gordonii, Streptococcus intermedius, Streptococcus macacae, Streptococcus mitis, Streptococcus mutans, Streptococcus oralis, Streptococcus parasanguinis, Streptococcus parauberis, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus ratti, Streptococcus salivarius, Streptococcus sanguinis, Streptococcus sobrinus, Streptococcus uberis, Streptococcus vestibularis, Vibrio cholerae, Yersinia enterocolitica, Yersinia pestis, Yersinia pseudotuberculosis.
656, 657, 271, 1136, 1137	for the detection and/or identification of *Enterococcus* sp.
701, 702	for the detection and/or identification of *Leishmania* sp.
703, 704, 705, 706, 793	for the detection and/or identification of *Entamoeba* sp.
794, 795	for the detection and/or identification of *Trypanosoma cruzi*
796, 797, 808, 809, 810, 811	for the detection and/or identification of *Clostridium* sp.
798, 799, 800, 801, 802, 803, 804, 805, 806, 807	for the detection and/or identification of *Cryptosporidium parvum*
816, 817, 818, 819	for the detection and/or identification of *Giardia* sp.
820, 821, 822	for the detection and/or identification of *Trypanosoma brucei*
823, 824	for the detection and/or identification of *Trypanosoma* sp.
825, 826	for the detection and/or identification of *Bordetella* sp.
923, 924, 925, 926, 927, 928	for the detection and/or identification of *Trypanosomatidae* family
933, 934	for the detection and/or identification of *Enterobacteriaceae* group
994, 995, 996, 997, 998, 999, 1000, 1001, 1200, 1210, 1211	for the detection and/or identification of *Streptococcus pyogenes*
1157, 2079, 2118	for the detection and/or identification of *Candida parapsilosis*

1158, 1159, 2078, 2110, 2111	for the detection and/or identification of *Candida glabrata*
1160, 2077, 2119, 2120	for the detection and/or identification of *Candida tropicalis*
1161, 2075, 2112, 2113, 2114	for the detection and/or identification of *Candida krusei*
1162	for the detection and/or identification of *Candida guilliermondii*
1162, 2080, 2115 2116, 2117	for the detection and/or identification of *Candida lusitaniae*
1165	for the detection and/or identification of *Candida zeylanoides*
1201	for the detection and/or identification of *Streptococcus pneumoniae*
1233	for the detection and/or identification of *Staphylococcus* sp. other than *S. aureus*
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of *Klebsiella pneumoniae*
1661, 1665	for the detection and/or identification of *Escherichia coli* and *Shigella* sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of *Acinetobacter baumanii*
1694, 1695, 2122	for the detection and/or identification of *Pseudomonas aeruginosa*
1971, 1972, 1973	for the detection and/or identification of *Cryptococcus sp.*
2081, 2082, 2083	for the detection and/or identification of *Legionella sp.*
2084	for the detection and/or identification of *Legionella pneumophila*
2093, 2094, 2095, 2096	for the detection and/or identification of *Mycoplasma pneumoniae*
2106, 2107	for the detection and/or identification of *Cryptococcus neoformans*
2131, 2132, 2133	for the detection and/or identification of *Campylobacter jejuni and C. coli*
2134, 2135, 2136	for the detection and/or identification of *Bacteroides fragilis*

2170	for the detection and/or identification of *Abiotrophia adiacens*
2171	for the detection and/or identification of *Gemella* sp.
2172	for the detection and/or identification of *Enterococcus* sp., *Gemella* sp., *A. adiacens*
2180, 2181, 2182	for the detection and/or identification of *Bordetella pertussis,*

said method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of hybridized probes or amplified products as an indication of the presence of said specificalgal, archaeal, bacterial, fungal or parasitical species, genus, family or group.

18. A method for the universal detection of any bacterium, fungus or parasite in a sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid as defined in claims 8 or 9, the method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions ofhybridization or of amplification and detecting the presence of any alga, archaeon, bacterium, fungus or parasite.

19. A method as set forth in claim 17 or 18, which further comprises probes or primers, or both, for the detection of at least one antimicrobial agent resistance gene.

20. A method as set forth in claim 17, 18 or 19, which further comprises probes or primers, or both, for the detection of at least one toxin gene.

21. A method as set forth in claim 19 or 20, wherein the probes or primers for the detection of said antimicrobial agent resistance gene or toxin gene have at least 12 nucleotides in length capable ofhybridizing with an antimicrobial agent resistance gene and/or toxin gene selected from SEQ ID NOs.:

1078, 1079, 1085	for the detection and/or identification of the *E. coli* Shiga-like toxin 2 (stx_2) gene

1080, 1081, 1084, 2012	for the detection and/or identification of the *E. coli* Shiga-like toxin 1 (stx_1) gene
1082, 1083	for the detection and/or identification of *E. coli* Shiga-like toxins 1 and 2 (*stx*) genes
1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292	for the detection and/or identification of the *vanA* resistance gene
1095, 1096, 1171, 1241, 2294, 2295	for the detection and/or identification of the *vanB* resistance gene
1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124	for the detection and/or identification of the *vanAB* resistance genes
1103, 1104, 1109, 1110	for the detection and/or identification of the *vanC1* resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the *vanC2* and *vanC3* resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the *vanC1, vanC2* and *vanC3* resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the *vanAXY* resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the *S. pneumoniae pbp1a* gene

1142, 1143, 1144, 1145	for the detection and/or identification of the *S. pneumoniae pbp2b* gene
1146, 1147, 1148, 1149	for the detection and/or identification of the *S. pneumoniae pbp2x* gene
1177, 1231	for the detection and/or identification of the *mecA* resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1936, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the *gyrA* resistance gene
1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the *gyrB* resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941, 1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the *parC* resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the *parE* resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the *aac(2')-Ia* resistance gene
1349, 1350	for the detection and/or identification of the *aac(3')-Ib* resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the *aac(3')-IIb* resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the *aac(3')-IVa* resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the *aac(3')-VIa* resistance gene

1367, 1368, 1369, 1370	for the detection and/or identification of the *aac(6')-Ia* resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the *aac(6')-Ic* resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the *ant(3')-Ia* resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the *ant(4')-Ia* resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the *aph(3')-Ia* resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the *aph(3')-IIa* resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the *aph(3')-IIIa* resistance gene
1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the *aph(3')-VIa* resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the *blaCARB* resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the blaCMY-2 resistance gene
1417, 1418	for the detection and/or identification of the *blaCTX-M-1*and *blaCTX-M -2* resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the *blaCTX-M-1* resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the *blaCTX-M-2* resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the *blaIMP* resistance gene
1434, 1435	for the detection and/or identification of the *blaOXA2* resistance gene
1436, 1437	for the detection and/or identification of the *blaOXA10* resistance gene
1440, 1441	for the detection and/or identification of the *blaPER-1* resistance gene

1443, 1444	for the detection and/or identification of the *blaPER-2* resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the *blaPER-1* and *blaPER -2* resistance genes
1450, 1451	for the detection and/or identification of the *dfrA* resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the *dhfrIa* and *dhfrXV* resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the *dhfrIa* resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the *dhfrIb* and *dhfrV* resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the *dhfrIb* resistance gene
1471, 1472, 1473, 1474	for the detection and/or identification of the *dhfrV* resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the *dhfrVI* resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the *dhfrVII* and *dhfrXVII* resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the *dhfrVII* resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the *dhfrVIII* resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the *dhfrIX* resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the *dhfrXII* resistance gene
1505, 1506	for the detection and/or identification of the *dhfrXIII* resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the *dhfrXV* resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the *dhfrXVII* resistance gene

1528, 1529	for the detection and/or identification of the *ereA* and *ereA2* resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the *ereB* resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the *linA* and *linA'* resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the *linB* resistance gene
1546, 1547	for the detection and/or identification of the *mefA* resistance gene
1549, 1550	for the detection and/or identification of the *mefE* resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the *mefA* and *mefE* resistance genes
1556, 1557, 1558, 1559	for the detection and/or identification of the *mphA* and *mphK* resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the *satG* resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the *tetM* resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the *vanD* resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the *vanE* resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the *vatB* resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the *vatC* resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the *vga* resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the *vgaB* resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the *vgb* and *vgh* resistance genes

1634, 1635, 1636, 1637	for the detection and/or identification of the *vgbB* resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the *blaSHV* resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the *blaTEM* resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the *sulII* resistance gene
1966, 1967, 1968, 1969	for the detection and/or identification of the *tetB* resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the *rpoB* resistance gene
2098, 2099, 2100	for the detection and/or identification of the *inhA* resistance gene
2102, 2103, 2104	for the detection and/or identification of the *embB* resistance gene
2123, 2124, 2125	for the detection and/or identification of the *C. difficile cdtA* toxin gene
2126, 2127, 2128	for the detection and/or identification of the *C. difficile cdtB* toxin gene
2142, 2143	for the detection and/or identification of the *mupA* resistance gene
2145, 2146	for the detection and/or identification of the *catI* resistance gene
2148, 2149	for the detection and/or identification of the *catII* resistance gene

2151, 2152	for the detection and/or identification of the *catIII* resistance gene
2154, 2155	for the detection and/or identification of the *catP* resistance gene
2157, 2158, 2160, 2161	for the detection and/or identification of the *cat* resistance gene
2163, 2164	for the detection and/or identification of the *ppflo*-like resistance gene.

22. A composition of matter comprising a specific nucleic acid as set forth in claim 10 or 11, which is specific for a bacterial, fungal or parasitical species, genus, family, or group, or a nucleic acid as set forth in claim 8 or 9 which is universal for a bacterium, fungus or parasite, or both specific and universal nucleic acids, in conjunction with a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene.

23. A composition as set forth in claim 22, wherein the nucleic acid capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene is any one of:

1078, 1079, 1085	for the detection and/or identification of the *E. coli* Shiga-like toxin 2 (stx_2) gene
1080, 1081, 1084, 2012	for the detection and/or identification of the *E. coli* Shiga-like toxin 1 (stx_1) gene
1082, 1083	for the detection and/or identification of *E. coli* Shiga-like toxins 1 and 2 (*stx*) genes
1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292	for the detection and/or identification of the *vanA* resistance gene
1095, 1096, 1171, 1241, 2294, 2295	for the detection and/or identification of the *vanB* resistance gene
1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124	for the detection and/or identification of the *vanAB* resistance genes

1103, 1104, 1109, 1110	for the detection and/or identification of the *vanC1* resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the *vanC2* and *vanC3* resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the *vanC1, vanC2* and *vanC3* resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the *vanAXY* resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the *S. pneumoniae pbp1a* gene
1142, 1143, 1144, 1145	for the detection and/or identification of the *S. pneumoniae pbp2b* gene
1146, 1147, 1148, 1149	for the detection and/or identification of the *S. pneumoniae pbp2x* gene
1177, 1231	for the detection and/or identification of the *mecA* resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1936, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the *gyrA* resistance gene

1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the *gyrB* resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941,1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the *parC* resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the *parE* resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the *aac(2')-Ia* resistance gene
1349, 1350	for the detection and/or identification of the *aac(3')-Ib* resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the *aac(3')-IIb* resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the *aac(3')-IVa* resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the *aac(3')-VIa* resistance gene
1367, 1368, 1369, 1370	for the detection and/or identification of the *aac(6')-Ia* resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the *aac(6')-Ic* resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the *ant(3')-Ia* resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the *ant(4')-Ia* resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the *aph(3')-Ia* resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the *aph(3')-IIa* resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the *aph(3')-IIIa* resistance gene

1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the *aph(3')-VIa* resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the *blaCARB* resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the blaCMY-2 resistance gene
1417, 1418	for the detection and/or identification of the *blaCTX-M-1* and *blaCTX-M -2* resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the *blaCTX-M-1* resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the *blaCTX-M-2* resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the *blaIMP* resistance gene
1434, 1435	for the detection and/or identification of the *blaOXA2* resistance gene
1436, 1437	for the detection and/or identification of the *blaOXA10* resistance gene
1440, 1441	for the detection and/or identification of the *blaPER-1* resistance gene
1443, 1444	for the detection and/or identification of the *blaPER-2* resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the *blaPER-1* and *blaPER -2* resistance genes
1450, 1451	for the detection and/or identification of the *dfrA* resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the *dhfrIa* and *dhfrXV* resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the *dhfrIa* resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the *dhfrIb* and *dhfrV* resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the *dhfrIb* resistance gene

1471, 1472, 1473, 1474	for the detection and/or identification of the *dhfrV* resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the *dhfrVI* resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the *dhfrVII* and *dhfrXVII* resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the *dhfrVII* resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the *dhfrVIII* resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the *dhfrIX* resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the *dhfrXII* resistance gene
1505, 1506	for the detection and/or identification of the *dhfrXIII* resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the *dhfrXV* resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the *dhfrXVII* resistance gene
1528, 1529	for the detection and/or identification of the *ereA* and *ereA2* resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the *ereB* resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the *linA* and *linA'* resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the *linB* resistance gene
1546, 1547	for the detection and/or identification of the *mefA* resistance gene
1549, 1550	for the detection and/or identification of the *mefE* resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the *mefA* and *mefE* resistance genes

1556, 1557, 1558, 1559	for the detection and/or identification of the *mphA* and *mphK* resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the *satG* resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the *tetM* resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the *vanD* resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the *vanE* resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the *vatB* resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the *vatC* resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the *vga* resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the *vgaB* resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the *vgb* and *vgh* resistance genes
1634, 1635, 1636, 1637	for the detection and/or identification of the *vgbB* resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the *blaSHV* resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the *blaTEM* resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the *sulII* resistance gene

1966, 1967, 1968, 1969	for the detection and/or identification of the *tetB* resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the *rpoB* resistance gene
2098, 2099, 2100	for the detection and/or identification of the *inhA* resistance gene
2102, 2103, 2104	for the detection and/or identification of the *embB* resistance gene
2123, 2124, 2125	for the detection and/or identification of the *C. difficile cdtA* toxin gene
2126, 2127, 2128	for the detection and/or identification of the *C. difficile cdtB* toxin gene
2142, 2143	for the detection and/or identification of the *mupA* resistance gene
2145, 2146	for the detection and/or identification of the *catI* resistance gene
2148, 2149	for the detection and/or identification of the *catII* resistance gene
2151, 2152	for the detection and/or identification of the *catIII* resistance gene
2154, 2155	for the detection and/or identification of the *catP* resistance gene
2157, 2158, 2160, 2161	for the detection and/or identification of the *cat* resistance gene
2163, 2164	for the detection and/or identification of the *ppflo*-like resistance gene.

24. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *tuf* sequences defined in SEQ ID NOs.: 1-73, 75-241, 399-457, 498-529, 612-618, 621-624, 675, 677, 717-736, 779-792, 840-855, 865, 868-888, 897-910, 932, 967-989, 992, 1266-1287, 1518-1526, 1561-1575, 1578-1580, 1662-1664, 1666-1667, 1669-1670, 1673-1683, 1685-1689, 1786-1843, 1874-1881, 1956-1960, 2183-2185, 2187-2188, 2193-2201, 2214-2249, 2255-2272.

25. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *atpD* sequences defined in SEQ ID NOs.: 242-270, 272-398, 458-497, 530-538, 663, 667, 673, 674, 676, 678-680, 737-778, 827-832, 834-839, 856-862, 866-867, 889-896, 929-931, 941-966, 1245-1254, 1256-1265, 1527, 1576-1577, 1600-1604,1638-1647, 1649-1660, 1671, 1684, 1844-1848, 1849-1865, 2189-2192.

26. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *recA* sequences defined in SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212.

27. A nucleic acid having at least 12 nucleotides in length, capable of selectively hybridizing with the nucleotide sequence of any one of the antimicrobial agent resistance gene sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280.

28. The nucleic acid sequences of the nucleic acids of any one of claims 24 to 27.

29. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the antimicrobial agent resistance genes sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280 for the detection and identification of microbial species.

30. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the toxin genes defined in SEQ ID NOs.: 1078-1085, 2012 and 2123 to 2128 for the detection and identification of microbial species.

31. A repertory of *hexA* nucleic acids used for the detection and/or identification of *Streptococcus pneumoniae*, which repertory is created by amplifying

the nucleic acids of any streptococcal species with any combination of primers SEQ ID NOs.: 1179, 1181 and 1182.

32. A repertory as defined in claim 31, which comprises the nucleic acids having a nucleotide sequence defined in SEQ ID NOs.: 1184 to 1191.

33. A repertory of nucleic acid sequences derived from the repertory of claim 31 or 32.

34. A nucleic acid used for the specific and ubiquitous detection and for identification of *Streptococcus pneumoniae*, which is derived from the repertory of claim 31.

35. A nucleic acid as set forth in claim 34 which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any *Streptococcus pneumoniae* and with any one of SEQ ID NOs.: 1184 to 1187.

36. A nucleic acid as set forth in claim 34, which has a nucleic acid sequence of at least 12 nucleotides capable ofhybridizing with the nucleic acids of *Streptococcus pneumoniae* and with any one of the nucleic acids having SEQ ID NOs.: 1179, 1180, 1181, 1182.

37. A peptide derived from the translation of the nucleic acids from the repertory obtained from the method of claim 1, 31 or 32, or of the nucleic acids defined in any one of claims 24 to 27, 35 and 36.

38. A peptide sequence derived from the peptide of claim 37.

39. A recombinant vector comprising a nucleic acid obtained from the method of claim 1, 31 or 32, or from the nucleic acids defined in any one of claims 24 to 27, 35 and 36.

40. A recombinant vector as defined in claim 39 which is an expression vector.

41. A recombinant host cell comprising the recombinant vector defined in claim 39 or 40.

42. The use of the nucleic acid sequences defined in claim 28 or 33, or obtained from the method of claim 2 and of the protein sequences deduced from said nucleic acid sequences, for the design of a therapeutic agent effective against said microorganisms.

43. The use as defined in claim 42, wherein said therapeutic agent is an antimicrobial agent, a vaccine or a genic therapeutic agent.

44. A method for identification of a microorganism in a test sample, comprising the steps of:

a) obtaining a nucleic acid sequence for a *tuf*, *atpD*, and/or *recA* genes of said microorganisms, and

b) comparing said nucleic acid sequence with the nucleic acid sequences of a bank as defined in claim 5, said repertory comprising a nucleic acid sequence obtained from the nucleic acids of said microorganism, whereby said microorganism is identified when said comparison results in a match between said sequences.

1/27

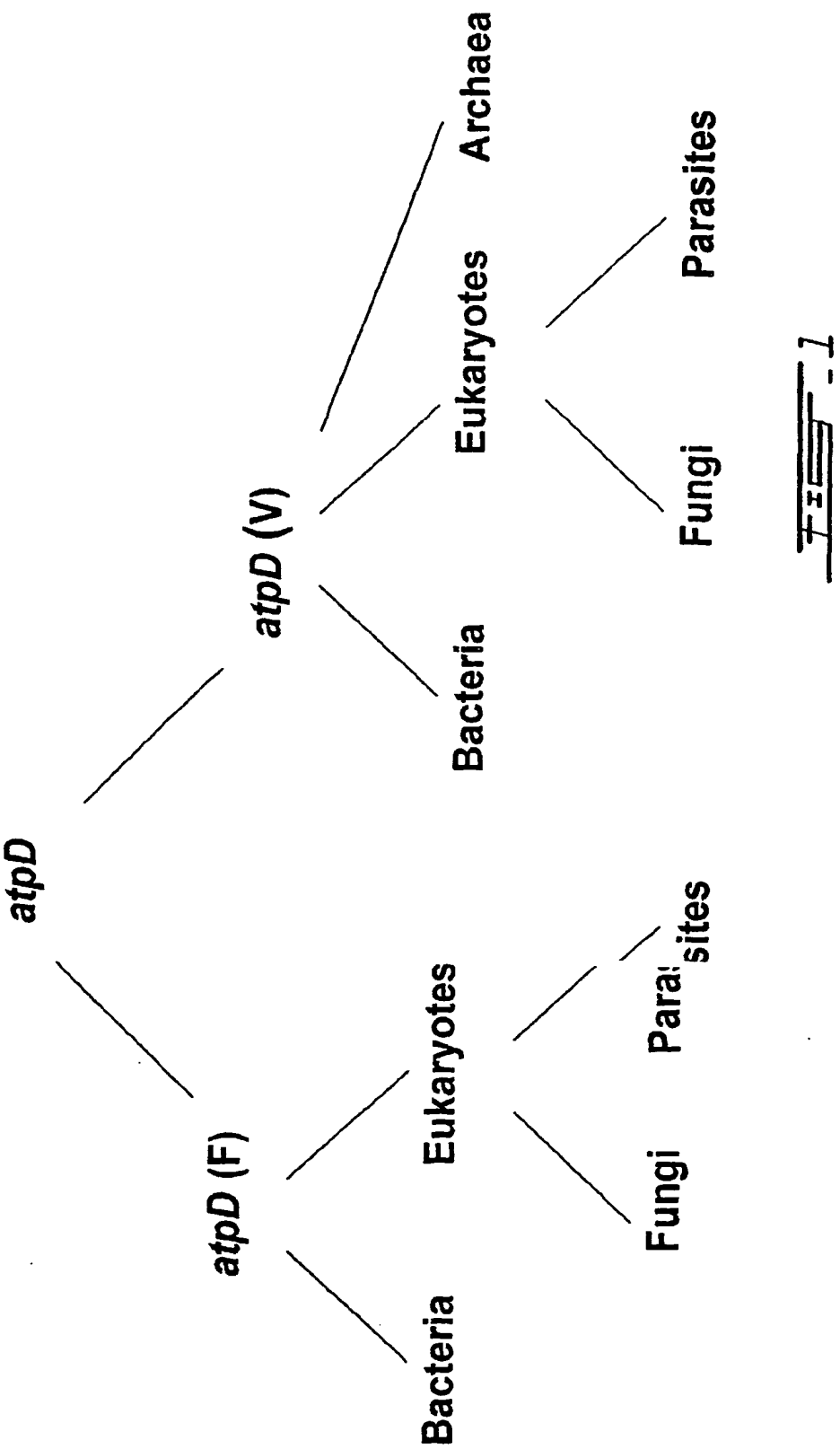

atpD
atpD (V)
Archaea
Eukaryotes
Parasites
Fungi
Bacteria
atpD (F)
Eukaryotes
Parasites
Fungi
Bacteria

Fig. 1

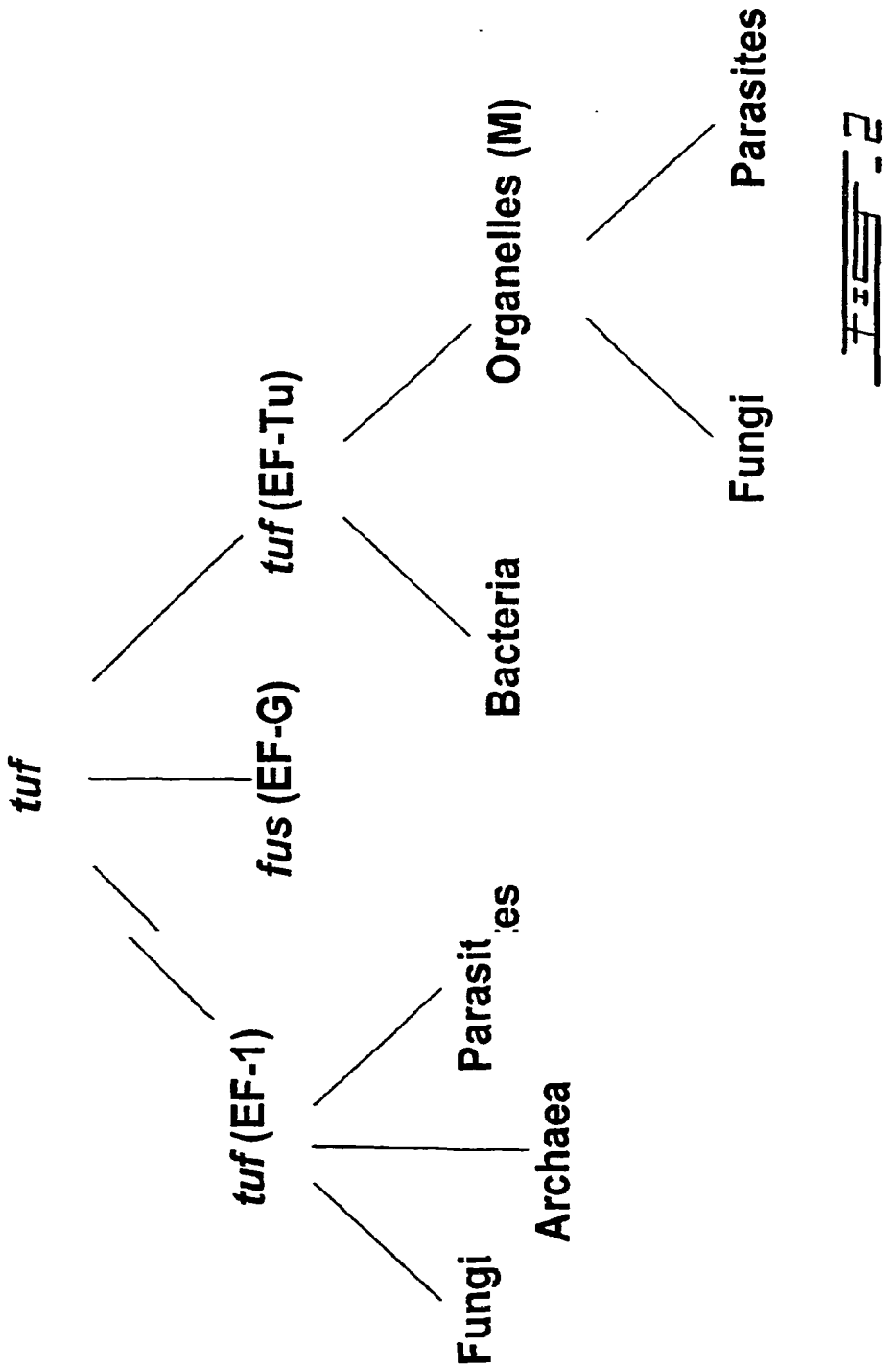

tuf
tuf (EF-Tu)
fus (EF-G)
Bacteria
Organelles (M)
Parasites
Fungi
tuf (EF-1)
Parasites
Archaea
Fungi

Fig. 2

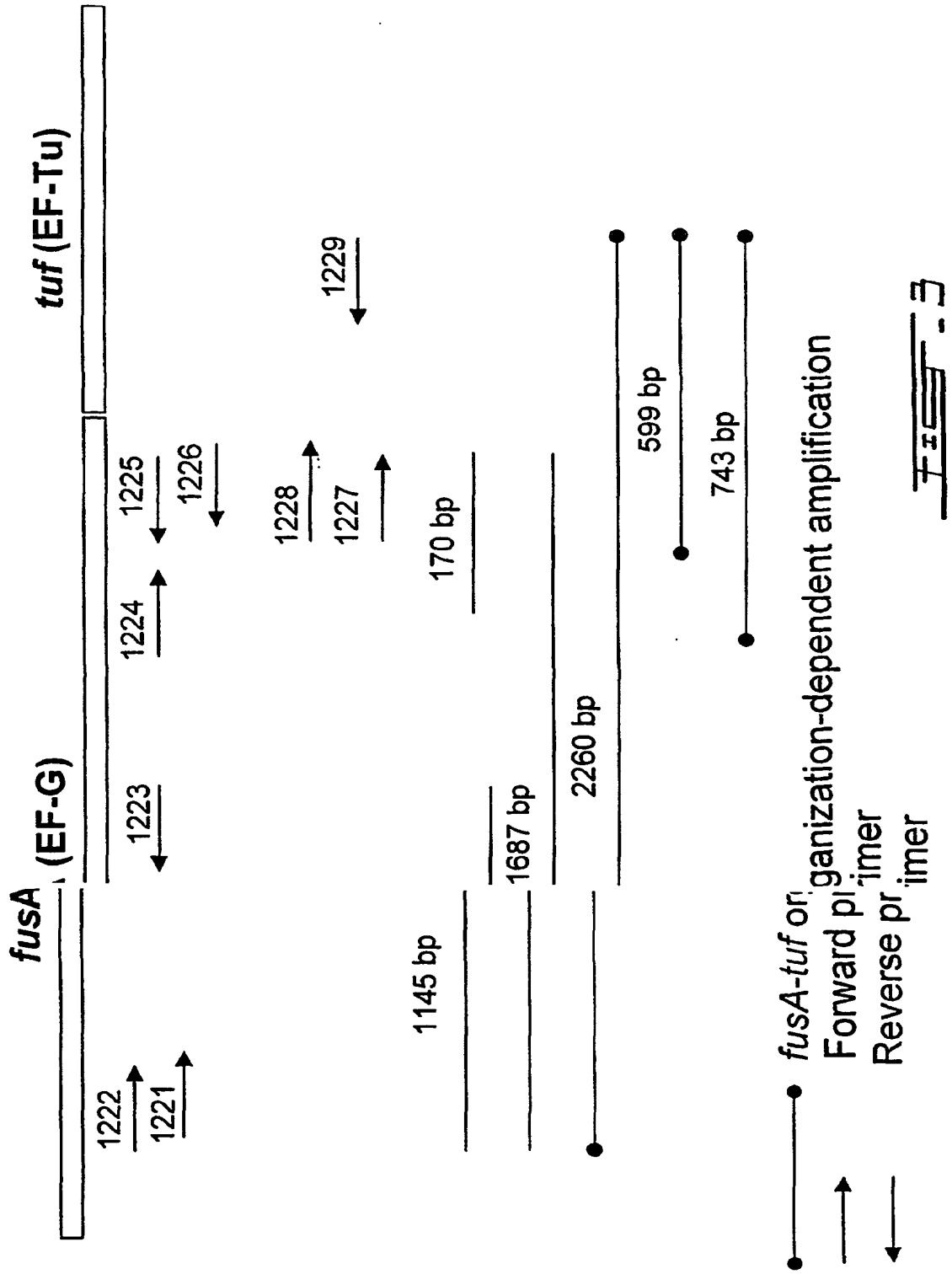

fusA (EF-G)
tuf (EF-Tu)
1222
1221
1223
1224
1225
1226
1228
1227
1229
170 bp
1145 bp
1687 bp
2260 bp
599 bp
743 bp
fusA-tuf organization-dependent amplification
Forward primer
Reverse primer

Fig. 3

120 130 140 150 160 170 180 190 200
S. aureus
S. epidermidis
E. durans (A)
E. hirae (A)
E. mundtii (A)
E. faecium (A)
E. cecorum
E. columbae
E. casseliflavus (A)
E. gallinarum (A)
E. faecalis
E. avium (A)
E. raffinosus (A)
E. dispar (A)
E. malodoratus (A)
E. pseudoavium (A)
E. sulfureus
E. saccharolyticus
E. solitarius

Fig - 4a

210 220 230 240 250 260 270 280 290
S. aureus TPERDSDKPFMMPVEDVI:SITGRGTVATGRVERGQIKVGEEVEIIGLH.DTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA
S. epidermidis TPERDSDKPFMMPVEDVI:SITGRGTVATGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA
E. durans (A) TPERDNDKPFMMPVEDVI:SITGRGTVATGRVERGQIKVGEEVEIIGMH.ETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA
E. hirae (A) TPERDNDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDVVDIVGIAEETAQTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. mundtii (A) TPERDNDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDVVDIVGIAEETAQTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. faecium (A) TPERDNDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDVDIVGLAEETAQTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREDIQRGQVLA
E. cecorum TPERDNDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEVVGIAEETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. casseliflavus (A) TPERDNDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIHDEISKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. gallinarum (A) TPERDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIADETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. faecalis TPERDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIADETAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. avium (A) TPVRDTDKPFMMPVEDVI:SITGRGTVATGRVERGEVRVGDEVEIVGIKDETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIERGQVLA
E. raffinosus (A) TPVRDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIADETAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. dispar (A) TPVRDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIAEETAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. malodoratus (A) TPVRDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIAEETAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. pseudoavium (A) TPVRDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIAEATAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLS
E. sulfureus TPVRDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIAEETAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. saccharolyticus TPTRDTDKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDEVEIVGIAEETAKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
E. solitarius TPERDTEKPFMMPVEDVI:SITGRGTVATGRVERGQVRVGDVVDIVGIADETAQTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
TPERDHDKPFMMPIEDVI FSITGRGTVATGRVERGQVRVGDVVEIVGIDEETAQTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA
FSITGRGTVATGRVERGTIKVGDEVDIIGIHEDVKKTTVTGVEMFRKLLDYAEAGDNIGTLLRGVSRDDIERGQVLA

Fig - 4b

L. monocytogenes
E. casseliflavus (B)
E. gallinarum (B)
E. durans (B)
E. faecium (B)
E. hirae (B)
E. mundtii (B)
E. avium (B)
E. pseudoavium (B)
E. malodoratus (B)
E. raffinosus (B)
E. dispar (B)
S. pneumoniae
S. suis
S. pyogenes
S. mutans
L. lactis
L. aquaticus
E. coli
C
f
D
g
E
F

Fig-4c

L. monocytogenes
E. casseli.flavus (B)
E. gallinarum (B)
E. durans (B)
E. faecium (B)
E. hirae (B)
E. mundtii (B)
E. avium (B)
E. pseudoavium (B)
E. malodoratus (B)
E. raffinosus (B)
S. dispar (B)
S. pneumoniae
S. suis
S. pyogenes
S. mutans
L. lactis
I. aquaticus
E. coli
a2
b2
c2
d2
e2
f2
g2
h2
i2
j2
k2

Fig - 4d

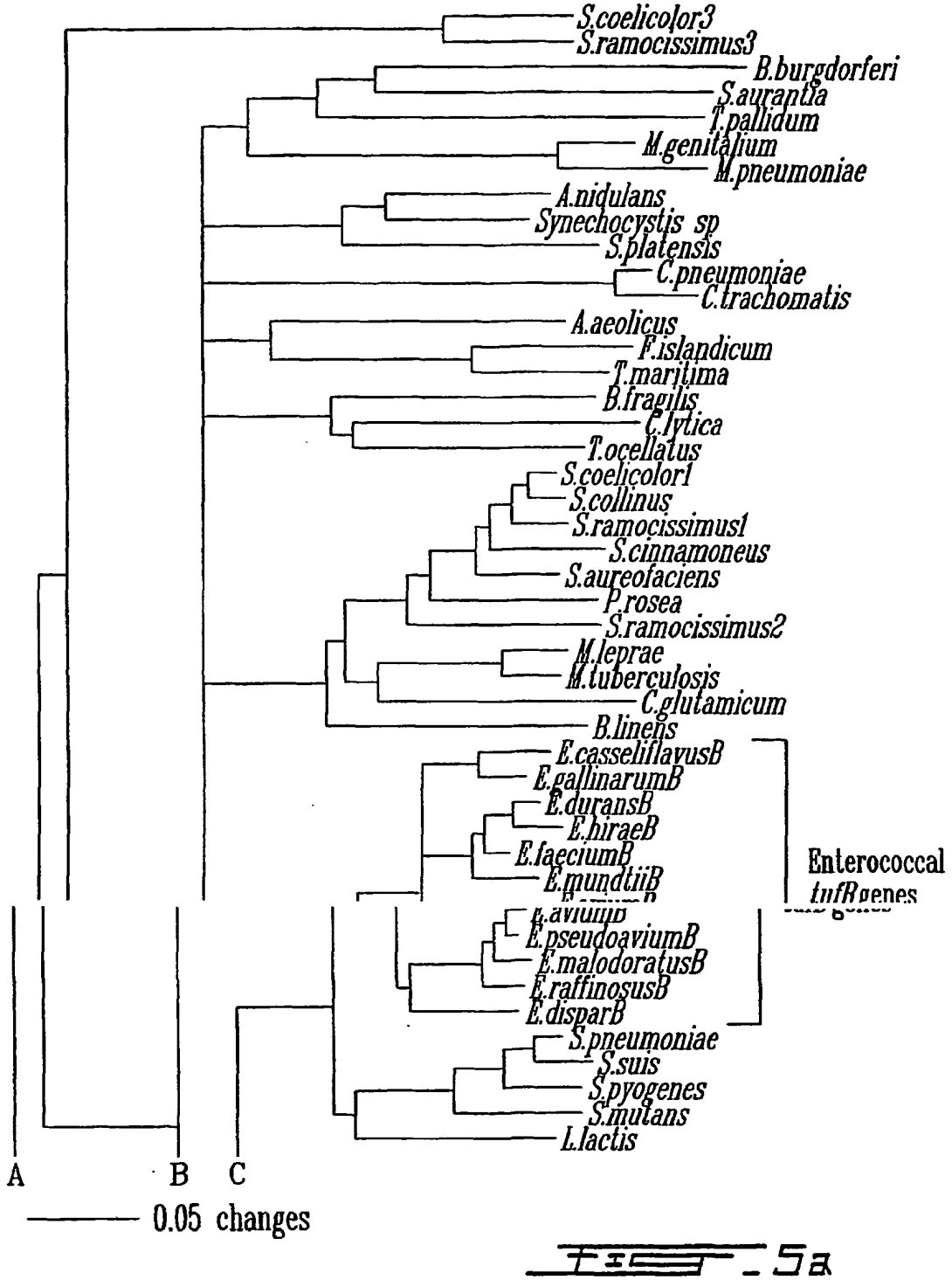

S.coelicolor3
S.ramocissimus3
B.burgdorferi
S.aurantia
T.pallidum
M.genitalium
M.pneumoniae
A.nidulans
Synechocystis sp
S.platensis
C.pneumoniae
C.trachomatis
A.aeolicus
F.islandicum
T.maritima
B.fragilis
C.lytica
T.ocellatus
S.coelicolor1
S.collinus
S.ramocissimus1
S.cinnamoneus
S.aureofaciens
P.rosea
S.ramocissimus2
M.leprae
M.tuberculosis
C.glutamicum
B.linens
E.casseliflavusB
E.gallinarumB
E.dransB
E.hiraeB
E.faeciumB
E.mundtiiB
E.aviumB
E.pseudoaviumB
E.malodoratusB
E.raffinosusB
E.disparB
S.pneumoniae
S.suis
S.pyogenes
S.mutans
L.lactis
Enterococcal
tufBgenes
A
B
C
0.05 changes

Fig. 5a

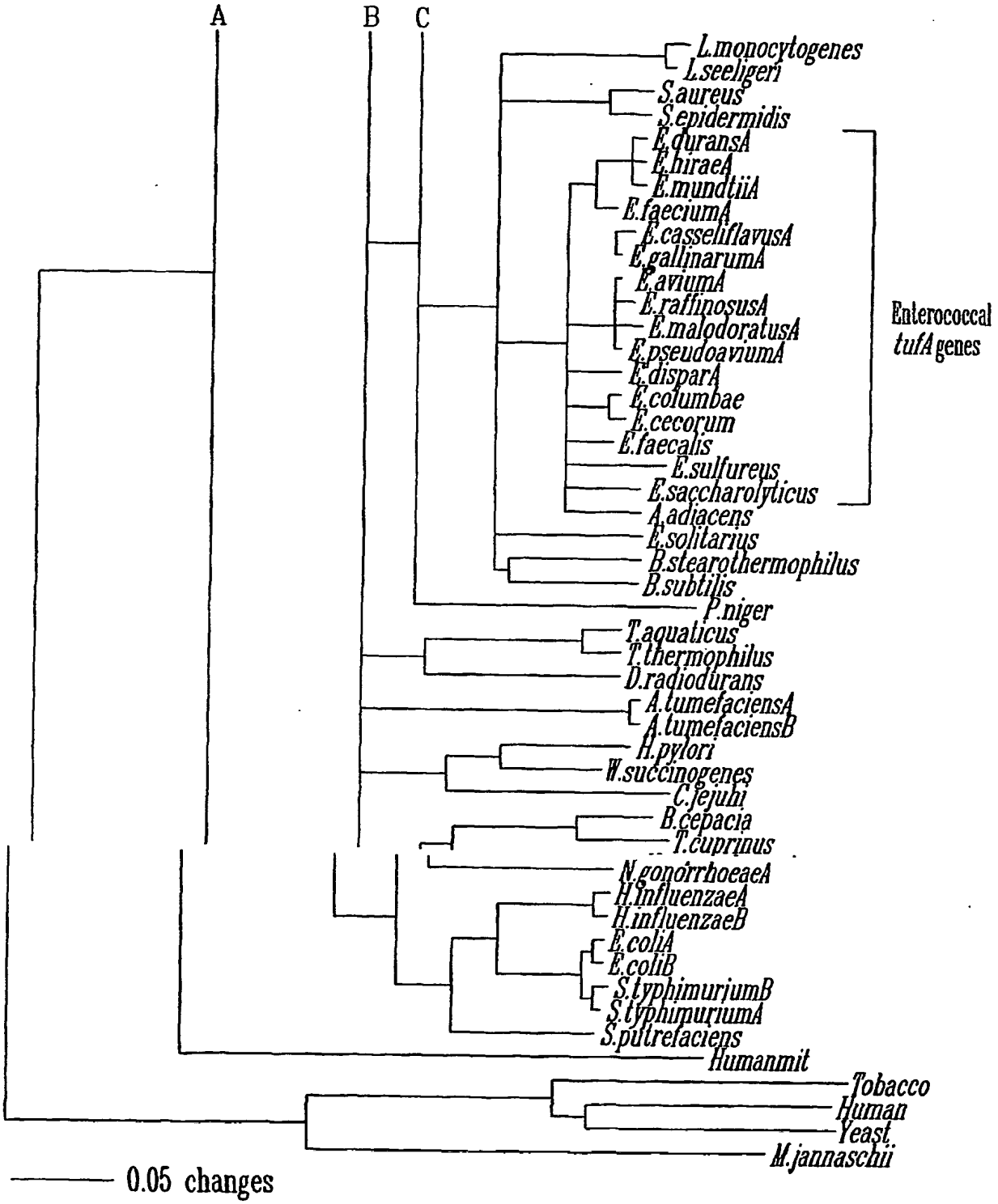

A
B
C
L.monocytogenes
L.seeligeri
S.aureus
S.epidermidis
E.duransA
E.hiraeA
E.mundtiiA
E.faeciumA
E.casseliflavusA
E.gallinarumA
E.aviumA
E.raffinosusA
E.malodoratusA
E.pseudoaviumA
E.disparA
E.columbae
E.cecorum
E.faecalis
E.sulfureus
E.saccharolyticus
A.adiacens
E.solitarius
B.stearothermophilus
B.subtilis
P.niger
T.aquaticus
T.thermophilus
D.radiodurans
A.tumefaciensA
A.tumefaciensB
H.pylori
W.succinogenes
C.jejuni
B.cepacia
T.cuprinus
N.gonorrhoeaeA
H.influenzaeA
H.influenzaeB
E.coliA
E.coliB
S.typhimuriumB
S.typhimuriumA
S.putrefaciens
Humanmit
Tobacco
Human
Yeast
M.jannaschii
Enterococcal tufA genes
0.05 changes

Fig - 5b

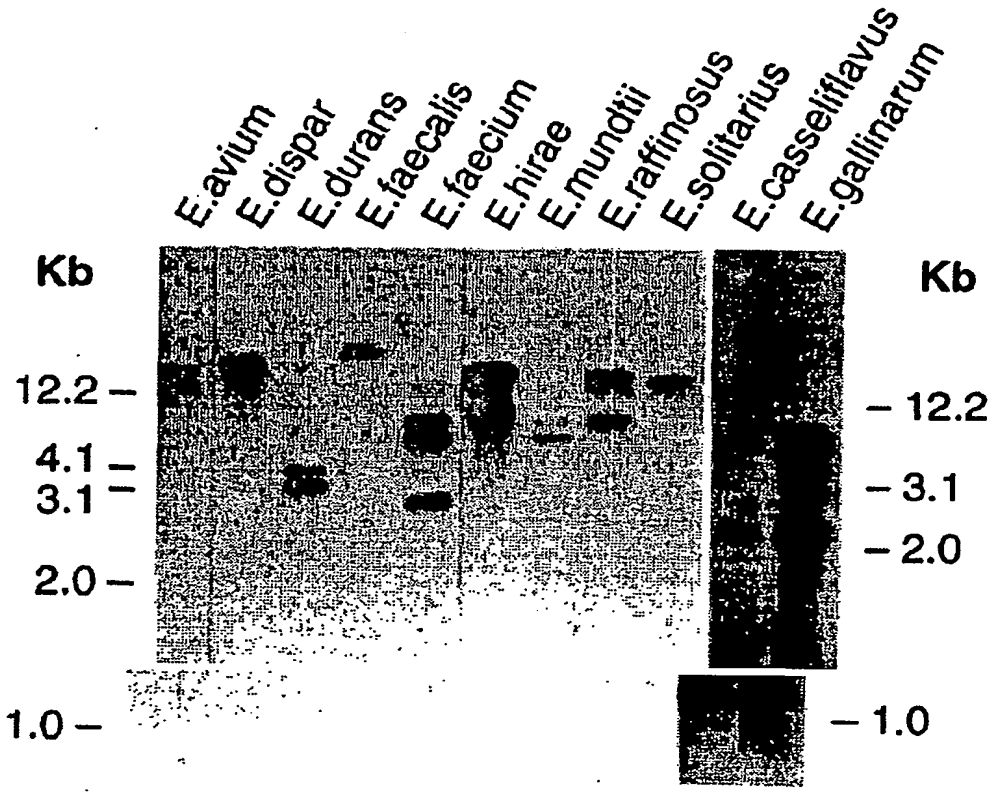

E.avium
E.dispar
E.durans
E.faecalis
E.faecium
E.hirae
E.mundtii
E.raffinosus
E.solitarius
E.casseliflavus
E.gallinarum
Kb
12.2
4.1
3.1
2.0
1.0
Kb
12.2
3.1
2.0
1.0

Fig. 6

```
                301        311        321        331
E. coli         GAGATCGGTG AAGAAGAGCG TTGGG..... .......... CGATTCACCG
E. agglomerans  GACATCGGTG AAGAAGAGCG TTGGG..... .......... CGATCCACCG
P. agglomerans  GAGCTGAAAG AAGAAGATGG CAGCGCAGTA GAGATCGCCT CTATTCACCG
P. dispersa     GACCTGAAAG AAGAAGACGG CAGCGCTGTA GAGGTTCCT  CTATTCATCG
T. ptyseos      GACCTGAAGA ACGAAGATGG TAGCAATGTT GAGGTGAACT CTATTCACCG

E. coli         ~I~~G~~E~  ~ E~~E~~R~~W ~~A~~ ..... .......... I~~H~~R~~
E. agglomerans  ~I~~G~~E~  ~ E~~E~~R~~W ~~A~~ ..... .......... I~~H~~R~~
P. agglomerans  ~L~~K~~E~  ~ E~~D~~G~~S ~~A~~V~~E~ ~I~~A~~S~~ I~~H~~R~~
P. dispersa     ~L~~K~~E~  ~ E~~D~~G~~S ~~A~~V~~E~ ~V~~S~~S~~ I~~H~~R~~
T. ptyseos      ~L~~K~~N~  ~ E~~D~~G~~S ~~N~~V~~E~ ~V~~N~~S~~ I~~H~~R~~
```

Fig-7

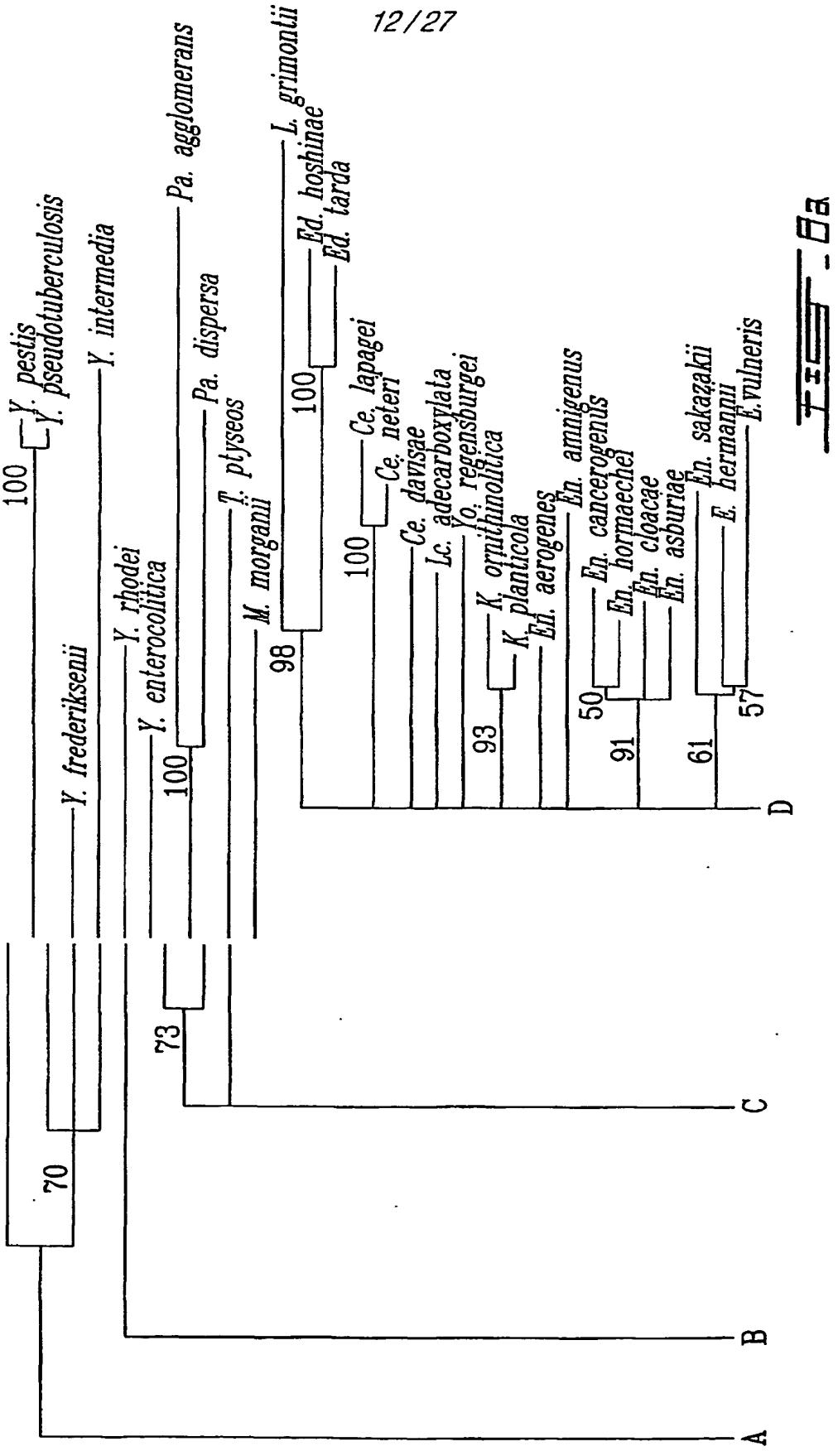

Y. pestis
Y. pseudotuberculosis
Y. frederiksenii
Y. intermedia
Y. rhodei
Y. enterocolitica
Pa. agglomerans
Pa. dispersa
T. ptyseos
M. morganii
L. grimontii
Ed. hoshinae
Ed. tarda
Ce. lapagei
Ce. neteri
Ce. davisae
Lc. adecarboxylata
Yo. regensburgei
K. ornithinolitica
K. planticola
En. aerogenes
En. amnigenus
En. cancerogenus
En. hormaechei
En. cloacae
En. asburiae
En. sakazakii
E. hermannii
E. vulneris
100
100
100
100
98
93
50
91
61
57
73
70
A
B
C
D

FIG. 8a

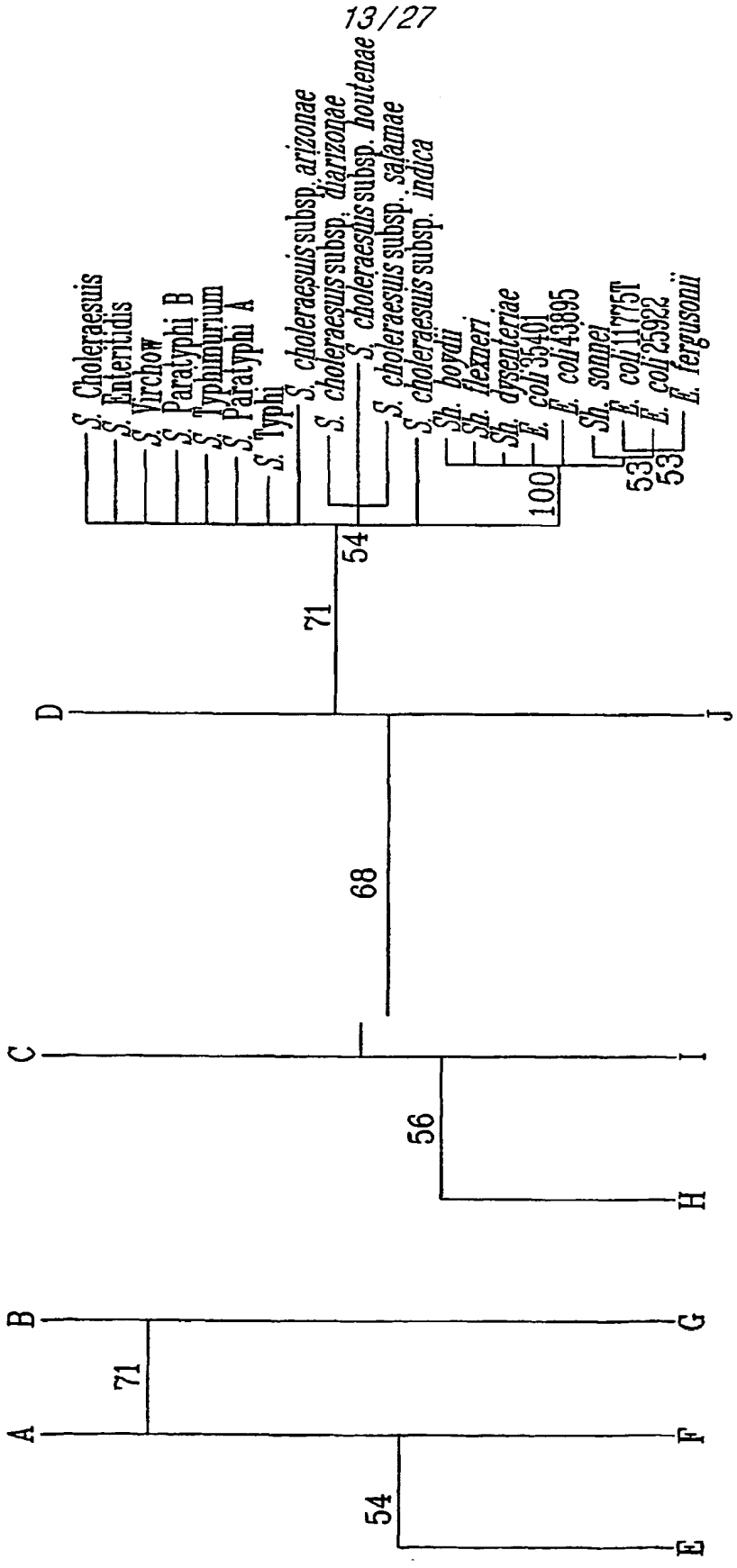

S. Choleraesuis
S. Enteritidis
S. Virchow
S. Paratyphi B
S. Typhimurium
S. Paratyphi A
S. Typhi
S. choleraesuis subsp. arizonae
S. choleraesuis subsp. diarizonae
S. choleraesuis subsp. houtenae
S. choleraesuis subsp. salamae
S. choleraesuis subsp. indica
Sh. boydii
Sh. flexneri
Sh. dysenteriae
E. coli 35401
E. coli 43895
Sh. sonnei
E. coli 11775T
E. coli 25922
E. fergusonii
A
B
C
D
E
F
G
H
I
J
71
54
68
71
54
56
100
53
53

Fig - 8b

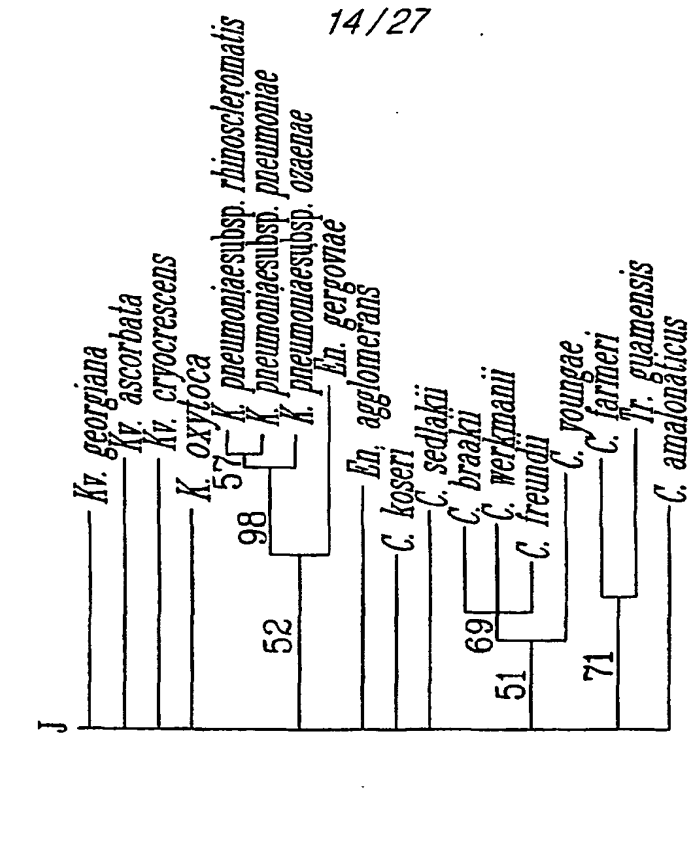

Kv. georgiana
Kv. ascorbata
Kv. cryocrescens
K. oxytoca
K. pneumoniaesubsp. rhinoscleromatis
K. pneumoniaesubsp. pneumoniae
K. pneumoniaesubsp. ozaenae
En. gergoviae
En. agglomerans
C. koseri
C. sedlakii
C. braakii
C. werkmanii
C. freundii
C. youngae
C. farmeri
Tr. guamensis
C. amalonaticus
57
98
52
69
51
71
J
I
O
H
N
G
75
F
M
E
L
K
85

Fig. 8C

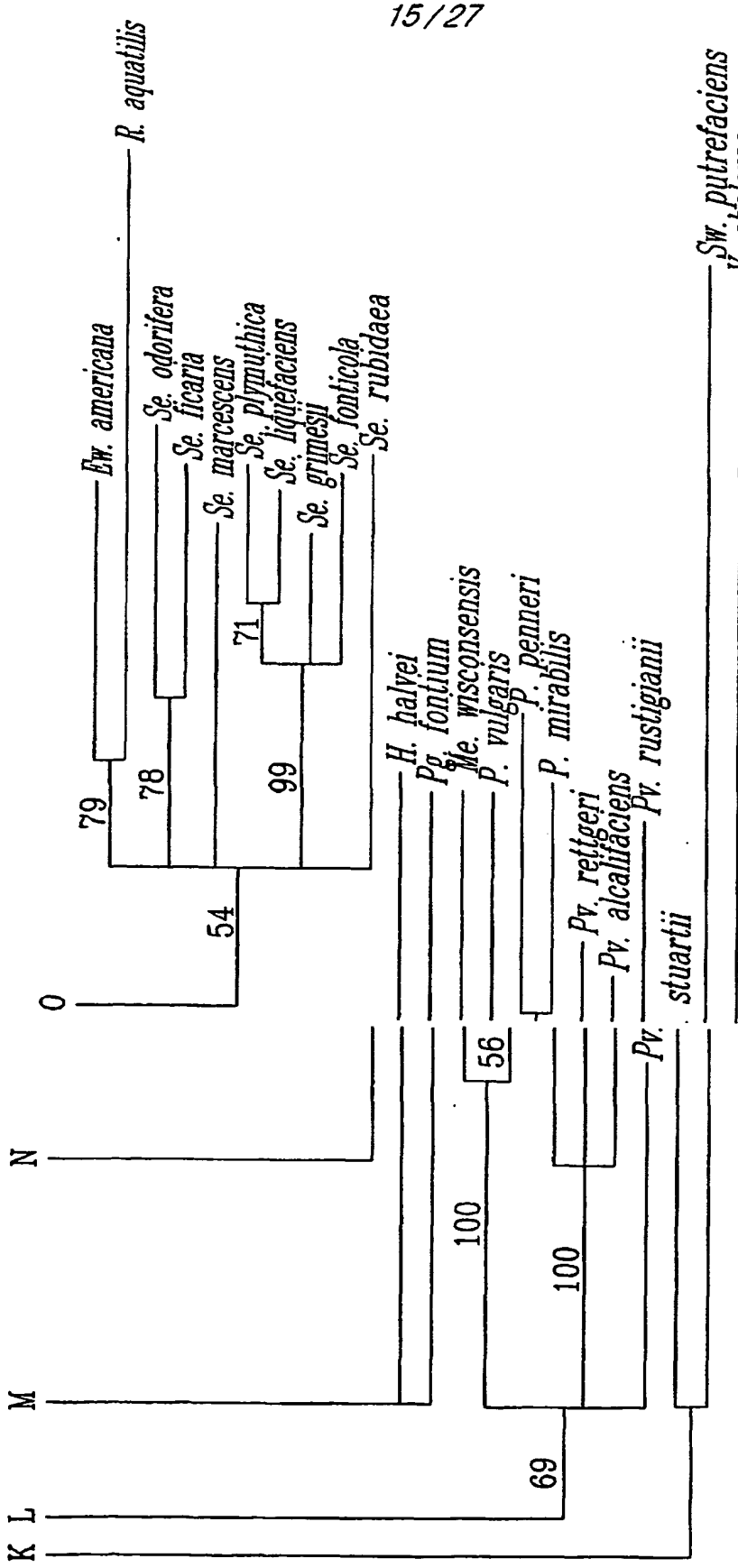

R. aquatilis
Ew. americana
Se. odorifera
Se. ficaria
Se. marcescens
Se. plymuthica
Se. liquefaciens
Se. grimesii
Se. fonticola
Se. rubidaea
H. halvei
Pg. fontium
Me. wisconsensis
P. vulgaris
P. penneri
P. mirabilis
Pv. rettgeri
Pv. alcalifaciens
Pv. rustigianii
Pv. stuartii
Sw. putrefaciens
V. cholerae
79
78
71
99
54
0
56
100
100
69
N
M
L
K
0.01 changes

FIG - 8d

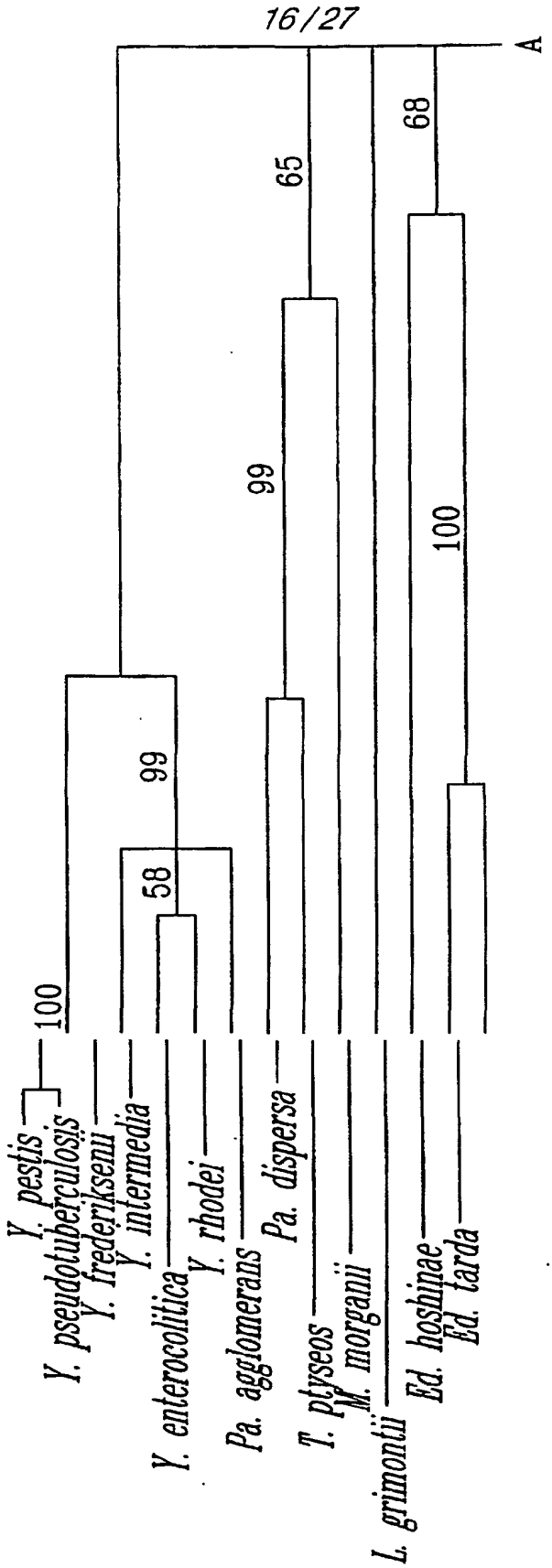

A
100
99
58
99
65
68
100
Y. pestis
Y. pseudotuberculosis
Y. frederiksenii
Y. intermedia
Y. enterocolitica
Y. rhodei
Pa. agglomerans
Pa. dispersa
T. ptyseos
M. morganii
L. grimontii
Ed. hoshinae
Ed. tarda

Fig. 8e

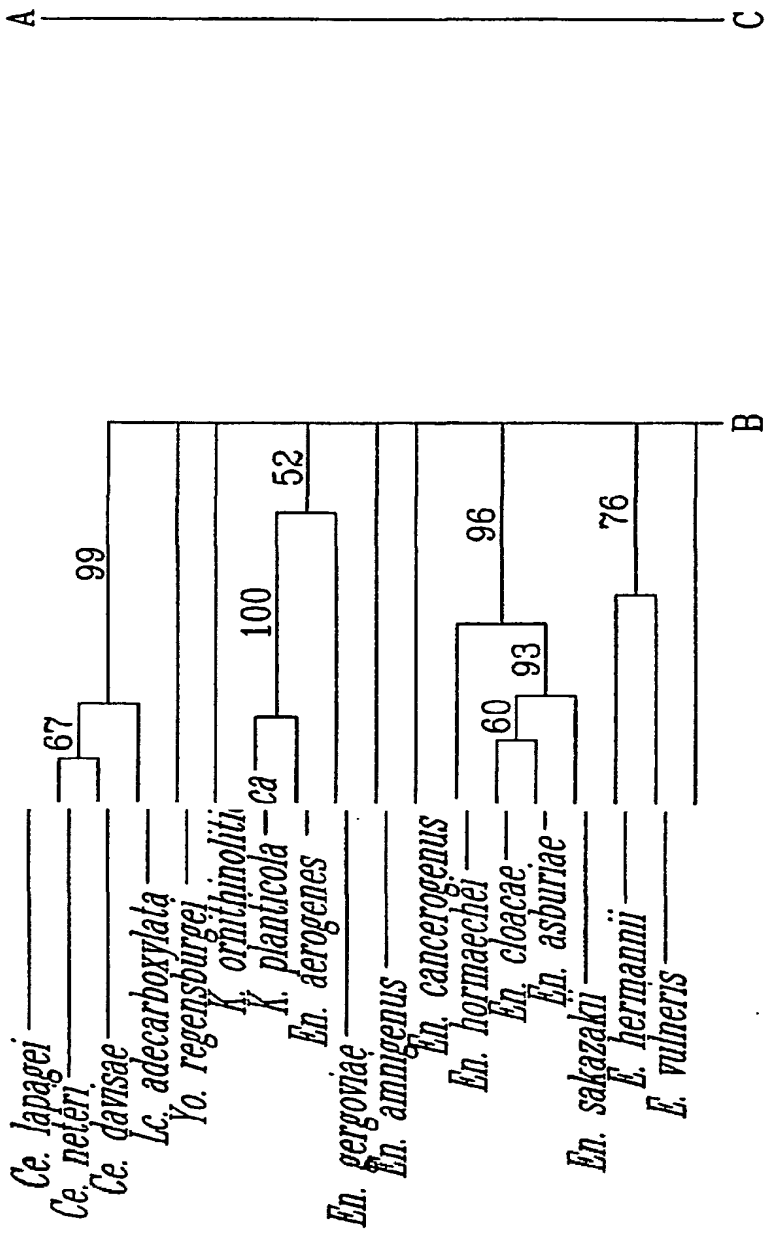
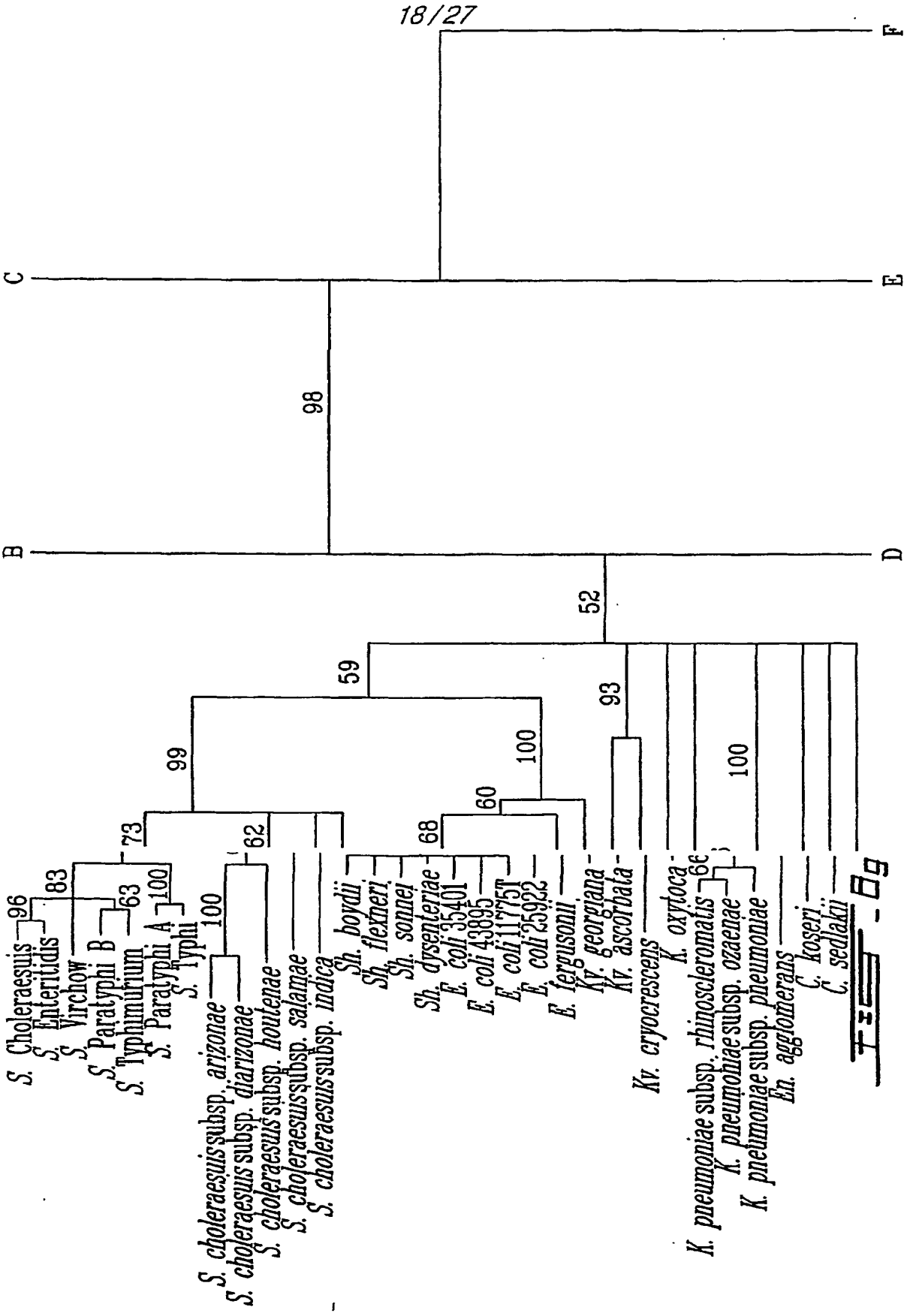
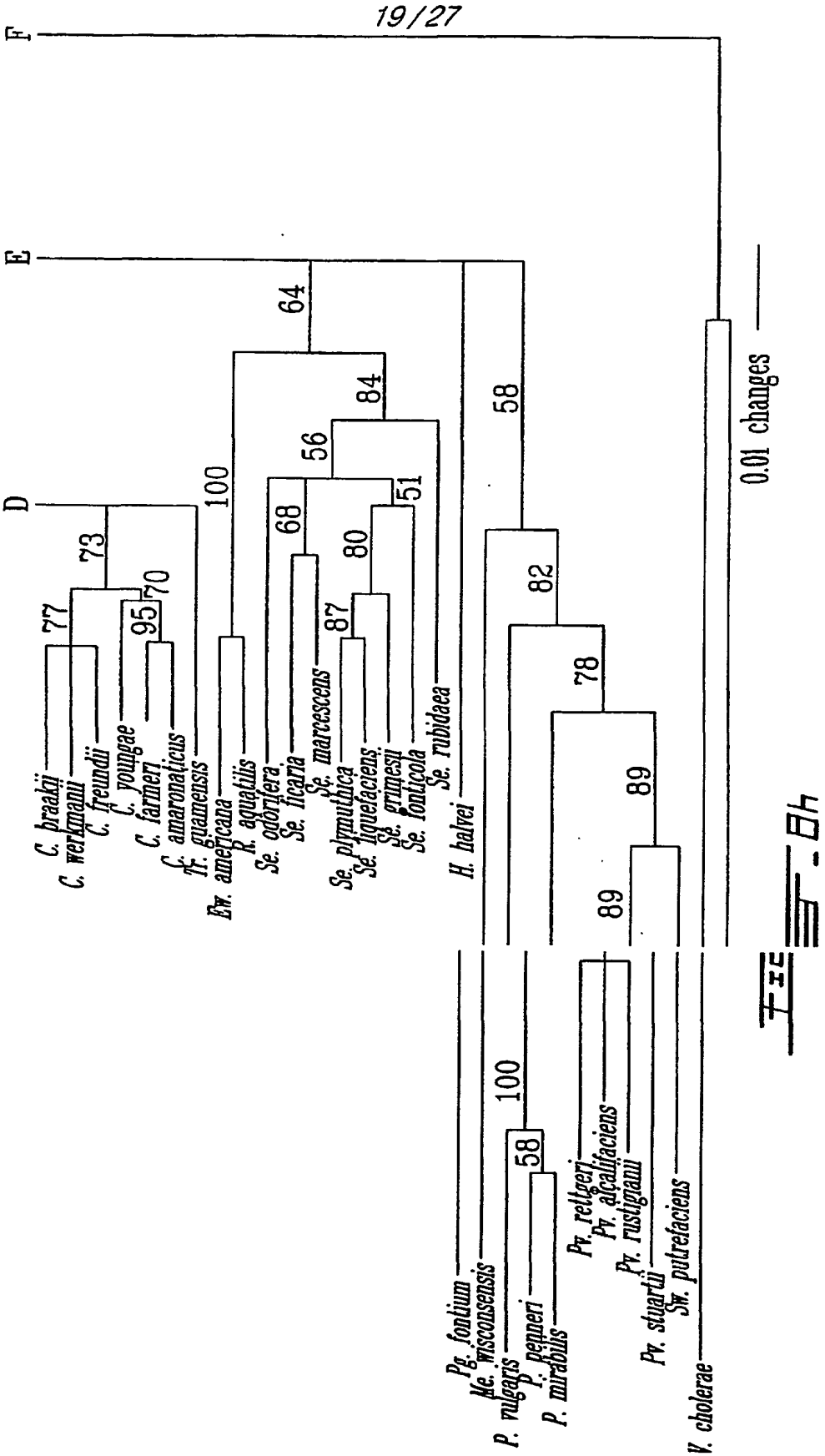

A
C
B
Ce. lapagei
Ce. neteri
Ce. davisae
Lc. adecarboxylata
Yo. regensburgei
K. ornithinolili
K. planticola
En. aerogenes
En. gergoviae
En. amnigenus
En. cancerogenus
En. hormaechei
En. cloacae
En. asburiae
En. sakazakii
E. hermannii
E. vulneris
67
99
100
52
60
96
93
76

Fig. 8F


F
E
D
C
B
98
52
59
99
73
83
96
63
100
62
100
68
60
100
93
100
S. Choleraesuis
S. Enteritidis
S. Virchow
S. Paratyphi B
S. Typhimurium
S. Paratyphi A
S. Typhi
S. choleraesuis subsp. arizonae
S. choleraesuis subsp. diarizonae
S. choleraesuis subsp. houtenae
S. choleraesuis subsp. salamae
S. choleraesuis subsp. indica
Sh. boydii
Sh. flexneri
Sh. sonnei
Sh. dysenteriae
E. coli 35401
E. coli 43895
E. coli 11775T
E. coli 25922
E. fergusonii
Kv. georgiana
Kv. ascorbata
Kv. cryocrescens
K. oxytoca
K. pneumoniae subsp. rhinoscleromatis
K. pneumoniae subsp. ozaenae
K. pneumoniae subsp. pneumoniae
En. agglomerans
C. koseri
C. sedlakii


F
E
D
0.01 changes
C. braakii
C. werkmanii
C. freundii
C. youngae
C. farmeri
C. amalonaticus
Tr. guamensis
Ew. americana
P. aquatilis
Se. odorifera
Se. ficaria
Se. marcescens
Se. plymuthica
Se. liquefaciens
Se. grimesii
Se. fonticola
Se. rubidaea
H. halrei
Pg. fonticum
Me. misconsensis
P. vulgaris
P. penneri
P. mirabilis
Pv. reitgeri
Pv. alcalifaciens
Pv. rustigianii
Pv. stuartii
Sw. putrefaciens
V. cholerae
64
84
56
100
51
68
80
87
58
82
78
89
89
100
58
77
73
95
70

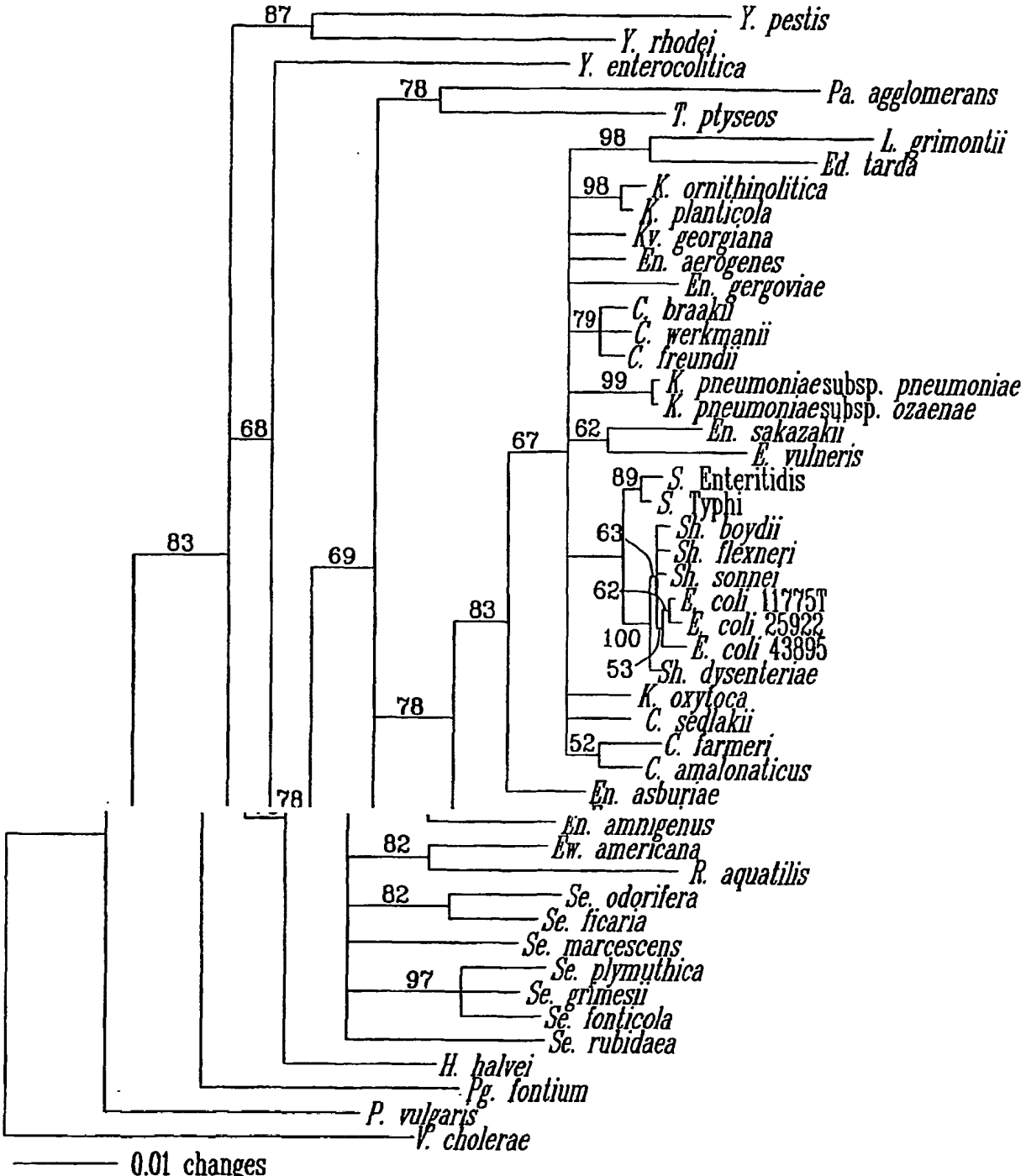

Y. pestis
Y. rhodei
Y. enterocolitica
Pa. agglomerans
T. ptyseos
L. grimontii
Ed. tarda
K. ornithinolitica
K. planticola
Kv. georgiana
En. aerogenes
En. gergoviae
C. braakii
C. werkmanii
C. freundii
K. pneumoniaesubsp. pneumoniae
K. pneumoniaesubsp. ozaenae
En. sakazakii
E. vulneris
S. Enteritidis
S. Typhi
Sh. boydii
Sh. flexneri
Sh. sonnei
E. coli 11775T
E. coli 25922
E. coli 43895
Sh. dysenteriae
K. oxytoca
C. sedlakii
C. farmeri
C. amalonaticus
En. asburiae
En. amnigenus
Ew. americana
R. aquatilis
Se. odorifera
Se. ficaria
Se. marcescens
Se. plymuthica
Se. grimesii
Se. fonticola
Se. rubidaea
H. halvei
Pg. fontium
P. vulgaris
V. cholerae
0.01 changes

Fig. 9a

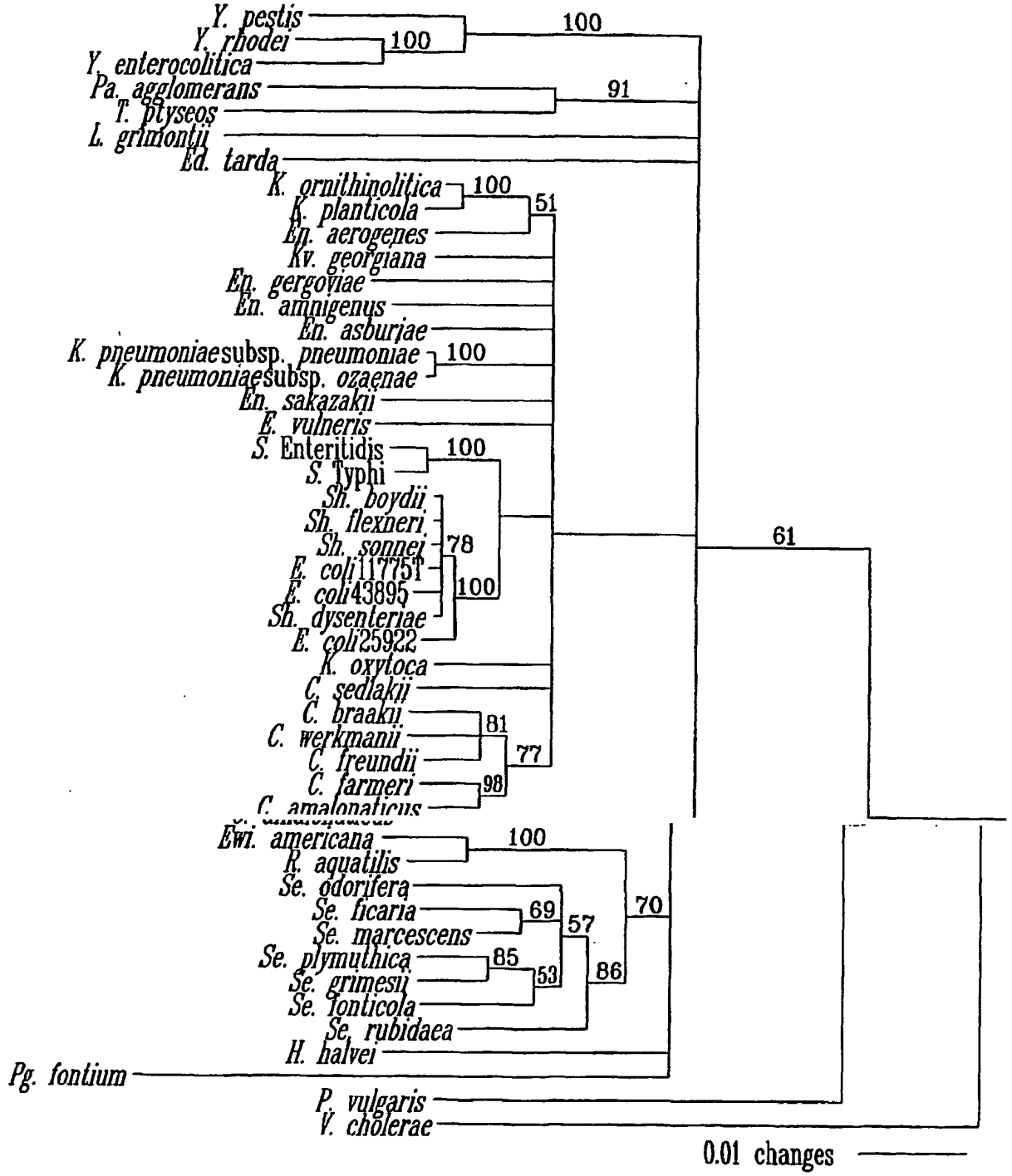

Y. pestis
Y. rhodei
Y. enterocolitica
Pa. agglomerans
T. ptyseos
L. grimontii
Ed. tarda
K. ornithinolitica
K. planticola
En. aerogenes
Kv. georgiana
En. gergoviae
En. amnigenus
En. asburiae
K. pneumoniae subsp. pneumoniae
K. pneumoniae subsp. ozaenae
En. sakazakii
E. vulneris
S. Enteritidis
S. Typhi
Sh. boydii
Sh. flexneri
Sh. sonnei
E. coli 11775T
E. coli 43895
Sh. dysenteriae
E. coli 25922
K. oxytoca
C. sedlakii
C. braakii
C. werkmanii
C. freundii
C. farmeri
C. amalonaticus
Ewi. americana
R. aquatilis
Se. odorifera
Se. ficaria
Se. marcescens
Se. plymuthica
Se. grimesii
Se. fonticola
Se. rubidaea
H. halvei
Pg. fontium
P. vulgaris
V. cholerae
100
100
91
100
51
100
78
100
81
77
98
100
69
57
85
53
86
70
61
0.01 changes

Fig. 9b

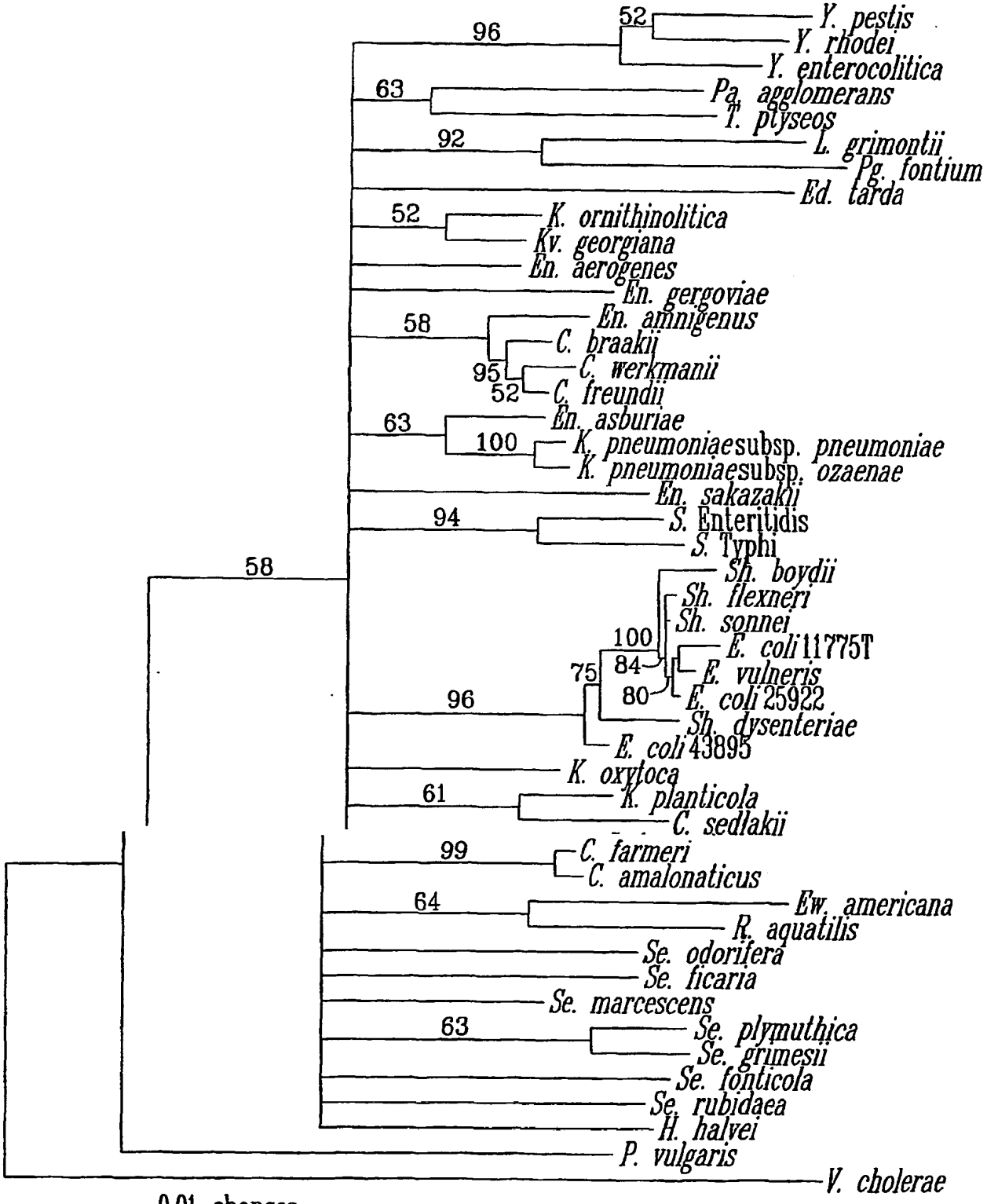

52
96
Y. pestis
Y. rhodei
Y. enterocolitica
63
Pa. agglomerans
T. plyseos
92
L. grimontii
Pg. fontium
Ed. tarda
52
K. ornithinolitica
Kv. georgiana
En. aerogenes
En. gergoviae
58
En. amnigenus
C. braakii
95
C. werkmanii
52
C. freundii
63
En. asburiae
100
K. pneumoniae subsp. pneumoniae
K. pneumoniae subsp. ozaenae
En. sakazakii
94
S. Enteritidis
S. Typhi
58
Sh. boydii
Sh. flexneri
Sh. sonnei
100
E. coli 11775T
75
84
E. vulneris
80
E. coli 25922
96
Sh. dysenteriae
E. coli 43895
K. oxytoca
61
K. planticola
C. sedlakii
99
C. farmeri
C. amalonaticus
64
Ew. americana
R. aquatilis
Se. odorifera
Se. ficaria
Se. marcescens
63
Se. plymuthica
Se. grimesii
Se. fonticola
Se. rubidaea
H. halvei
P. vulgaris
V. cholerae
0.01 changes

Fig. 9c

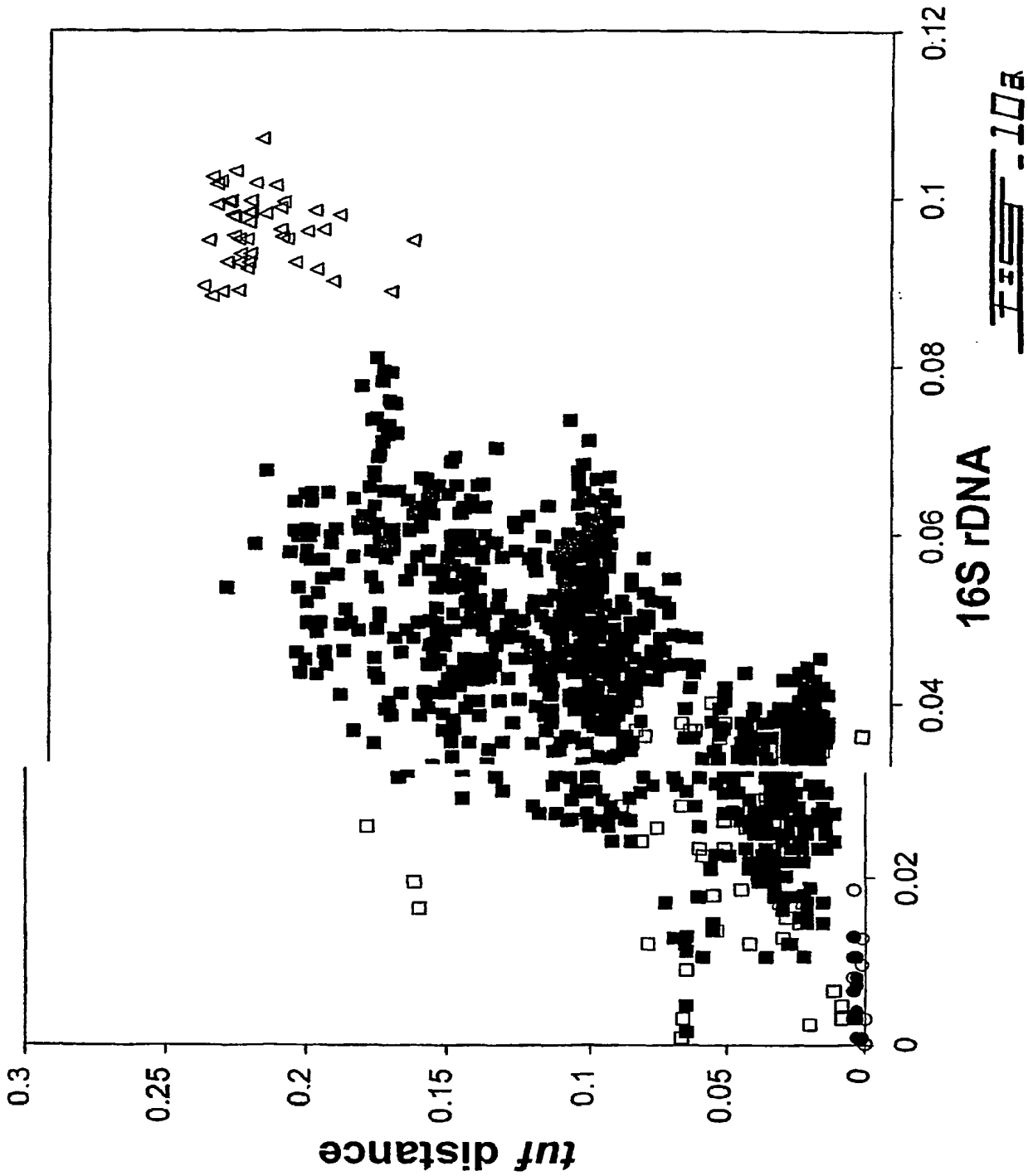

0.3
0.25
0.2
0.15
0.1
0.05
0
tuf distance
0
0.02
0.04
0.06
0.08
0.1
0.12
16S rDNA

Fig. 10a

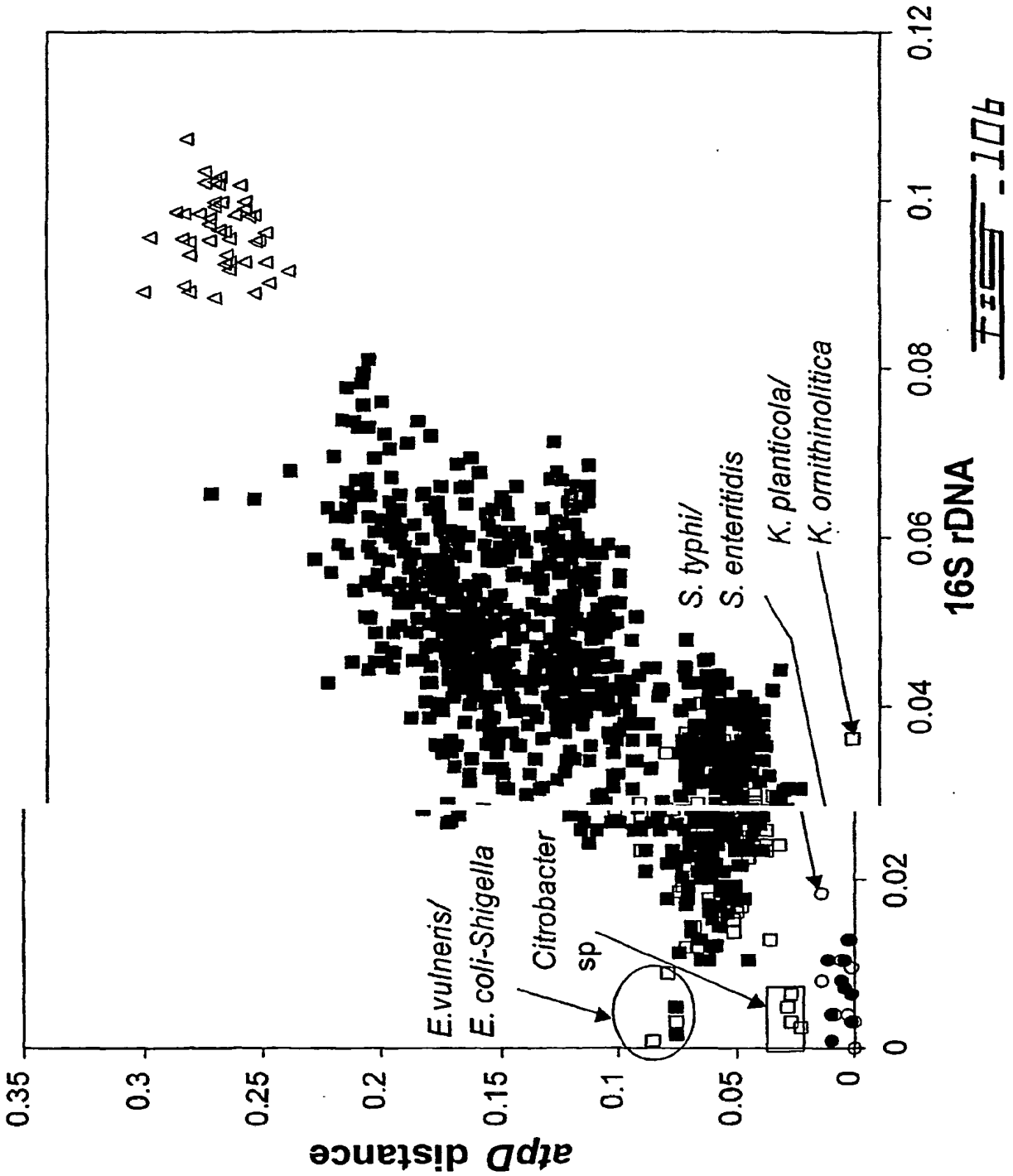

atpD distance
16S rDNA
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0.02
0.04
0.06
0.08
0.1
0.12
E.vulneris/
E. coli-Shigella
Citrobacter
sp
S. typhi/
S. enteritidis
K. planticola/
K. ornithinolitica

Fig - 10b

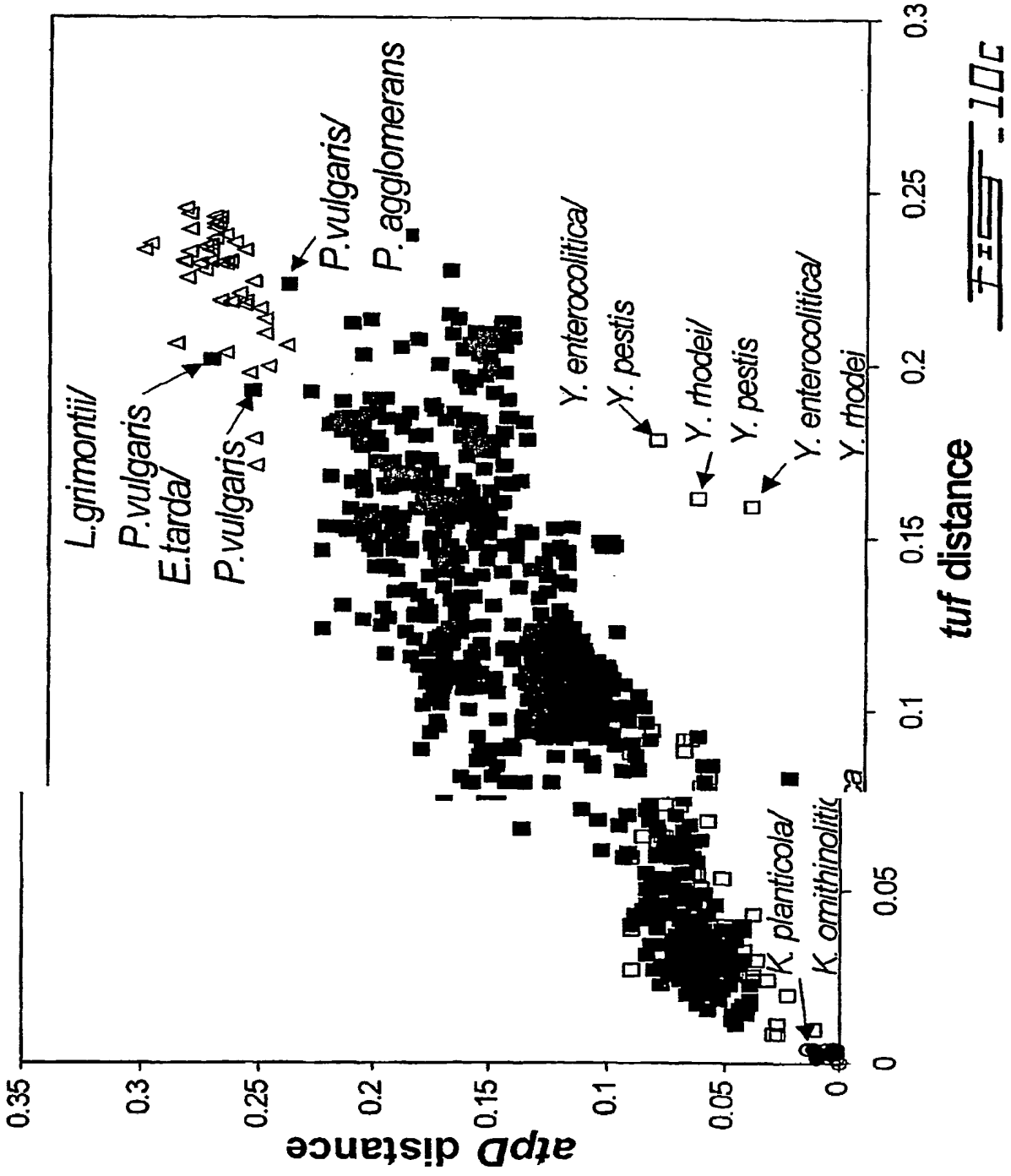

atpD distance
tuf distance
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0.05
0.1
0.15
0.2
0.25
0.3
L.grimontii/
P.vulgaris
E.tarda/
P.vulgaris
P.vulgaris/
P. agglomerans
Y. enterocolitica/
Y. pestis
Y. rhodei/
Y. pestis
Y. enterocolitica/
Y. rhodei
K. planticola/
K. ornithinolitic
a

Fig. 10c

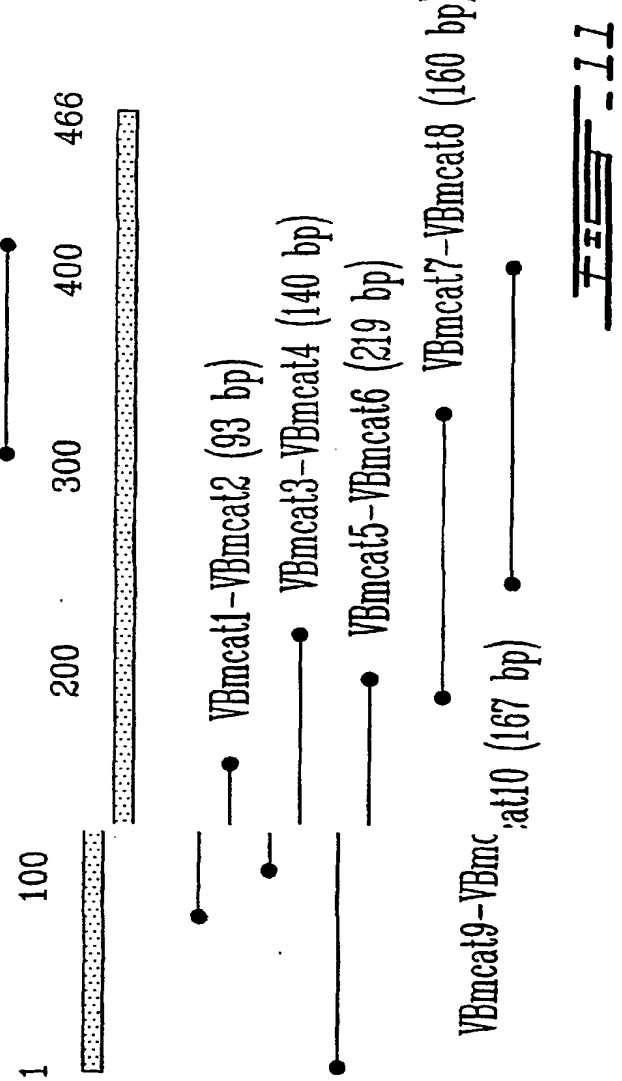

SEQ ID NO: 118+SEQ ID NO: 119 (118 bp)
1
100
200
300
400
466
VBmcat1-VBmcat2 (93 bp)
VBmcat3-VBmcat4 (140 bp)
VBmcat5-VBmcat6 (219 bp)
VBmcat7-VBmcat8 (160 bp)
VBmcat9-VBmc ;at10 (167 bp)

Fig - 11

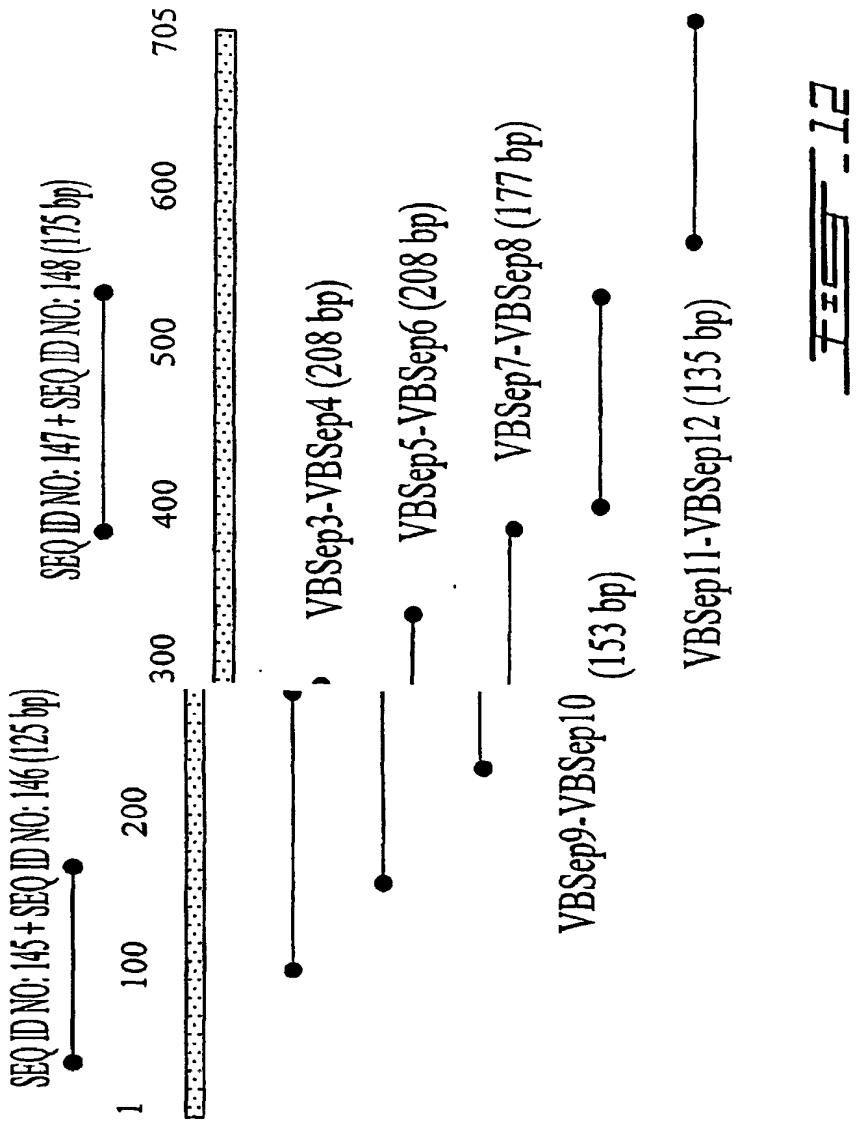

SEQ ID NO: 145 + SEQ ID NO: 146 (125 bp)
SEQ ID NO: 147 + SEQ ID NO: 148 (175 bp)
1
100
200
300
400
500
600
705
VBSep3-VBSep4 (208 bp)
VBSep5-VBSep6 (208 bp)
VBSep7-VBSep8 (177 bp)
VBSep9-VBSep10 (153 bp)
VBSep11-VBSep12 (135 bp)

Fig - 12

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

BERGERON, Michel G. [1], 1145 des Érables, Québec City, Québec, Canada, G2K 1T8
BOISSINOT, Maurice [1], 109 Jean-Bruchési, St-Augustin-de-Desmaures, Québec, Canada, G3A 2N2
HULETSKY, Ann [1], 1231 Av des Pins, Sillery, Québec, Canada, G1S 4J3
MÉNARD, Christian [1], 1174 Rue du Pont, St-Lambert-de-Lévis, Québec, Canada, G0S 2W0
OUELLETTE, Marc [1], 1035 de Ploërmel, Sillery, Québec, Canada, G1S 3S1
PICARD, François J. [1], 1245 de la Sapinière, Cap-Rouge, Québec, Canada, G1Y 1A1
ROY, Paul H. [2], 28 Charles Garnier, Loretteville, Québec, Canada, G2A 2X8

[1]:Canadian citizenship
[2]:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL, FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 2297

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(v) COMPUTER READABLE:

(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING:
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:
(B) REGISTRATION NUMBER:

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE:
(B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

```
CAAACTCGTG AGCACATCCT TCTTTCTCGT CAGGTAGGTG TACCTTACAT      50
CATCGTATTC TTAAACAAAT GCGACCTTGT TGATGACGAA GAATTACTTG     100
AATTAGTAGA AATGGAAGTA CGTGAACTTC TTTCTACTTA TGACTTCCCA     150
GGTGATGACA CTCCAGTAAT CCGTGGTTCA GCTCTTGCAG CGCTTAACGG     200
TGAAGCTGGT CCTTACGGTG AAGAATCAGT TCTTGCTCTT GTAGCAGCAC     250
TTGACTCTTA CATCCCAGAG CCAGAGCGTG CAATCGACAA AGCATTCTTG     300
ATGCCAATCG AAGACGTATT CTCAATTTCT GGTCGTGGTA CAGTAGTAAC     350
AGGCCGTGTT GAAGCTGGTA TCATCAAAGT TGGTGAAGAA GTAGAGATCG     400
TTGGTATTAA AGATACAGTT AAAACAACTG TAACTGGCGT AGAAATGTTC     450
CGTAAACTTC TTGACGAAGG CCGTGCAGGT GAGAACTGTG GTATCTTACT     500
TCGTGGTACT AAGCGTGAAG AAGTACAACG TGGTCAAGTA CTTGCTAAAC     550
CAGGTACAAT CAAGCCGCAC ACTAAATTCG ACGCAGAAGT ATACGTACTT     600
TCTAAAGAAG AAGGTGGTCG TCACACTCCA TTCTTAAATG GTTACCGTCC     650
ACAGTTCTAC TTCCGTACAA CTGACGTAAC TGGTGCRATC CAGTTGAAAG     700
AAGGCGTTGA AATGGTAATG CCAGGTGACA ACGTTGAAAT GTCAGTAGAA     750
```

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Actinomyces meyeri*
(B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

```
CGGTGCGATC CTCGTGGTCG CCGCGACCGA CGGCCCCATG GCCCAGACCC      50
GCGAGCACGT CCTGCTCGCC CGTCAGGTCG GCGTTCCCAC CATCCTCATC     100
GCCCTCAACA AGTCCGACAT GGTTGACGAC GAGGAAATGA TGGAACTGGT     150
CGAGGAGGAG TGCCGCGACC TGCTGGAGTC CCAGGACTTC GATCGCGATG     200
CCCCGATCGT CCAGGTTTCC GCTCTGAAGG CCCTCGAGGG CGACGCGGAG     250
TGGGTTGCCA AGATCGAGGA GCTCATGGAG GCTGTGGATT CCTACATCCC     300
CACCCCCGAG CGCGATATGG ACAAGCCCTT CCTCATGCCG ATCGAGGACG     350
TCTTCACGAT CACAGGTCGT GGCACGGTCG TCACGGGGCG TGTTGAGCGT     400
GGCAAGCTGC CGATCAACTC CGAGGTCGAG ATCCTCGGTA TCCGTGATCC     450
```

```
CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG      500
AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC      550
GATGAGGTTG AGCGCGGCCA GGTTGTGGCC ATTCCCGGCT CCATCACGCC      600
TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG      650
GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT      700
ACCACGGACG TGACCGGCGT CATCACCCTC CCCGAGGGCA CCGACATGGT      750
CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG      800
CCATGGAGCC CGGCTGGGCT TCGCCA                               826
```

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aerococcus viridans*
- (B) STRAIN: ATCC 11563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

```
TGGTGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC       50
GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTTCCTGC ATTCGTAGTA      100
TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG      200
ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA      250
GCTCAAGAAG CTAAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT      300
TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG      350
ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA      400
CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA      450
ACAAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTC CGTAAAAACT      500
TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGTT      550
CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT      600
CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG      650
AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC      700
TTCCGTACTA CTGACATTAC TGGTGTTATC ACTTTACCAG AAGACGTAGC      750
TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCACC      800
CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC                     835
```

2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

```
CCTGGTGGTG TCGGCCGCTG ACGGCCCGAT GCCGCAAACG CGCGAACACA      50
TCCTGCTGAG CCGCCAGGTT GGCGTGCCGT ACATCATCGT CTTCCTGAAC     100
AAGGCCGACA TGGTTGACGA CGCCGAGCTG CTTGAGCTGG TGGAAATGGA     150
AGTTCGCGAR CTGCTGAGCA AGTACGACTT CCCGGGCGAC GACACCCCGA     200
TCGTGAAGGG TTCGGCCAAG CTGGCGCTGG AAGGCGACAA GGGCGAACTG     250
GGCGAACAGG CCATCATGGC GCTGGCCGCT GCGCTGGACT CGTACATCCC     300
GACGCCTGAG CGTGCCGTTG ACGGCGCGTT CCTGATGCCG GTTGAAGACG     350
TGTTCTCGAT CTCGGGTCGC GGCACCGTGG TGACCGGCCG TATCGAACGC     400
GGCATCATCA AGGTCGGCGA GGAAATCGAA ATCGTCGGTC TGGTGCCGAC     450
GGTGAAGACG ACCTGCACGG GCGTGGAAAT GTTCCGCAAG CTGCTGGACC     500
AAGGTCAAGC CGGCGACAAC GTGGGCATCC TRCTGCGCGG CACCAAGCGT     550
GAAGACGTCC AGCGCGGCCA GGTTCTGGCC AAGCCGGGCT CGATCACCCC     600
GCACACGGAC TTCACGTCCG AGGTGTACAT CCTGTCCAAG GAAGAAGGCG     650
GCCGTCACAC TCCGTTCTTC CAAGGCTATC GTCCCCAGTT CTACTTCCGC     700
ACGACGGACG TGACGGGCAC GATCGAGCTG CCGGCCGACA AGGAAATGGT     750
CCTGCCGGGC GACAACGTGG CCATGACGGT CAAGCTGCTG GCTCCGATCG     800
CCATGGAAGA AGGCCTGCGT TCGCCAC                              827
```

2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Anaerorhabdus furcosus*
(B) STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

```
TGGATCAATC CTAGTAGTTG CTGCAACTGA TGGACCAATG CCTCAAACTC      50
GTGAACATAT CTTACTTGCT CGTCAAGTAG GTGTTCCAAG AATGGTTGTA     100
TTCTTGAACA AATGCGACAT GGTTGAAGAT GAAGAATTAA TCGACCTTGT     150
TGAAATGGAA GTTCGTGAAC TTCTAAGTGC TTACGGTTTC GAAGGTGATG     200
ATACACCAGT TATCCGTGGT TCTGCATTAA AATCTCTTGA AGGAAATGCT     250
GATTGGGAAG CAAAAGTTGC TGAATTAATG GATGCAGTTG ACTCTTGGAT     300
TCCAACTCCA ACTCATGAAA CAGACAAACC ATTCTTAATG GCTGTTGAAG     350
ATGTATTCAC AATTACAGGT CGTGGTACAG TTGCTACTGG ACGTGTTGAA     400
CGTGGACACT TAAACCTTAA CGAAGAAGTT GAAATCGTTG GTATTCATGA     450
TACTAAGAAA TCAGTTGTTA CTGGTATCGA AATGTTCCGT AAATTATTAG     500
ACTATGCTGA AGCAGGAGAC AACATTGGTG CATTATTACG TGGTGTTTCT     550
CGTGATGAAA TCGAACGTGG ACAATGTCTA GCTAAACCTG GATCAGTTAC     600
TCCACATACA GCTTTCAAAG CTCAAGTATA CGTATTAACT AAAGAAGAAG     650
GTGGACGTCA TACACCATTC GTAACTAACT ACCGTCCTCA ATTCTATTTC     700
CGTACAACTG ACGTAACAGG AGTTGTTAAA CTTCCTGAAG GTACTGAAAT     750
GGTTATGCCT GGAGACAACA TCGAAATGAT CGTTGAATTA ATCGCTCCAA     800
TCGCTGTTGA ACAAGGAACT AAG                                  823
```

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

```
CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACTC      50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTACCTTA CATCGTTGTA     100
TTCTTAAACA AATGCGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT     150
AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG     200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT     250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT     300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG     350
ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG     400
CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA     450
AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC     500
TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT     550
GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT     600
AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG     650
AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC     700
TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA     750
AATGGTAATG CCTGGTGACA ACATCGAAAT GACTATCGAA CTTATCGCTC     800
CAATCGCTAT CGAAGAGGGA ACTAA                               825
```

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

```
CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACAC      50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTTCCTTA CATCGTTGTA     100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAATTAT TAGAATTAGT     150
AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG     200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT     250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT     300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG     350
ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG     400
```

CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA 450
AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC 500
TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT 550
GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT 600
AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG 650
AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA 750
AATGGTAATG CCTGGTGACA ACATTGAAAT GACTATCGAA CTTATCGCTC 800
CAATCGCTAT CGAAGAGGGA ACTAAATTC 829

2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacteroides distasonis*
(B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

CGGTGCTATC ATCGTAGTTG CTGCTACTGA TGGTCCTATG CCTCAAACTC 50
GCGAGCACAT CCTTTTGGCT CGTCAGGTAA ACGTTCCGAG ATTGGTTGTA 100
TTCATGAACA AGTGTGACAT GGTTGACGAC GAGGAAATGT TGGAATTGGT 150
TGAGATGGAG ATGAGAGAGT TGCTTTCATT CTATCAATTC GACGGTGACA 200
ACACTCCGAT CATCCGTGGT TCTGCTCTTG GTGCATTGAA CGGTGATGCT 250
CAATGGGAAG ATAAAGTAAT GGAGTTGATG GAAGCTTGTG ATACTTGGAT 300
TCCTCTGCCT CCGCGCGAAA TCGACAAGCC GTTCTTGATG CCGGTTGAGG 350
ACGTATTCTC AATCACGGGT CGTGGTACTG TTGCTACAGG TCGTATCGAG 400
ACAGGTATTG TTAAGGTTGG TGAGGAAGTT CAGATCATCG GTCTTGGCGC 450
TGCTGGTAAG AAATCTGTTG TTACAGGTGT TGAGATGTTC CGTAAGTTAT 500
TGGATCAAGG TGAGGCTGGT GATAACGTTG GTTTGTTGCT TCGCGGTATC 550
GATAAGAATG AGATCAAGCG TGGTATGGTA ATCTGCCACC CGGGTCAGGT 600
TAAAGAGCAT TCTAAGTTCA AGGCTGAGGT TTATATCTTG AAGAAAGAGG 650
AAGGTGGTCG TCACACTCCG TTCCACAACA AATATCGTCC TCAGTTCTAT 700
ATCCGTACAT TGGATGTAAC TGGTGAGATC ACTTTGCCGG AAGGAACTGA 750
AATGGTAATG CCGGGTGATA ACGTAACGAT CGAGGTTGAG TTGATCTATC 800
CGGTAGCATG TAGCGTAG 818

2) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 639 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

GGTCCTATGC CTCAAACACG TGAACACATC TTGTTATCAC GTAACGTTGG 50
TGTACCATAC ATCGTTGTTT TCTTAAACAA AATGGATATG GTTGATGACG 100
AAGAATTACT AGAATTAGTT GAAATGGAAG TTCGTGACTT ATTGTCAGAA 150
TATGACTTCC CAGGCGACGA TGTTCCTGTA ATCGCTGGTT CTGCTTTGAA 200
AGCTCTTGAA GGCGATGCTT CATACGAAGA AAAAATCATG GAATTAATGG 250
CTGCAGTTGA CGAATACGTT CCAACTCCAG AACGTGACAC TGACAAACCA 300
TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT 350
TGCTACAGGC CGTGTTGAAC GTGGACAAGT TCGCGTTGGT GACGAAGTTG 400
AAATCGTTGG TATTGCTGAA GAAACTGCTA AAACAACTGT AACTGGTGTT 450
GAAATGTTCC GTAAATTGTT AGACTATGCT GAAGCAGGGG ATAACATTGG 500
TGCATTGCTA CGTGGTGTTG CTCGTGAAGA CATCCAACGT GGACAAGTAT 550
TGGCTAAAGC TGGTACAATC ACACCTCATA CAAAATTTAA AGCTGAAGTT 600
TACGTTTTAA CAAAAGAAGA AGGTGGACGT CACACACCA 639

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 692 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: CSG 197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

GAACACATTC TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT 50
CTTAAACAAA GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG 100
AAATGGAAGT TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT 150
GTACCTGTAA TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA 200
CTATGAGCAA AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC 250
CAACACCAGA ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC 300
GTATTCTCAA TCACTGGTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG 350
TGGTCAAATC AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG 400
AATCAAGCAA AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA 450
GACTACGCTG AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTTC 500
ACGTGATGAC GTACAACGTG GTCAAGTTTT AGCTGCTCCT GGTACTATTA 550
CACCACATAC AAAATTCAAA GCGGATGTTT ACGTTTTATC TAAAGATGAA 600
GGTGGTCGTC ATACACCATT CTTCACTAAC TACCGCCCAC AATTCTATTT 650
CCGTACTACT GACGTAACTG GTGTTGTTAA CTTACCAGAA GG 692

2) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacteroides ovatus*
(B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

```
CGGTGCTATC ATCGTTTGTG CTGCAACTGA TGGTCCGATG CCTCAAACTC      50
GCGAACACAT TCTGTTAGCT CGTCAGGTAA ACGTACCTCG TCTGGTTGTA     100
TTCTTGAACA AATGCGATAT GGTAGACGAC GAAGAAATGT TGGAACTCGT     150
TGAAATGGAA ATGAGAGAAC TCCTTTCATT CTATGATTTC GATGGTGACA     200
ATACTCCTAT CATCCGTGGT TCTGCTCTTG GCGCATTGAA CGGTGTTGAA     250
AAATGGGAAG ACAAAGTTAT GGAACTGATG GATGCAGTTG ATAACTGGAT     300
TCCACTGCCT CCGCGCGATG TTGATAAACC ATTCTTGATG CCGGTTGAAG     350
ACGTGTTCTC TATCACAGGT CGTGGTACTG TAGCAACAGG TCGTATCGAA     400
ACAGGTGTCA TCCACGTTGG TGATGAAGTC GAAATTCTTG GTTTAGGTGA     450
AGATAAGAAA TCAGTTGTAA CTGGTGTTGA AATGTTCCGT AAACTGTTGG     500
ATCAAGGTGA AGCTGGTGAC AACGTAGGTC TTTTGCTTCG TGGTATTGAC     550
AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAACCAG GTCAGATTAA     600
ACCGCACTCT AAATTCAAAG CTGAGGTTTA TATCTTGAAG AAAGAAGAAG     650
GTGGTCGTCA CACTCCGTTC CACAACAAAT ACCGTCCTCA GTTCTACTTG     700
CGTACTATGG ACTGTACAGG TGAAATCACT TTGCCGGAAG GAACAGAAAT     750
GGTAATGCCG GGTGATAACG TAACTATTAC AGTTGAGTTG ATTTACCCAG     800
TAGCATTGAA CCCGGGCTTC G                                    821
```

2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

```
TGGTGCGATT TTGGTTGTTT CAGCTGCTGA TGGTCCGATG CCTCAAACAC      50
GTGAGCATAT TCTTCTTGCC CGTCAGGTTG GTGTTCCAGC GATTGTTGTT     100
TTTCTTAATA AGGTTGATCA GGTTGATGAT GCTGAGCTTT TGGAGCTTGT     150
TGAGCTTGAA GTTCGGGAGT TATTGTCGAA ATATGATTTT CCAGGAGACG     200
ATATTCCGAT CGTTAAAGGT TCTGCTTTGG CAGCGCTTGA AGATAAAGAT     250
AAAAGCATTG GTGAAGATGC GGTTCGTCTT TTGATGAGTG AAGTTGATAA     300
TTATATACCG ACGCCTGAAC GTCCTGTTGA TCAGCCGTTT TTGATGCCAA     350
TTGAAGATGT TTTTTCGATT TCGGGTCGTG GAACTGTTGT GACGGGTCGT     400
GTTGAGCGTG GTGTTATTAA GGTTGGTGAA GAAGTTGAGA TTATCGGCAT     450
TCGTCCAACT TCTAAGACAA CAGTTACAGG GGTTGAAATG TTCCGCAAGC     500
TTTTAGATCA GGGGCAAGCG GGTGATAATA TTGGAGCGCT GCTTCGTGGT     550
ATTGATCGTG AAGGGATTGA GCGTGGACAA GTTTTGGCGA AGCCTGCTTC     600
GGTTACACCT CATACGAGAT TTAAAGCAGA GGCTTACATT TTGACGAAAG     650
ATGAAGGTGG TCGTCATACT CCATTTTTCA CGAATTATCG TCCTCAGTTT     700
TATTTCCGTA CTACGGATGT AACGGGAATT GTTACGCTTC CAGAAGGTAC     750
```

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
TTCCAATTGC CATGGAAGAA AAACTTCGTT TTGCTATC 838

2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bifidobacterium adolescentis*
(B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
GCTCTGAACA AGTGCGATAT GGTCGACGAC GACGAGCTCA TCGAGCTCGT 150
TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC 400
CGTGTCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG 700
TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bifidobacterium dentium*
(B) STRAIN: ATCC 27534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
GCCCTGAACA AGTGCGATAT GGTCGACGAC GAAGAGCTCA TCGAGCTCGT 150

```
TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAACGGCTTC GATCGCGATT      200
GCCCGGTCAT CCACACCTCC GCCTACGGCG CGCTGCACGA TGACGCTCCG      250
GACCACGACA AGTGGGTTGA GTCCGTCAAG GAACTCATGA AGGCCGTCGA      300
CGAGTACATC CCGACCCCGA CCCACGATCT GGACAAGCCG TTCCTGATGC      350
CGATCGAAGA TGTGTTCACC ATCTCCGGCC GTGGCACCGT GGTTACCGGC      400
CGTGTCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTTG AGATCGTCGG      450
CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA      500
AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC      550
GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG      600
CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA      650
AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG      700
TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG      750
CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA      800
TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG                  839
```

2) INFORMATION FOR SEQ ID NO: 15

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 838 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
- (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

```
TGGCGCGATC CTGGTGGTTT CGGCTGCTGA CGGCCCGATG CCGCAGACCC       50
GCGAGCACAT CCTGCTTGCC CGTCAGGTTG GCGTTCCGGC GATCGTCGTG      100
TTCCTCAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT      150
TGAACTGGAA GTGCGCGAAC TTCTGTCGAA GTACGAATTC CCCGGCGACG      200
AAATCCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCC      250
AAGGAACTGG GCGAAGATGC CATCCGCAAC CTGATGGACG CGGTTGACAG      300
CTACATTCCG ACCCCGGAAC GCCCGATCGA CCAGCCGTTC CTGATGCCGA      350
TCGAAGACGT GTTCTCGATC TCCGGCCGTG GTACGGTTGT GACGGGTCGC      400
GTTGAGCGCG GTATCGTTAA GGTCGGTGAA GAAGTTGAAA TCGTCGGCAT      450
CAAGGCGACG ACGAAGACCA CGGTTACCGG CGTTGAAATG TTCCGCAAGC      500
TGCTCGACCA GGGCCAGGCT GGCGACAACA TTGGCGCGCT GATCCGCGGC      550
GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTC      600
TGTGAAGCCG CACACCAAGT TTAAGGCAGA AGCCTATATT CTGACCAAGG      650
ACGAAGGTGG CCGTCATACG CCGTTCTTCA CCAACTACCG TCCGCAGTTC      700
TACTTCCGTA CGACGGACGT GACGGGTGTT GTGACGCTTC CGGCTGGCAC      750
GGAAATGGTC ATGCCTGGCG ATAACGTCGC CATGGACGTT ACCCTGATCG      800
TGCCGATCGC CATGGAAGAG AAGCTTCGCT TCGCTATC                   838
```

2) INFORMATION FOR SEQ ID NO: 16

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 771 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Burkholderia cepacia*
(B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

```
GGCAGCAGAC GGCCCGATGC CGCAAACGCG TGAGCACATC CTGCTGGCGC      50
GTCAGGTTGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA GTGCGACATG     100
GTGGACGACG CCGAACTGCT CGAGCTGGTC GAGATGGAAG TTCGCGAACT     150
CCTGTCGAAG TACGACTTCC CGGGCGACGA CACGCCGATC GTGAAGGGTT     200
CGGCGAAGCT GGCGCTGGAA GGCGACACGG GCGAGCTGGG CGAAGTGGCG     250
ATCATGAGCC TGGCCGACGC GCTGGACACG TACATCCCGA CGCCGGAGCG     300
TGCAGTTGAC GGCGCGTTCC TGATGCCGGT GGAAGACGTG TTCTCGATCT     350
CGGGCCGCGG TACGGTGGTG ACGGGTCGTG TCGAGCGCGG CATCGTGAAG     400
GTCGGCGAAG AAATCGAAAT CGTCGGTATC AAGCCGACGG TGAAGACGAC     450
CTGCACGGGC GTTGAAATGT TCCGCAAGCT GCTGGACCAA GGTCAAGCAG     500
GCGACAACGT TGGTATCCTG CTGCGCGGCA CGAAGCGTGA AGACGTGGAG     550
CGTGGCCAGG TTCTGGCGAA GCCGGGTTCG ATCACGCCGC ACACGCACTT     600
CACGGCTGAA GTGTACGTGC TGAGCAAGGA CGAAGGCGGC CGTCACACGC     650
CGTTCTTCAA CAACTACCGT CCGCAGTTCT ACTTCCGTAC GACGGACGTG     700
ACGGGCTCGA TCGAGCTGCC GAAGGACAAG GAAATGGTGA TGCCGGGCGA     750
CAACGTGTCG ATCACGGTGA A                                   771
```

2) INFORMATION FOR SEQ ID NO: 17

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cedecea davisae*
(B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

```
GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTTGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTA     150
GAAATGGAAG TTCGTGAACT TCTGTCCCAG TACGACTTCC CGGGCGACGA     200
TACTCCAATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGAAGCAG     250
AGTGGGAAGC TAAAATCGTT GAGCTGGCTG GCTACCTGGA TTCTTACATC     300
CCTGAGCCAG AGCGTGCTAT CGATAAGCCG TTCCTGCTGC CAATCGAAGA     350
CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT     450
ACTGCGAAAT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCAGG CTCTATCAAG     600
CCACACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC     700
GTACAACTGA CGTGACCGGC ACCATCGAAC TGCCAGAAGG CGTTGAGATG     750
GTAATGCCTG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT     800
```

CGCGATGGAT GACGGTCTGC GTTTCGCAA

2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cedecea neteri*
(B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

```
CGCTATCCTG GTTGTTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG      50
AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC     100
CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA     150
AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGACTTCCCG GGCGATGACA     200
CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG     250
TGGGAAGCTA AAATYGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC     300
AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG     350
TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC     400
GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC     450
TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG     500
AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT     550
GAAGAAATCG AACGTGGTCA GGTTCTGGCT AAGCCAGGCT CTATCAAGCC     600
GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG     650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT     700
ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT     750
AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG     800
CGATGGACGA CGGTCTGCGT TTCG                                 824
```

2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cedecea lapagei*
(B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

```
CGCTATTCTG GTTGTTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG      50
AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTC     100
CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA     150
AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGACTTCCCA GGCGATGATA     200
```

CCCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCG TGTAGAGCGC 400
GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
TGCGAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTTCTGGCT AAGCCAGGCT CTATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG 650
GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT 700
ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
AATGCCAGGT GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
CGATGGACGA CGGTCTGCGT TTCGCAA 827

2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydia pneumoniae*
(B) STRAIN: CWL 029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAAACT 50
AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT 100
TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG 150
ACCTTGTTGA GATGGAACTT AGTGAGCTTC TTGAAGAAAA AGGCTACAAA 200
GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC 250
AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA 300
TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA 350
GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA 400
GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG 450
AGACTAAAGA AACAATCGTT ACTGGAGTCG AAATGTTCAG GAAAGAACTT 500
CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTACTCCTCA GAGGTATTGG 550
AAAGAACGAT GTTGAAAGAG GTATGGTGGT TTGTCAGCCT AACAGCGTGA 600
AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCTTCA GAAAGAAGAA 650
GGCGGACGTC ATAAGCCTTT CTTCAGCGGA TACAGACCTC AGTTCTTCTT 700
CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAACTGAAA 750
TGGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA 800
GTTGCTCTTG AAGAAGGAAT GAGATTTGCA A 831

2) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydia psittaci*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

```
TGGAGCGATT CTCGTTGTTT CCGCTACTGA CGGTGCGATG CCTCAGACCA      50
AAGAACATAT TCTTTTGGCG AGACAGGTTG GTGTTCCTTA CATCGTTGTT     100
TTCCTTAACA AAATCGATAT GATTTCTCAA GAAGATGCTG AGCTCGTAGA     150
CTTAGTTGAA ATGGAATTGT CCGAACTTCT AGAAGAAAAA GGTTATAAAG     200
GTTGCCCAAT TATCCGTGGT TCTGCTTTGA AAGCCTTAGA AGGTGATGCA     250
AGCTACGTTG AAAAAATTCG CGAGTTAATG CAAGCAGTGG ATGATAACAT     300
CCCTACTCCA GAGCGTGAAG TTGATAAGCC TTTCTTAATG CCTATCGAAG     350
ACGTATTCTC TATTTCTGGT CGTGGTACTG TGGTCACAGG ACGTATCGAG     400
CGTGGAATCG TTAAAGTGGG TGATAAAGTA CAGATTGTTG GTTTAAGAGA     450
TACTAGAGAG ACAATTGTTA CCGGTGTGGA AATGTTCAGA AAAGAACTTC     500
CAGAAGGTCA AGCAGGGGAA AACGTTGGTT TGCTCCTCAG AGGTATCGGT     550
AAGAATGACG TTGAACGTGG TATGGTTATC TGCCAACCTA ATAGCGTGAA     600
ATCTCACACA CAATTTAAAG GTGCTGTCTA CATTCTACAA AAAGAAGAGG     650
GTGGACGTCA TAAACCTTTC TTTACCGGAT ACAGACCTCA GTTCTTCTTC     700
CGTACAACAG ATGTTACAGG TGTTGTAACT CTCCCAGAAG GTACAGAGAT     750
GGTTATGCCA GGCGATAACG TTGAATTCGA AGTTCAATTA ATTAGCCCAG     800
TAGCTCTAGA AGAAGGTATG AGATTT                               826
```

2) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydia trachomatis*
(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

```
GGGGCTATTC TAGTAGTTTC TGCAACAGAC GGAGCTATGC CTCAAACTAA      50
AGAGCATATT CTTTTGGCAA GACAAGTTGG GGTTCCTTAC ATCGTTGTTT     100
TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC     150
TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG     200
GTGTCCAATC ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGGGATGCTG     250
CATACATAGA GAAAGTTCGA GAGCTAATGC AAGCCGTCGA TGATAATATC     300
CCTACTCCAG AAAGAGAAAT TGACAAGCCT TTCTTAATGC CCATTGAGGA     350
CGTGTTCTCT ATCTCCGGAC GAGGAACTGT AGTAACTGGA CGTATTGAGC     400
GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT     450
ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTCAGAA AAGAACTCCC     500
AGAAGGTCGT GCAGGAGAGA ATGTTGGATT GCTCCTCAGA GGTATTGGTA     550
AGAACGATGT GGAAAGAGGA ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA     600
CCTCATACAC GGTTTAAGTG TGCTGTTTAC GTTCTGCAAA AAGAAGAAGG     650
TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA TTCTTCTTCC     700
GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG     750
GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAGTTGA TTAGCCCTGT     800
GGCTTTAGAA GAAGGTATGA GA                                   822
```

2) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chryseobacterium meningosepticum*
(B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAACTA 50
GAGAACACAT CCTACTTTGC CGTCAGGTAA ACGTACCTAG AATTGTTGTG 100
TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAATTGT TAGAGCTTGT 150
TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA 200
ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTTAA CGGTGATGCT 250
AAGTGGGTAG CTACTGTAGA AGCTCTAATG GATGCTGTTG ATACTTGGAT 300
CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCCTTATG CCAATCGAAG 350
ACGTATTCTC TATTACAGGT AGAGGTACTG TAGCAACTGG TAGAATCGAG 400
GCTGGTGTAA TCAACACAGG TGATCCTGTT GACATCGTAG GTATGGGTGA 450
CGAGAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC 500
TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT 550
GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTCAGT 600
TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG 650
AAGGTGGACG TCACACTCCA TTCCACAACA AATACCGTCC TCAGTTCTAT 700
GTAAGAACTA CTGACGTTAC AGGTGAAATC TTCTTACCAG AAGGTGTAGA 750
AATGGTAATG CCTGGTGATA ACTTAACTAT CACTGTAGAA TTGTTACAAC 800
CAATCGCTCT TAACGAGGGT CTTAGATTCG CGATC 835

2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter amalonaticus*
(B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG 200
ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250

GAGTGGGAAG CGAAAATCAT CGAACTGGCC GGCTTCCTGG ATTCTTACAT 300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTGCCAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCWCCATCAA 600
GCCGCACACC ATGTTCGAAT CYGAAGTGTA CATCCTGTCC AAAGACGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTTGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGG 816

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter braakii*
(B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CGCGATCCTG GTTGTTGCTG CAACTGACGG CCCGATGCCG CAGACTCGTG 50
AGCACATCCT GCTGGGTCGY CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA 150
AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGATTTCCCG GGCGACGACA 200
CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAWGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATCCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCT ATCGAAGACG 350
TATTCTCCAT CTCTGGTCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC 400
GGTATCATCA AAGTTGGTGA AGAAGTTGAA ATCGTTGGTA TCAARGACAC 450
TGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAGCGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCT CTATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG 650
GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCGCAGTT CTACTTCCGT 700
ACTACTGACG TGACTGGTAC CATCGAACTG CCGGAAGGCG TTGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
CGATGGACGA CGGTCTGCGT TTCGC 825

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter koseri*
(B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
TGAGATGGAA GTGCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG     200
ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAMGCT     250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT     300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG     400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATYGTTG GTATCAAAGA     450
GACTGCGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GYTCCATCAA     600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATYCTGTCY AAAGATGAAG     650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA     800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA                           830
```

2) INFORMATION FOR SEQ ID NO: 27

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter farmeri*
(B) STRAIN: ATCC 51112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

```
CGCGATCCTG GTTGTTGCTG CGACTGACGG CCCGATGCCG CAGACTCGTG      50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTC     100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA     150
GATGGAAGTT CGTGAACTGC TGTCTCAGTA CGATTTCCCG GGCGACGACA     200
CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG     250
TGGGAAGCGA AAATCATCGA ACTGGCAGGC TTCCTGGATT CTTACATCCC     300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG     350
TATTCTCCAT CTCTGGTCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC     400
GGTATCATCA AAGTGGGTGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC     450
TGCCAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG     500
AAGGCCGTGC TGGTGAGAAC GTAGGTGTTC TGCTGCGTGG TATCAAACGT     550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCW CCATCAAGCC     600
RCACACTATG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG     650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT     700
ACGACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGTG TTGAGATGGT     750
TATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG     800
CGATGGACGA CGGTCTGCGT TTCGCAA                              827
```

2) INFORMATION FOR SEQ ID NO: 28

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter freundii*
(B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC 100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TAGAAATGGA 150
AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACTCCGA 200
TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGAAGC AGAGTGGGAA 250
GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCAGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCTATCGAA GACGTATTCT 350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTGCTAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
GTGCTGGTGA GAACGTTGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCTCTATCA AGCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGACGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
GACGTGACTG GTACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCGA 797

2) INFORMATION FOR SEQ ID NO: 29

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter sedlakii*
(B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

CGGCGCGATC CTGGTTGTTG CCGCGACTGA CGGCCCGATG CCGCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG 200
ACACGCCGAT CGTTCGTGGT TCAGCTCTGA AAGCGCTGGA AGGCGACGCA 250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300

TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTGCGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCGGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCGAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA TATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGTCTG CGTTTC 826

2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter werkmanii*
(B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

GCGATCCTGG TTGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA 50
GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC 100
TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150
ATGGAAGTTC GTGAACTTCT GTCTCAGTAC GATTTCCCGG GCGACGACAC 200
TCCGATCGTT CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GAAGCAGAGT 250
GGGAAGCGAA AATCATCGAA CTGGCTGGCT TTCTGGATTC TTACATCCCG 300
GAACCAGAGC GTGCGATTGA CAAGCCGTTC CTGCTRCCTA TCGAAGACGT 350
ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG 400
GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGACACC 450
GCTAAGTCTA CCTGTACCGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA 500
AGGCCGTGCT GGTGAGAACG TTGGTGTTCT GCTGCGTGGT ATCAAACGTG 550
AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCTC TATCAAGCCG 600
CACACCAAGT TCGAATCTGA AGTGTACATC CTGTCCAAAG ACGAAGGCGG 650
CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA 700
CTACTGACGT GACTGGTACC ATCGAACTGC CGGAAGGCGT AGAGATGGTA 750
ATGCCGGGCG ACAACATYAA AATGGTTGTT ACYCTGATCC ACCCGATCGC 800
GATGGACGAC GGTCTGCGTT TCG 823

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter youngae*
(B) STRAIN: ATCC 29935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

```
GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTA     150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC CGGGCGACGA     200
TACGCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGAAGCAG     250
AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC     300
CCGGAACCAG AACGTGCTAT CGATAAGCCG TTCCTGCTGC CAATCGAAGA     350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACTGGT CGTGTAGAAC     400
GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG     450
ACTGCCAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCTATCAAG     600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     700
GTACTACTGA CGTGACGGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG     750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT     800
CGCGATGGAT GACGGTCTGC GTTTCG                               826
```

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium perfringens*
(B) STRAIN: ATCC 13124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

```
CGGAGCTATA TTAGTTTGTT CAGCAGCTGA TGGTCCAATG CCTCAAACAA      50
GAGAGCACAT CTTATTATCA TCAAGAGTTG GAGTTGACCA CATCGTAGTA     100
TTCTTAAACA AAGCAGATAT GGTTGACGAC GAAGAATTAT TAGAATTAGT     150
TGAAATGGAA GTTAGAGAGT TATTAAGCGA GTACAACTTC CCAGGAGACG     200
AYATTCCAGT AATCAARGGA TCAGCTTTAG TAGCATTAGA AAACCCAACT     250
GACGAAGCTG CAACAGCTTG TATCAGAGAG TTAATGGATG CTGTAGATAG     300
CTACATCCCA ACACCAGAAA GAGCAACAGA TAAGCCATTC TTAATGCCAG     350
TAGAGGACGT ATTCACAATC ACTGGTAGAG GAACAGTTGC AACAGGAAGA     400
GTTGAAAGAG GAGTTCTACA TGTAGGAGAC GAAGTAGAAG TAATCGGATT     450
AACTGAAGAA AGAAGAAAAA CTGTTGTAAC AGGAATCGAA ATGTTCAGAA     500
AGTTATTAGA TGAAGCACAA GCTGGAGATA ACATCGGAGC ATTATTAAGA     550
GGTATCCAAA GAACTGAYAT CGAAAGAGGT CAAGTTTTAG CTCAAGTTGG     600
AACAATCAAC CCACACAAAA AATTCGTAGG TCAAGTATAC GTACTTAAAA     650
AAGAAGAAGG TGGAAGACAT ACTCCATTCT TCGATGGATA CAGACCACAA     700
TTCTACTTCA GAACAACAGA CGTTACAGGA TCAATCAAAT TACCAGAAGG     750
AATGGAAATG GTTATGCCTG GAGACCACAT CGACATGGAA GTTGAATTAA     800
TCACAGAAAT CGCTATGGAY GAAGGATTAA GATTCGCTAT C             841
```

2) INFORMATION FOR SEQ ID NO: 33

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Comamonas acidovorans*
(B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

```
CGGCGCCATC CTGGTGTGCT CGGCCGCTGA CGGCCCCATG CCCCAGACCC      50
GCGAGCACAT CCTGCTGGCC CGTCAGGTGG GCGTGCCCTA CATCATCGTG     100
TTCCTGAACA AGTGCGACAT GGTGGACGAC GAAGAGCTGC TGGAACTGGT     150
CGAAATGGAA GTGCGCGAGC TGCTTGCCAA GTACGACTTC CCCGGCGACG     200
ACACCCCCAT CATCCGCGGC TCGGCCAAGC TGGCCCTGGA AGGCGACCAG     250
TCCGACAAGG GCGAACCTGC CATCCTGCGC CTGGCTGAAG CACTGGACTC     300
CTACATCCCC ACGCCCGAGC GCGCTGTGGA CGGCGCCTTT GCAATGCCCG     350
TGGAAGACGT GTTCTCGATC TCTGGCCGTG GCACCGTGGT GACTGGCCGT     400
ATCGAGCGCG GCATCATCAA GGTCGGCGAA GAAATCGAAA TCGTCGGTAT     450
CCGCGACACC CAGAAGACCA TCGTCACCGG CGTGGAAATG TTCCGCAAGC     500
TGCTGGACCA AGGTCAAGCT GGCGACAACG TGGGTCTGCT GCTGCGCGGC     550
ACCAAGCGTG AAGACGTGGA ACGCGGCCAA GTGCTGTGCA AGCCCGGCTC     600
CATCAAGCCC CACACCCACT TCACGGCTGA GGTGTACGTG CTGTCCAAGG     650
ACGAAGGTGG TCGCCACACT CCGTTCTTCA ACAACTACCG TCCCCAGTTC     700
TATTTCCGTA CGACCGACGT GACCGGCTCC ATCGAGCTGC CCGCCGACAA     750
GGAAATGGTG ATGCCTGGCG ACAACGTGTC GATCACCGTC AAGCTGATCG     800
CCCCCATCGC CATGGAAGAA GG                                   822
```

2) INFORMATION FOR SEQ ID NO: 34

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium bovis*
(B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

```
GCCGCAGACC CGTGAGCACG TCCTCCTGGC CCGTCAGGTC GGTGTGCCCT      50
ACATCCTCGT CGCCCTCAAC AAGTGCGACA TGGTCGACGA CGAGGACCTC     100
ATCGAGCTCG TCGAGATGGA GGTCCGTGAG CTCCTCGCCG AGCAGGACTA     150
CGACGAGGAC GCCCCGATCA TCCACATCTC CGCCCTCAAG GCCCTCGAGG     200
GTGACCCGGA GTGGACGCAG CGCATCGTCG ACCTCATGAA GGCCTGCGAC     250
GACGCCATCC CGGATCCGGA GCGCGAGACG GACAAGCCGT TCCTCATGCC     300
```

GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC 350
GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT 400
ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA 450
CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC 500
GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG 550
GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC 600
CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTCGACAAC TACCGTCCGC 650
AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG 700
GG 702

2) INFORMATION FOR SEQ ID NO: 35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium cervicis*
(B) STRAIN: NCTC 10604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GGCGTTCCGA 50
CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG 100
CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT 150
CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG 200
GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC 250
ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC 300
GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC 350
GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT 400
ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA 450
GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG 500
GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT 550
TCGATCACCC CGCACACCAA CTTCACCGGA CAGGTCTACA TCCTCAAGAA 600
GGAAGAAGGC GGTCGTCACA ACCCGTTCTT CTCGAACTAC CGTCCGCAGT 650
TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC 689

2) INFORMATION FOR SEQ ID NO: 36

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium flavescens*
(B) STRAIN: ATCC 10340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

GGTTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTC 50
TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG 100
TGCGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT 150
CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC 200
ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC 250
ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG 300
CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA 350
CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG 400
GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAGT CCATCTCCAC 450
CACCGTTACC GGTATCGAAA TGTTCCGCAA GATGATGGAC TACACCGAGG 500
CTGGCGACAA CTGTGGTCTG CTTCTGCGTG GTACCAAGCG TGAAGAGGTC 550
GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA 600
GTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA 650
CCCCGTTCAT GGACAACTAC CGTCCGCAGT TCTACTTCCG TACCACTGAC 700
GTGACCGGCG TTGTTCACCT GCCTGAGGGC ACCGAGATGG TCATGCCTGG 750
CGACAACGTT GATATGACCG TTGAGCTCAT CCAGCCCGTC GCTAGGATGA 800
GGGC 804

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 692 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium kutscheri*
(B) STRAIN: ATCC 15677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

TGCCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCT 50
TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT 100
CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT 150
ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG 200
GGCGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTGA 250
TGACTCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC 300
CTATCGAGGA TATCTTCACC ATCACCGGTC GTGGCACCGT TGTTACCGGT 350
CGTGTTGAGC GCGGTTCCTT GAAGGTGAAT GAGGACGTCG AGATCATCGG 400
CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC 450
GTAAGCTTCT TGATTACACC GAAGCTGGCG ATAACTGTGG TCTGCTTCTT 500
CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTCAGGTTG TTGTTAAGCC 550
AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT 600
CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA 650
CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG 692

2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium minutissimum*
(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

```
CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG      50
TTCTTCTGGC CCGCCAGGTT GGCGTTCCGT ACATCCTCGT TGCACTGAAC     100
AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA     150
GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG     200
TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG     250
TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA     300
GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA     350
TTACCGGCCG CGGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG     400
AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC     450
CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG     500
AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG     550
GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GGCGCTTACA CCCCGCACAC     600
CAAGTTCGAG GGTTCCGTCT ACGTCCTGAA GAAGGAAGAG GGCGGCCGCC     650
ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC     700
GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC     750
GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA       797
```

2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium mycetoides*
(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```
GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT      50
ACATCCTCGT TGCGCTGAAC AAGTGCGACA TGGTTGATGA TGAGGAGATC     100
ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA     150
CGACGAGGAC GCCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG     200
GCGACGAGAA GTGGGTTCAG TCCGTGCTCG ACCTCATGCA GGCGTGCGAC     250
GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC     300
GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC     350
GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACGAGGTCGA GATCATCGGC     400
ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA     450
CAAGCTGCTC GATACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC     500
GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG     550
GGCGCCTACA CCCCGCACAC CAAGTTCGAG GGTTCCGTCT ACGTCCTGTC     600
CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC     650
AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG     700
GG                                                        702
```

2) INFORMATION FOR SEQ ID NO: 40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 674 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium pseudogenitalium*
(B) STRAIN: ATCC 33038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGCGCTGA ACAAGTGCGA 50
CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG 100
AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC 150
TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT 200
TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA 250
CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC 300
CGCGGTACCG TTGTTACCGG CCGTGTTGAG CGTGGCCGTC TGAACGTCAA 350
CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG 400
TTACCGGTAT CGAGATGTTC CGCAAGATGA TGGACTACAC CGAGGCTGGC 450
GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG 500
TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCG 550
AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG 600
TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC 650
CGGTGTTGTT CACCTGCCAG AGGG 674

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 694 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium renale*
(B) STRAIN: ATCC 19412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT 50
TACATCCTCG TTGCACTGAA CAAGTGCGAC ATGGTCGACG ACGAAGAAAT 100
CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT 150
ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC 200
GGCGAGCAGA AGTGGGTTGA CTCCATCGTC GAACTGATGG AAGCTTGCGA 250
CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC 300
CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC 350
CGTGTCGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG 400

TATCAAGGAC AAGTCCCAGA AGACCACCGT CACCGGTATC GAGATGTTCC 450
GCAAGATGCT GGACTACACC GAAGCTGGCG ACAACTGTGG TCTGCTGCTC 500
CGCGGCATCG GCCGTGAGGA TGTCGAGCGT GGCCAGGTTA TCATCAAGCC 550
AGGCGCTTAC ACCCCTCACT CTGAGTTCGA GGGCTCTGTC TACGTCCTGT 600
CCAAGGACGA GGGTGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA 650
CAGTTCTACT TCCGCACCAC CGACGTGACC GGCGTTGTGC ACCT 694

2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium ulcerans*
(B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

GCCGCAGACC CGCGAGCACG TTCTGCTGGC TCGCCAGGTT GGCGTTCCKT 50
ACATCCTSGT TGCACTGAAC AAGTGCGACA TGGTTGACGA TGAGGARCTC 100
CTSGAGCTCG TCGAGATGGA GGTCCGCGAG CTGCTGGCTG AGCAGGACTA 150
CGACGAGGAA GCTCCGRTCG TTCACATCTC CGCWCTGAAC GCCCTGGACG 200
GCGACSAGAA GTGGGCTVAC TCCATCCTCG AGCTGATGCA GGCTTGCGAC 250
GAGTCCATCC CGGATCCGGA GCGCGAGACC GACAAGCCGT TCCTGATGCC 300
GATTGAGGAC ATCTTCACCA TTACCGGTCG CGGYACCGTT GTTACCGGCC 350
GTGTTGAGCG TGGCDTCCTG AACGTSAACG ACGASGTTGA GATCATGGGY 400
ATCCGGGAGA AGTCCCAGAA GACCACCGTY ACCKSCATCG AGATGTTCAA 450
CAAGMTGMTG GACWCCGCAG AGGCTGGCGA CAACGCTGSW CTGCTGCTGC 500
GTGGTMTSAA GCGTGAGGAC GTTGAGCGTG GCCAGATCAT CGYTAAGCCG 550
GGCGCKTACA CCCCGCACAC CGAGTTCGAG GGCTCCGTCT ACGTCCTGTC 600
CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC 650
AGTTCTACTT CCGCACCACC GACGTSACCG GTGTTGT 687

2) INFORMATION FOR SEQ ID NO: 43

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 778 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium urealyticum*
(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT 50
TCTGCTGGCT CGCCAGGTTG GCGTTCCGTA CATCCTCGTT GCACTGAACA 100

AGTGCGACAT GGTTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG 150
GTCCGCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCGT 200
CCCGATCTCC GCACTGGGCG CCCTGGACGG CGATCAGAAG TGGGTCGACT 250
CCATCCTCGA GCTCATGAAG GCTTGCGACG AGTCCATCCC GGACCCGGAG 300
CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT 350
TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTTGAGCGT GGCGTCCTGA 400
ACCTGAACGA CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG 450
ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA 500
GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG 550
TCGAGCGAGG CCAGATCATC GCTAAGCCGG GCGCTTACAC CCCGCACACC 600
GAGTTCGAGG GCTCCGTCTA CGTCCTGTCC AAGGACGAGG GCGGCCGTCA 650
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGTACCACCG 700
ACGTCACCGG TGTCGTTACC CTGCCAGAGG GCACCGACAT GGTCATGCCG 750
GGCGACAACG TTGAGATGAG CGTCAAGC 778

2) INFORMATION FOR SEQ ID NO: 44

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 703 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium xerosis*
(B) STRAIN: ATCC 373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

CGCAGACCCG TGAGCACGTC CTCCTGGCCC GCCAGGTCGG CGTCCCCTAC 50
ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT 100
CGAGCTCGTG GAGATGGAGG TGCGTGAGCT TCTCGCCGAG CAGGACTACG 150
ACGAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGGCGC CCTCAATGGC 200
GAAGAGAAGT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA 250
GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCCG 300
TCGAGGACAT CTTCACCATC ACCGGCCGCG GCACCGTCGC CACCGGTCGC 350
GTGGAGCGCG GCACCCTGAA GGTCAACGAC GAGGTCGAGA TCCTGGGCAT 400
CCAGGAGAAG TCCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA 450
AGCTGCTGGA CTCCGCCGAG GCCGGCGACA ACTGTGGCCT GCTGCTCCGC 500
GGCATCAAGC GCGAGGACAT CGAGCGCGGC CAGATCATCG CGAAGCCGGG 550
CGCCTACACC CCGCACACCG AGTTCGAGGG CTCCGTCTAC ATCCTGGCCA 600
AGGACGAGGG CGGCCGCCAC ACCCCGTTCT TCGACAACTA CCGTCCGCAG 650
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCGTGAAGC TGCCGGAGGG 700
CAC 703

2) INFORMATION FOR SEQ ID NO: 45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Coxiella burnetii*
(B) STRAIN: Nine Mile phase II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

```
GGAGCGATAT TGGTGGTGAG CGCAGCGGAC GGCCCGATGC CGCAAACGCG      50
GGAACACATT GTATTGGCGA AGCAAGTGGG TGTTCCGAAC ATAGTGGTTT     100
ACTTGAACAA AGCGGACATG GTGGATGACA AAGAGCTGTT GGAATTAGTG     150
GAAATGGAAG TGAGGGATTT ATTGAACAGT TATGATTTCC CTGGGGATGA     200
GACGCCGATA ATAGTGGGGT CAGCGTTAAA GGCGTTAGAA GGTGACAAGA     250
GTGAGGTTGG GGAGCCATCG ATAATCAAAT TAGTGGAAAC GATGGACACG     300
TACTTCCCGC AGCCGGAGCG AGCGATAGAC AAACCGTTTT TAATGCCGAT     350
CGAAGATGTG TTTTCGATAT CGGGCCGAGG GACGGTGGTG ACGGGACGCG     400
TAGAGCGAGG GATCATCAAA GTGGGCGACG AGATAGAGAT TGTGGGGATC     450
AAGGACACGA CGAAGACGAC GTGCACGGGC GTTGAGATGT TTCGCAAATT     500
ATTGGATGAA GGTCAAGCGG GTGACAACGT AGGAATTTTA TTGAGAGGGA     550
CGAAACGCGA AGAAGTGGAG CGTGGTCAAG TATTGGCGAA ACCGGGATCG     600
ATCACGCCAC ACAAGAAATT TGAGGCGGAG ATTTATGTGT TGTCGAAGGA     650
AGAAGGGGGA CGCCACACAC CGTTTTTACA AGGCTATCGA CCGCAATTTT     700
ATTTCCGCAC GACGGACGTG ACGGGCCAGT TATTGAGTTT ACCGGAGGGG     750
ATAGAGATGG TGATGCCGGG AGATAACGTG AAAGTGACGG TTGAATTGAT     800
TGCGCCGGTA GCGATGGATG AAGGGCTACG AT                        832
```

2) INFORMATION FOR SEQ ID NO: 46

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Edwardsiella hoshinae*
(B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

```
GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
TGAGCACATC CTGCTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT     150
GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA     200
TACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG     250
AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACGCTGGA CTCCTACATT     300
CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA     350
CGTATTCTCA ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTAGG TATCAAGCCG     450
ACCACCAAGA CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTACCAAGC     550
GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT     600
CCGCACACCA AGTTCGAATC AGAAGTGTAC ATCCTGAGCA AGGATGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGTTA CCGTCCGCAG TTCTACTTCC     700
GTACCACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG     750
GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT     800
CGCCATGGAC GATGGT                                         816
```

2) INFORMATION FOR SEQ ID NO: 47

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Edwardsiella tarda*
(B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
TGAGCACATC CTGTTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT 150
GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA 200
CACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG 250
AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACTCTGGA CTCCTACATC 300
CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCT ATCTCTGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTTGG TATCAAGCCG 450
ACCACCAAGA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAGC 550
GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT 600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGAGCA AGGATGAAGG 650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT 800
CGCCATGGAC GATGGTCTGC G 821

2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Eikenella corrodens*
(B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

CGGTGCCATC CTGGTGGTAT CCGCTGCTGA CGGCCCCATG CCTCAGACTC 50
GCGAACACAT CCTGTTGGCT CGTCAGGTAG GTGTACCCTA CATCCTCGTA 100
TTCATGAACA AATGCGACAT GGTAGATGAT GCCGAGCTGC TTGAGTTGGT 150
TGAGATGGAA ATCCGCGACC TGCTCTCCAG CTATGACTTC CCTGGTGACG 200
ACTGCCCGAT CGTACAAGGT TCCGCTCTCA AAGCCCTCGA AGGCGATGCC 250

GGTTACAAAG AAAAAATCTT CGAACTAGCT GCTGCTTTGG ATAGCTACAT 300
CCCCACTCCT CAACGTGCTG TAGACAAACC CTTCCTGTTG CCGATCGAAG 350
ACGTATTCTC TATCTCCGGC CGTGGTACCG TAGTAACCGG TCGTGTAGAG 400
CGCGGCATCA TCAAAGTAGG TGAAGAGATC GAAATCGTTG GTCTGAAGCC 450
CACTCAGAAA ACTACCTGTA CTGGCGTGGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGTCA GGCCGGTGAC AACGTAGGCG TACTGCTGCG CGGTACCAAA 550
CGTGAAGAAG TTGAGCGTGG TCAAGTATTG GCTAAACCCG GCACCATCAC 600
TCCGCACACC AAGTTCAAAG CCGAAGTATA CGTATTGAGC AAAGAAGAAG 650
GTGGTCGTCA CACCCCGTTC TTTGCCAACT ACCGTCCACA GTTCTACTTC 700
CGTACTACTG ACGTAACCGG TGCTGTAGAG CTGGAGCCTG GTGTAGAAAT 750
GGTTATGCCT GGTGAGAACG TAACCATCAC CGTAGAACTG ATTGCTCCGA 800
TTGCTATGGA AGAAGGTCTG CGCTTTGCGA 830

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter aerogenes*
(B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT 150
GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA 200
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC 300
CCRGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAC 450
ACCGCGAAAA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCTGGTGAGA ACGTAGGYGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CAGCATCAAG 600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG 650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGRTG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCGATGG 808

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter agglomerans*
(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AATGTGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG     200
ATACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAMGCW     250
GAGTGGGAAG CGAAAATCAT CGARCTGGCT GGCCACCTGG ATACCTATAT     300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG     350
ACGTATTCTC CATCTCCGGT CGCGGTACCG TTGTTACCGG TCGTGTAGAG     400
CGCGGTATCA TYAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
TACYGCGAAA TCAACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA     600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG     650
GCGGTCGTCA CACTCCGTTC TTCAAAGGCT ACCGTCCSCA GTTCTACTTC     700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA     800
TCGCGATGGA CGACGGTCTG CGTTCGCA                             828
```

2) INFORMATION FOR SEQ ID NO: 51

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter amnigenus*
(B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

```
TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACGC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG     200
ACACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAAGCA     250
GAGTGGGAAG CTAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCTTACAT     300
CCCGGAACCA GAACGTGCTA TCGATAAGCC ATTCCTGCTG CCAATCGAAG     350
ACGTATTCTC TATCTCCGGC CGTGGTACTG TTGTAACCGG TCGTGTAGAG     400
CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCAG GCTCAATCAA     600
GCCGCACACC AAATTCGAAT CTGAAGTTTA TATTCTGTCC AAAGATGAAG     650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC     700
CGTACAACTG ACGTGACCGG CACCATCGAA CTGCCAGAAG GCGTAGAGAT     750
GGTAATGCCA GGCGACAACA TTCAGATGGT TGTTACCCTG ATCCACCCAA     800
TCGCGATGGA TGACGGTCTG CGTTT                                825
```

2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter asburiae*
(B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTT CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG     200
ATACTCCAAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA     250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT     300
CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG     400
CGCGGTATCA TCAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA     600
GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG     650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC     700
CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT     750
GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA     800
TCGCGATGGA CGACGGTCTG CG                                   822
```

2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter cancerogenus*
(B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG     100
TTCCTGAACA AGTGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
AGAAATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCAGGCGACG     200
ACACTCCAAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAAGCT     250
```

GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
TACTGCKAAA TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
CGCGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA 600
GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACGCTG ATCCACCCAA 800
TCGCGATGGA CGACGGTCTG CGTTTC 826

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter cloacae*
(B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

GATCCTGGTA GTAGCTGCGA CTGACGGCCC AATGCCTCAG ACTCGTGAGC 50
ACATCCTGCT GGGTCGTCAG GTAGGCGTTC CTTACATCAT CGTGTTCCTG 100
AACAAATGCG ACATGGTTGA TGACGAAGAG CTGCTGGAAC TGGTAGAGAT 150
GGAAGTTCGT GAACTGCTGT CTCAGTACGA TTTCCCAGGC GACGATACCC 200
CAATCGTTCG TGGTTCTGCT CTGAAAGCGC TGGAAGGCGA CGCAGAGTGG 250
GAAGMGAAAA TCATCGAACT GGCTGGCTAC CTGGATTCTT ACATCCCAGA 300
ACCAGAGCGT GCGATTGAYA AGCCATTCCT GCTGCCAATC GAAGACGTAT 350
TCTCCATCTC CGGTCGTGGT ACCGTTGTTA CCGGTCGTGT AGAGCGCGGT 400
ATCATCAAAG TGGGTGAAGA AGTTGAAATC GTTGGTATCA AAGAGACTGC 450
GAAGTCTACC TGTACTGGCG TTGAAATGTT CCGCAAACTG CTGGACGAAG 500
GCCGTGCTGG TGAGAACGTT GGTGTTCTGC TGCGTGGTAT CAAACGTGAA 550
GAAATCGAAC GTGGTCAGGT TCTGGCGAAG CCAGGCTCAA TCAAGCCACA 600
CACCAAGTTC GAATCTGAAG TGTACATCCT GTCCAAAGAC GAAGGCGGCC 650
GTCATACTCC GTTCTTCAAA GGCTACCGTC CACAGTTCTA CTTCCGTACA 700
ACTGACGTGA CCGGTACCAT CGAACTGCCA GAAGGCGTAG AGGTGGTAAT 750
GCCAGGCGAC AACATCAAGA TGGTTGTGAC TCTGATCCAC CCAATCGCGA 800
TGGACG 806

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter gergoviae*
(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AGTGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG     200
ACACCCCGAT CGTTCGCGGT TCTGCGCTGA AAGCGCTGGA AGGCGACGCA     250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCCACCTGG ATACCTAYAT     300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG     350
ACGTATTCTC CATTTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG     400
CGCGGTATCA TCAAGGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
CACCGCGAAA ACCACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTCGGCG TTCTGCTGCG TGGTATCAAG     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCCATCAA     600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG     650
GCGGCCGTCA CACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAGATGGT TGTTACCCTG ATCCACCCGA     800
TCGCGATGGA CGACGGTCTG CGTTTC                               826
```

2) INFORMATION FOR SEQ ID NO: 56

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter hormaechei*
(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

```
GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTA     150
GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CAGGCGACGA     200
CACCCCAATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAMGCAG     250
AGTGGGAAGM GAAAATCATC GARCTGGCTG GCTTCCTGGA TTCTTACATC     300
CCAGAACCAG AGCGTGCGAT TGACAAGCCA TTCCTGCTGC CAATCGAAGA     350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTWGAGC     400
GCGGTATCAT CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG     450
ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CGAAGCCAGG CTCAATCAAG     600
CCACACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC     700
GTACAACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG     750
GTAATGCCAG GCGACAACAT CAAGATGGTT GTGACGCTGA TCCACCCAAT     800
CGCGATGGAC GACGGTCTGC GTTTCGCAA                            829
```

2) INFORMATION FOR SEQ ID NO: 57

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter sakazakii*
(B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT 150
GAGATGGAAG TGCGCGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA 200
CACCCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCTG 250
AGTGGGAAGC GAAAATCATC GAGCTGGCAG GTCACCTGGA TTCCTACATC 300
CCGGAACCGG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCC ATCTCYGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
GCGGTATCAT CAAGGTTGGT GAAGAAGTTG AAATCGTGGG CATCAAAGAC 450
ACCGCGAAAT CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCGGGCGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCCATCAAG 600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 650
CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACRACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCGATGGAC GACGGTCTGC GTTTCGCAAT C 831

2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACAC 50
GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT 100
TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATATGACTTC CCAGGCGACG 200
ATGTTCCTGT AATCGCTGGT TCTGCTTTGA AAGCTCYTGA AGGCGATGCT 250

TCATACGAAG AAAAAATCAT GGAATTAATG GCTGCAGTTG ACGAATACGT 300
TCCAACTCCA GAACGTGACA CTGACAAACC ATTCATGATG CCAGTCGAAG 350
ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTTG GTATTGCTGA 450
AGAAACTGCT AAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTGT 500
TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGTGTT 550
GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT 600
CACACCTCAT ACAAAATTTA AAGCTGAAGT TTACGTTTTA ACAAAAGAAG 650
AAGGTGGACG TCACACACCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTGTTGTT GAATTACCAG AAGGAACTGA 750
AATGGTTATG CCTGGTGATA ACGTAACAAT CGACGTTGAA TTGATCCACC 800
CAATCGCTAT CGAAGACGGA ACTCGTTTCT CAATT 835

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus cecorum*
(B) STRAIN: ATCC 43198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

GGTGCTATCT TAGTAGTATC TGCTGCTGAT GGTCCTATGC CACAAACTCG 50
TGAACACATT CTTTTATCAC GTAACGTTGG TGTTCCATAC ATCGTTGTTT 100
TCTTAAACAA AGTTGATATG GTTGACGACG AAGAATTATT AGAATTAGTT 150
GAAATGGAAG TACGTGACTT ATTAACTGAA TACGACTTCC CAGGAGACGA 200
TGTTCCTGTA ATCGCTGGTT CTGCATTAAA AGCTTTAGAA GGCGACCCAT 250
CTTACGAAGA AAAAATCTTA GAATTAATGG CTGCAGTTGA CGAATACATC 300
CCAACTCCAG AACGTGACAA CGATAAACCA TTCATGATGC CAGTCGAAGA 350
CGTATTTTCA ATCACTGGTC GTGGTACTGT TGCTACAGGT CGTGTTGAAC 400
GTGGACAAGT ACGTGTTGGT GACGAAGTTG AAATAGTTGG TATCCATGAT 450
GAAATTTCTA AAACAACAGT TACTGGTGTT GAAATGTTCC GTAAATTATT 500
AGATTACGCT GAAGCTGGAG ACAACATCGG TGCATTATTA CGTGGTGTGG 550
CTCGTGAAGA TATCCAACGT GGTCAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CAAAATTCAC TGCTGAAGTG TACGTTTTAA CTAAAGAAGA 650
AGGTGGACGT CATACTCCAT TCTTCACTAA CTACCGTCCA CAATTCTACT 700
TCCGTACAAC TGACGTTACA GGTGTAGTTA ACTTACCAGA AGGTACTGAA 750
ATGGTTATGC CTGGTGATAA CGTAACTATG GAAGTTGAAT TAATCCACCC 800
AATCGCTATC GAAGACGGAA CTCGTT 826

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus dispar*
(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

```
CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACTC      50
GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTTCCTTA CATCGTCGTT     100
TTCTTGAACA AAATGGACAT GGTTGATGAC GAAGAATTAT TAGAATTAGT     150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG     200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT     250
TCATATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT     300
CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG     350
ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA     400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA     450
AGAAACTGCT AAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTGT     500
TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG     550
GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAAC CAGGTTCAAT     600
CACTCCACAT ACAAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG     650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC     700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA     750
AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC     800
CAATCGCGAT CGAAGACGGT ACTCGTTTCT CAATC                     835
```

2) INFORMATION FOR SEQ ID NO: 61

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus durans*
(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

```
CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCCTATG CCTCAAACTC      50
GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTTCCTTA CATCGTYGTA     100
TTCTTGAACA AAGTAGATAT GGTCGATGAC GAAGAATTAC TAGAATTAGT     150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG     200
ATGTTCCTGT AATCGCTGGT TCAGCTTTGA AAGCTTTAGA AGGCGACGCT     250
TCATACGAAG AAAAAATCCT TGAATTAATG GCTGCAGTTG ACGAATATAT     300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG     350
ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA     400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA     450
AGAAACAGCT CAAACAACAG TTACTGGTGT TGAAATGTTC CGTAAATTAT     500
TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGTT     550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT     600
CACKCCTCAT ACAAAATTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG     650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC     700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA     750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC     800
CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC                     835
```

2) INFORMATION FOR SEQ ID NO: 62

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 680 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT 50
TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA 100
ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT 150
TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA 200
TCGCAGGTTC TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA 250
AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA 300
ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA 350
TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT 400
CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA 450
AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG 500
AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT 550
ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC 600
AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC 650
ACACTCCATT CTTCACTAAC TACCGTCCTC 680

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 680 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: R487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT 50
TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA 100
ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT 150
TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA 200
TCGCAGGTTC TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA 250
AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA 300
ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA 350
TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT 400

CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA 450
AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG 500
AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT 550
ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC 600
AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC 650
ACACTCCATT CTTCACTAAC TACCGTCCTC 680

2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACTCGT GAACACATCC 50
TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA 100
GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT 150
TCGTGACCTA TTAACAGAAT ACGAATTCCC TGGTGACGAT GTTCCTGTAG 200
TTGCTGGATC AGCTTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA 250
AAAATTCTTG AATTAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA 300
ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA 350
TTACTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT 400
CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AAACTTCAAA 450
AACAACAGTT ACTGGTGTTG AAATGTTCCG TAAATTGTTA GACTACGCTG 500
AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTTGC ACGTGAAGAC 550
ATCCAACGTG GACAAGTTTT AGCTAAACCA GGTACAATCA CACCTCATAC 600
AAAATTCTCT GCAGAAGTAT ACGTGTTGAC AAAAGAAGAA GGTGGACGTC 650
ATACTCCATT CTTCACTAAC TACCGTCCTC AATTT 685

2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC 50
GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT 100

TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATATGACTTC CCAGGCGACG 200
ATGTTCCTGT AATCGCTGGT TCTGCTTTGA AAGCTCTTGA AGGCGATGCT 250
TCATACGAAG AAAAAATCAT GGAATTAATG GCTGCAGTTG ACGAATACGT 300
TCCAACTCCA GAACGTGACA CTGACAAACC ATTCATGATG CCAGTCGAAG 350
ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTTG GTATTGCTGA 450
AGAAACTGCT AAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTGT 500
TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGGGTT 550
GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAG CTGGTACAAT 600
CACACCTCAT ACAAAATTTA AAGCTGAAGT TTACGTTTTA ACAAAAGAAG 650
AAGGTGGACG TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTGTTGTT GAATTACCAG AAGGAACTGA 750
AATGGTTATG CCTGGTGATA AMGTAACAAT CGACGTTGAA TTGATCCACC 800
CAATCGCTAT CGAAGACGGA ACTCG 825

2) INFORMATION FOR SEQ ID NO: 66

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 636 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

TCCTATGCCT CAAACTCGTG AACACATCTT GTTATCACGT AACGTTGGCG 50
TACCATACAT CGTTGTTTTC TTGAACAAAA TGGATATGGT TGATGACGAA 100
GAATTGCTAG AATTAGTTGA AATGGAAGTT CGTGACCTAT TGTCTGAGTA 150
TGACTTCCCA GGCGACGATG TTCCTGTAAT CGCCGGTTCT GCTTTGAAAG 200
CTCTTGAAGG AGATCCTTCA TACGAAGAAA AAATCATGGA ATTGATGGCT 250
GCAGTTGACG AATACGTTCC AACTCCAGAA CGTGATACTG ACAAACCATT 300
CATGATGCCA GTCGAAGACG TATTCTCAAT CACTGGACGT GGTACTGTTG 350
CTACAGGCCG TGTTGAACGT GGACAAGTTC GCGTTGGTGA TGAAGTAGAA 400
ATCGTTGGTA TTGCTGACGA AACTGCTAAA ACAACTGTAA CAGGTGTTGA 450
AATGTTCCGT AAATTGTTAG ACTATGCTGA AGCAGGGGAT AACATTGGTG 500
CATTGCTACG TGGGGTTGCT CGTGAAGACA TCCAACGTGG ACAAGTATTG 550
GCTAAAGCTG GTACAATCAC ACCTCATACA AAATTCAAAG CTGAAGTTTA 600
TGTTTTGACA AAAGAAGAAG GTGGACGTCA CACTCC 636

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus hirae*
(B) STRAIN: ATCC 8043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

```
CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACTC      50
GTGAACATAT CCTAYTATCT CGTCAAGTTG GTGTTCCATA CATCGTTGTA     100
TTCTTGAACA AAGTAGATAT GGTTGACGAC GAAGAATTAC TAGAATTAGT     150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG     200
ATGTTCCTGT AGTTGCTGGT YCAGCTTTGA AAGCTTTAGA AGGCGACGCT     250
TCATACGAAG AAAAAATCCT TGAATTGATG GCTGCAGTTG ACGAATATAT     300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTCGAAG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA     400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA     450
AGAAACAGCT CAAACAACAG TTACTGGTGT TGAAATGTTC CGTAAATTAT     500
TAGACTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGTT     550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT     600
CACACCTCAT ACAAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAAGAAG     650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC     700
TTCCGTACRA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA     750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC     800
CAATCGCTAT CGAAAACGGT ACTAAATTCT CAATC                     835
```

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus mundtii*
(B) STRAIN: ATCC 43186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

```
CGGAGCAATC TTAGTTGTTT CTGCTGCTGA CGGCCCTATG CCTCAAACTC      50
GTGAACACAT CCTATTATCT CGTCAAGTTG GTGTACCATA CATCGTTGTA     100
TTCTTGAACA AAGTAGATAT GGTTGATGAC GAAGAATTAC TTGAATTAGT     150
TGAAATGGAA GTTCGTGACC TATTAACAGA ATACGAATTC CCTGGTGACG     200
ATGTTCCTGT AATCGCTGGT TCAGCTTTAA GAGCTTTAGA AGGCGACGCT     250
KCATACGAAG AAAAAATTCT TGAATTGATG GCTGCAGTTG ACGAATATAT     300
CCCAACTCCA GAACGTGATA ACGACAAACC ATTCATGATG CCAGTTGAGG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG ACGTGTTGAA     400
CGTGGACAAG YTCGTGTTGG TGACGTTATC GATATCGTTG GTATCGCAGA     450
AGAAACAGCT CAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTAT     500
TAGACTACGC TGAAGCAGGC GATAACATTG GTGCGTTACT ACGTGGTGTT     550
TCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTAAAC CAGGTACAAT     600
CACACCTCAT ACAAAATTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG     650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC     700
TTCYGTACGA CTGACGTAAC TRGTGTTGTY GAATTACCAG AAGGAACTGA     750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC     800
CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC                     835
```

2) INFORMATION FOR SEQ ID NO: 69

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 836 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACAC 50
GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCTTA CATCGYTGTA 100
TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAC TAGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGATTTC CCAGGCGACG 200
ACACTCYAGT TATCGCTGGT TCAGCYTTGA AAGCTTTAGA AGGCGACCCT 250
TCATACRAAG AAAAAATCTT AGAATTAATG SCTGCTGTTG ACGAATACAT 300
CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA 400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA 450
AGAAACTGCT AAAACAACTG TTACAGGTGT TGAAATGTTC CGTAAATTGT 500
TAGACTACGC TGAAGCAGGC GATAACATCG GTGCATTATT ACGTGGTGTT 550
GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT 600
CACTCCACAT ACAAAATTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG 650
AAGGCGGGCG TCACACTCCG TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTGTTGTT GATCTACCAG AAGGTACTGA 750
AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC 800
CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATTC 836

2) INFORMATION FOR SEQ ID NO: 70

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus raffinosus*
(B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

CGGAGCTRTC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACTC 50
GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCTTA CATCGTTGTA 100
TTCTTAAACA AAATGGATAT GGTTGACGAT GAAGAATTAC TAGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTAACTGA ATACGACTTC CCAGGCGACG 200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT 250
TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ATGAATACAT 300

CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGYGGAAG 350
ACGTAYTCTC AATCACTGGT CGTGGAACTG TTGCAACTGG TCGTGTTGAA 400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATTGCTGA 450
AGAAACTGCT AAAACAACTG TTACAGGTGT TGAAATGTTC CGTAAATTGT 500
TGGATTACGC TGAAGCGGGC GACAACATTG GTGCATTATT ACGTGGTGTT 550
GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT 600
CACTCCACAT ACAAAATTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG 650
AAGGCGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA 750
AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC 800
CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATT 835

2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus saccharolyticus*
(B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACTC 50
GTGAACACAT CTTGTTATCT CGTAACGTAG GTGTTCCTTA CATCGTTGTA 100
TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGACT TATTATCAGA ATACGATTTC CCAGGCGATG 200
ACACTCCAGT TATTGCAGGT TCTGCTTTGA AAGCTTTAGA AGGCGATCCA 250
GTTTACGAAG AAAAAATCTT CGAATTAATG GCTGCAGTTG ACGAATATAT 300
CCCAACTCCA GAACGTGATA CTGAAAAACC ATTCATGATG CCAGTTGAGG 350
ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GAAATCGTTG GTATCGACGA 450
AGAAACAGCT CAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTAT 500
TAGACTACGC TGAAGCAGGC GATAACATCG GTGCTTTATT ACGTGGGGTT 550
GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAC CAGGAACAAT 600
CACTCCTCAT ACAAAATTCG TAGCTGAAGT TTACGTTTTA ACTAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTGTTGTA GAATTACGCG AAGGTACTGA 750
AATGGTAATG CCTGGTGACA ACGTAACTAT CGACGTTGAA TTAATCCACC 800
CAATCGCTAT CGAAGACGGA ACTCGTTTCT CTATT 835

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus solitarius*
(B) STRAIN: ATCC 49428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

```
GAGCTATCTT GGTAGTTTCT GCAGCTGATG GCCCAATGCC ACAAACTCGT      50
GAACATATTT TGTTGTCACG TAATGTAGGT GTACCTTACA TCGTTGTGTT     100
CTTGAACAAA ATGGATATGG TTGATGACGA AGAATTACTT GAGTTAGTTG     150
AAATGGAAGT ACGTGATCTA TTATCTGAAT ACGACTTCCC AGGAGATGAT     200
ACTCCAGTTA TTTCCGGTTC AGCTTTGAAA GCTTTAGAAG GCGACGAAGA     250
ATATGAACAA AAAATTATGG ACTTAATGGA TGCAGTTGAT GACTACATTC     300
CAACTCCTGA ACGTGACCAT GACAAACCAT TCATGATGCC AATTGAAGAT     350
GTATTTTCAA TTACAGGCCG TGGTACTGTT GCTACAGGAC GTGTTGAACG     400
CGGGACTATC AAAGTCGGCG ATGAAGTTGA CATTATTGGT ATTCATGAAG     450
ACGTTAAAAA GACAACAGTT ACTGGTGTAG AAATGTTCCG TAAATTGTTG     500
GACTACGCTG AAGCAGGCGA TAACATTGGT ACTTTGTTAC GTGGTGTTTC     550
TCGTGATGAT ATCGAACGTG GTCAAGTATT AGCTAAACCA GGTTCAATCA     600
CACCACATAC AAGATTCTCT GCTGAAGTTT ATGTTTTGAC TAAAGAAGAA     650
GGCGGACGTC ATACTCCATT CTTCTCAAAC TATCGTCCTC AATTCTACTT     700
CCGTACAACT GATATCACTG GTGTCATTGA ATTGCCAGAA GGTACTGAAA     750
TGGTAATGCC AGGTGATAAT GTAACAATGG ATGTTGAATT AATCCACCCA     800
GTCGCTATCG AAGAAGGAAC TCG                                  823
```

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

```
CGGTGCAATC TTGGTCGTAT CAGCGACAGA TGGCCCAATG CCACAAACAC      50
GGGAGCATAT TTTGCTTTCT CGTCAAGTGG GTGTGAAACA TTTGATCGTC     100
TTTTTGAATA AGACGGACCT TGTCGATGAT GACGAGTTGA TCGATTTAGT     150
TGAAATGGAA GTCAGAGAAT TGCTGACTGA ATATGATTTT CCTGGCGACG     200
ACATTCCTGT GATCAAGGGC TCTGCGTTAA AAGCCTTGGA AGGGGACCCA     250
GATGCTGAAG CAGCGATCTT AACGCTGATG GATACAGTAG ATGAATATAT     300
CCCAACGCCA GAACGTGATA CTGACAAACC ATTGTTGTTA CCGATCGAAG     350
ATGTCTTTTC GATCACAGGA CGGGGGACCG TTGCTTCTGG TCGGATCGAT     400
CGCGGCATGG TAAAAGTCGG GGATGAAGTA GAAATCGTCG GAATCAAACC     450
TGAAACACAA AAAGCAGTCG TGACAGGGGT AGAAATGTTC CGCAAAACGA     500
TGGACTTCGG AGAAGCTGGC GATAACGTAG GGGTATTGTT ACGGGGCATC     550
ACCCGTGATG AAATTGAACG TGGCCAAGTG TTAGCAAAAC CAGGTTCTAT     600
CACACCGCAT ACGAAATTCC AAGCGGAAGT CTATGTGTTG ACAAAAGAAG     650
AAGGCGGTCG CCATACCCCA TTCTTTAATA ATTATCGCCC ACAATTTTAC     700
TTCCGTACAA CGGACGTAAC TGGGAATATC GTTTTACCAG AAGGAACGGA     750
AATGGTGATG CCTGGTGACA ACGTAACGAT CGATGTGGAA TTGATCCATC     800
CGATCGCTGT AGAAAATGGA ACGACCTTCT CGATT                     835
```

2) INFORMATION FOR SEQ ID NO: 74

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

```
TAACGGGCGT CTCGATAGAA AAACACGTGA AAATCCCAAT GATTATAAAC      50
AATCAATATA CGATTTTGCT GAAGCTGTAA CAAAAGGTAT TAAGGAACAA     100
ACAAATAAAA ATTAATAGGC AACTTAACCA GAATCGTTAA AACTATATGA     150
AGATTCTGGT TTTTTAAATT CAAAAAGTTT TCTAAAAAAT TTACTTGCTT     200
TTTTAAGTAT AGGTATAAAA TACGATTGAT TAAAACAGTA AAGGAAATGA     250
ATCATGAAAC AATTAACTAA GCCTTTATAC TTTTACCTAT TACTTTTTAT     300
TACAACAACG CTGATTGGCG CGTTACTATT ATATTTGCCA ATCACAGGTA     350
AACATCCTAT TGATTTTGTG GACGCCCGTT                           380
```

2) INFORMATION FOR SEQ ID NO: 75

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 666 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

```
GCAATCTTGG TCGTATCAGC GACAGATGGC CCAATGCCAC AAACACGGGA      50
GCATATTTTG CTTTCTCGTC AAGTGGGTGT GAAACATTTG ATCGTCTTTT     100
TGAATAAGAC GGACCTTGTC GATGATGACG AGTTGATCGA TTTAGTTGAA     150
ATGGAAGTCA GAGAATTGCT GACTGAATAT GATTTTCCTG GCGACGACAT     200
TCCTGTGATC AAGGGCTCTG CGTTAAAAGC CTTGGAAGGG GACCCAGATG     250
CTGAAGCAGC GATCTTAACG CTGATGGATA CGGTAGATGA ATATATCCCA     300
ACGCCAGAAC GTGATACTGA CAAACCATTG TTGTTACCGA TCGAAGATGT     350
CTTTTCGATC ACAGGACGGG GGACCGTTGC TTCTGGTCGG ATCGATCGCG     400
GCATGGTAAA AGTCGGGGAT GAAGTAGAAA TCGTCGGAAT CAAACCTGAA     450
ACACAAAAAG CAGTCGTGAC AGGGGTAGAA ATGTTCCGCA AAACGATGGA     500
CTTCGGAGAA GCTGGCGATA ACGTAGGGGT ATTGTTACGG GGCATCACCC     550
GTGATGAAAT TGAACGTGGC CAAGTGTTAG CAAAACCAGG TTCTATCACA     600
CCGCATACGA AATTCCAAGC GGAAGTCTAT GTGTTGACAA AAGAAGAAGG     650
CGGTCGCCAT ACCCCA                                         666
```

2) INFORMATION FOR SEQ ID NO: 76

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

TGGTGCGATT TTAGTTGTAT CCGCAACAGA TGGTCCAATG CCTCAAACCC 50
GGGAACATAT CTTGCTTTCG AGACAAGTTG GTGTGAAACA TCTGATTGTT 100
TTCTTGAACA AAATCGATTT AGTCGATGAC GAAGAATTGA TTGATTTAGT 150
AGAAATGGAA GTAAGAGAAC TGCTATCTGA ATATAATTTT CCAGGGGATG 200
ACATTCCTGT TATCAAAGGT TCGGCATTAA AAGCGTTGGA AGGAGACCCT 250
GATGCAGAAG CTGCCATCAT GGAATTAATG GATACAGTAG ACAGCTATAT 300
CCCAACACCT GAGCGTGATA CAGACAAACC ATTACTCTTG CCAGTTGAAG 350
ATGTCTTTTC GATTACTGGA CGAGGAACAG TTGCTTCCGG ACGGATCGAT 400
CGGGGAACAG TTCGGGTAGG CGATGAAGTA GAAATCGTCG GTATCAAACC 450
TGAAACCCAA AAAGCTGTAG TGACAGGCGT CGAAATGTTC CGCAAGACGA 500
TGGACTTTGG GGAAGCCGGT GACAATGTAG GTGTCTTGCT GAGAGGGATC 550
ACTCGTGACG AAATTGAACG AGGACAAGTG TTGGCTAAAC CAGGTTCGAT 600
CACACCACAT ACAAAATTCC AAGCAGAAGT TTATGTATTG ACGAAAGAAG 650
AAGGTGGTCG TCATACACCA TTCTTCAACA ACTATCGTCC ACAATTTTAT 700
TTCCGTACAA CGGATGTGAC AGGGAACATT ACATTGCCTG AAGGAACAGA 750
A 751

2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Ehrlichia canis*
(B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

TGCAGCAATA TTAGTAGTGT CTGCAACTGA TGGAGCAATG CCACAAACAA 50
GAGAACATAT ATTATTAGCA AAGCAAGTAG GTGTAAAAGA TATAGTAGTG 100
TGGATGAATA AGTGTGATGT TGTAGATGAT GAAGAAATGT TGTCATTAGT 150
TGAAATGGAA ATAAGGGAAT TGTTATCAAA ATATGGGTAT CCTGGGGATG 200
ATATAGATGT AGTTAGAGGA TCTGCAGTTA AAGCATTAGA AGAAGAAACA 250
GGCTCAGGTG TGTGGAGTGA AAAAATAATG GAATTGATGA ATGCTTTAGA 300
AAAAATAAGT TTACCAGTAA GAGAAAAAGA TAAGCCATTT TTAATGTCAA 350

TAGAAGATGT GTTTTCAATA CCTGGAAGAG GTACAGTAGT AACAGGAAGA 400
ATAGAAAGAG GAGTAATTAG AGTAGGGGAT AAAATAGAGA TAGTAGGATT 450
GCGTGAGATA CAAAGTACAG TATGTACAGG TGTTGAAATG TTTCATAAAG 500
CATTAGATGC AGGAGAAGCA GGGGATAATG CTGGAATATT GTTAAGAGGG 550
ATAAAAAAAG AAGATGTAGA AAGAGGGCAA GTATTGAGTG CACCTGGACA 600
GATACATTCA TATAAGAGAT TTAAGGCAGA GGTATATATA TTGAAAAAAG 650
AAGAAGGAGG AAGACATACT CCATTTTTCT CAAATTACCA GCCGCAATTT 700
TATGTTAGAA CAACAGATGT AACAGGGAAT ATAAAGTTAC CAGAAGGAGT 750
AGAAATGGTA ATGCCAGGGG ATAATATAAA TATCGAAGTG AGTTTGGATA 800
AGCCTGTTGC TATTGATCAA GGATTGAGAT TTGC 834

2) INFORMATION FOR SEQ ID NO: 78

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*
(B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
GAGTGGGAAG CGAAAATCCT GGAACTGGCT GGCTTCCTGG ATTCTTAYAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGT 817

2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
(B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

```
CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG      50
CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTCCT     100
GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA     150
TGGAAGTTCG TGAACTTCTG TCTCAGTACG ACTTCCCGGG CGACGACACT     200
CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG     250
GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG     300
AACCAGAGCG TGCGATTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG     350
TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG     400
TATCATCAAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC     450
AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAAACT GCTGGACGAA     500
GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA     550
AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC     600
ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCCAAAGA TGAAGGCGGT     650
CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC     700
TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA     750
TGCCGGGCGA CAACATCAAA ATGGTTGTTA CCCTGATCCA CCCGATCGCG     800
ATGGACGACG GTCTGCGTTT CGCAA                                825
```

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia hermannii*
(B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

```
GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT     150
GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA     200
CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG     250
AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC     300
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA     350
CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT     450
ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG     600
CCKCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     700
GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG     750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT     800
CGCGATGGAC GACGGTCTGC GTTTCGCAA                            829
```

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia vulneris*
(B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
TGAGATGGAA GTGCGTGAAC TTCTGTCCCA GTACGACTTC CCGGGCGACG     200
ACACCCCGAT CATTCGTGGT TCTGCGCTGA AAGCGCTGGA AGGCGAAGCT     250
GAGTGGGAAG AGAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCCTACAT     300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG     400
CGCGGTATCA TCAARGTKGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA     450
TACTGCGAAA TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGTCG TGCAGGCGAG AACTGCGGCG TTCTGCTGCG TGGTATCAAG     550
CGTGAAGAGA TCCAGCGTGG CCAGGTTCTG GCTAAGCCGG GCTCAATCAA     600
GCCGCACACC AAGTTCGAAT CCGAAGTGTA CATCCTGTCC AAAGACGAAG     650
GCGGCCGTCA CACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCATCCGA     800
TCGCGATGGA CGACGG                                         816
```

2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Eubacterium lentum*
(B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

```
CGGCGCCTCC TCGTTATCGC CGCCACCGAC GGCCCGATGG CCCAGACCCG      50
CGAGCACATC CTGCTCGCCC GTCAGGTCGG CGTGCCCTAC ATCGTGGTCT     100
TCCTGAACAA GTGCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC     150
GAGATGGAAG TTCGCGAGCT GCTCGACTCT TACGAGTTCC CGGGCGACGA     200
CACCCCGATC ATCCGCGGCT CCGCTTTGAA GGCCCTCGAG GGCGACAAAG     250
AGTGGCAGGA GAAGGTCTGG GAGCTCATGG ACGCCGTCGA CTCCTACATC     300
CCGACGCCGG AGCGCATGGT CGACAAGCCG TTCCTGATGG CCGTCGAGGA     350
```

CACGATGACC ATCACCGGCC GCGGCACCGT TGCCACCGGT CGTGTGGAGC 400
GTGGTACGCT GCATGTCAAC GACCCGCTGG AGATCGTCGG TATCAAGGAG 450
ACCCAGAACA CGGTCTGCAC CGGTATCGAG ATGTTCCGCA AGCTGCTCGA 500
CGAGGCTCAG GCCGGCGACA ACATCGGCTG CCTGCTCCGC GGTGTCAAGC 550
GCGAGGAGAT CGTTCGCGGC CAGGTTCTCT GCAAGCCCGG TAGCGTGACC 600
CCGCACACCG AGTTCGAGGG TCAGGTCTAC ATCCTGACGA AGGAAGAGGG 650
CGGCCGCCAC ACGCCGTTCT TCGACGGCTA CCGTCCGCAG TTCTACTTCC 700
GCACGACGGA CGTGACGGGT GTTGCCCACC TTCCCGAGGG CACCGAGATG 750
GTCATGCCGG GCGACAACGT GGAGATCAAG GGCGAGCTCA TTCACCCGAT 800
CGCCAGGAAG AGGGCTGCGT TCGCTAAC 828

2) INFORMATION FOR SEQ ID NO: 83

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Eubacterium nodatum*
(B) STRAIN: ATCC 33099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

GGAGCAATTC TGGTTTGTGC AGCAACKGAC GGACCAATGC CTCAGACAAG 50
AGAACATATC CTTTTGTCAA GGCAGGTAGG AGTGCCATAT ATCATCGTAT 100
TCCTGAATAA ATGTGACATG GTGGATGAYG AAGAGCTTCT GGACTTGGTA 150
GAGATGGAAG TAAGAGAACT TCTCAGTGAG TATGAATTCC CGGGAGATGA 200
TACCCCGATA GTAAGAGGTT CAGCCCTGAA GGCACTGGAA GAACCCAATG 250
GAGAATGGGC AGACAAGATT GTAGAGCTGA TGGAGGAAGT AGATAAATAC 300
ATTCCTGAAC CAAAGAGAGA TAACGACAAA CCGTTCCTGA TGCCTGTAGA 350
GGACGTATTC TCAATAACAG GAAGAGGAAC AGTAGCGACA GGAAGRGTTG 400
AAAGAGGAAT CCTGAAGGTC GGTGATGAAG TAGAAATCGT GGGAATGAGC 450
GAAGAGAGAA GAAAGGTAGT AGTAACGGGA GTTGAAATGT TCAGAAAGCT 500
TCTGGATGAA GCAGAGACAG GAGACAACAT CGGAGCACTG CTGAGAGGAG 550
TTCAGAGAAC RGAGATCCAG AGAGGTCAGG TATTGGCRGC ACCTGGAACG 600
ATCAACCCAC ATACAAAGTT CAAGGGTCAG GTATATGTAC TGAAGAAGGA 650
AGAAGGAGGA AGGCATACGC CGTTCTTCAA YGGATACAGW CCACAGTTCT 700
ACTTCAGAAC AACAGACGTA ACAGGAGATT TGCAGCTGCC GGAAGGARCA 750
GAGATGTGCA TGCCGGGAGA TAATGTGGTA ATGAACRTCA GCCTGATCAC 800
TCCGATTGCT ATAGAAGAGG GWCTGAGATT TGCCA 835

2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*
(B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

```
GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA      50
GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA     100
TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA     150
ATGGAAGTTC GYGAACTTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT     200
CCCAGTTGTT AAAGGTTCAG CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT     250
GGGAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA     300
GAACCAGAGC GTGCGATTGA CAAGCCATTC CTGCTGCCAA TCGAAGACGT     350
ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG     400
GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT     450
GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA     500
AGGCCGTGCY GGTGAGAACG TTGGTGTTCT GCTGCGTGGT ATCAAGCGTG     550
AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTC AATCAAACCA     600
CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG     650
CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA     700
CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA     750
ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC     800
GATGGATGAC GGTCTGCGTT TCGCAA                               826
```

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) *STRANDEDNESS*: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Francisella tularensis*
(B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

```
TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC      50
GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAAA AATCGTTGTT     100
TTCTTAAACA AGTGTGACAT GGTTGATGAT GAAGAGTTAT TAGAGCTAGT     150
TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG     200
ACACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA     250
GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT     300
TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG     350
ATGTATTCTC AATTTCAGGT CGTGGTACTG TTGTAACTGG TCGTATTGAG     400
CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTCGTCC     450
AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG     500
ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTCG TGGACTTAAG     550
AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA     600
GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG     650
GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC     700
CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCCAGAGG GTGTAGAAAT     750
GGTTATGCCT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA     800
TCGCTAGGAT GAAGGGTTAC GTTTTGCA                             828
```

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

```
CGGTGCTATC ATCGTAGKTG CTGCTACTGA TGGTCCGATG CCTCARACTC      50
GTGAGCAYAT CYTGCTGGCT CGTCAGGTAA ACGTWCCKAG ACTGGTTGTA     100
TTCATGAACA AGTGYGACAT GGTAGACGAC GCTGAAATGY TGGAACTCGT     150
TGAAATGGAA ATGCGTGAAC TGCTTTCAGC YTACGAATTC GAYGGYGACA     200
ACACTCCKTT CATTCAGGGT TCTGCTCTTG GTGCRTTGAA YGGCGTTGAA     250
AAGTGGGAAG AGAAGGTTAT GGANCTGATG GATGCTTGCG ACACTTGGAT     300
TCCTTTGCCT CCGCGTGATA TTGAYAAACC GTTCTTGATG CCGGTTGAAG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCTACTGG TCGTATCGAA     400
GCTGGTGTTA TCCATGTAGG TGACGAAGTT GAAATCCTCG GTTTGGGTGA     450
AGACAAGAAG TCTGTTGTAA CTGGTGTTGA AATGTTCCGC AAGTTGCTGG     500
ATCAAGGTGA AGCTGGTGAC AACGTAGGTY TGTTGCTCCG TGGTATCGAC     550
AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAGCCCG GTCAGATTAA     600
ACCTCACTCT AAGTTCAAAG CTTCTATCTA CGTTTTGAAG AAAGAAGAAG     650
GTGGTCGTCA CACTCCGTTC CACAACAAAT ACCGTCCTCA GTTCTATCTG     700
CGTACTATGG ACTGTACAGG TGAAATCWCT CTTCCGGAAG GAACTGAAAT     750
GGTAATGCCT GGTGATAACG TAGAAATCAC TGTAGAACTG ATCTACCCGG     800
TAGCATTGAA CGTAGGTTTG CGTTTCGCT                            829
```

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Gemella haemolysans*
(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

```
CTATCTTAGT AATCGCTGCT ACAGATGGAC CAATGGCTCA AACTCGTGAG      50
CACATCCTAT TATCTCGTAA CGTTGGAGTA CCAAAAATCG TTGTATTCTT     100
AAACAAATGT GATATGGTTG ATGACGAAGA GTTATTAGAA TTAGTTGAAA     150
TGGAAGTTCG TGAACTATTA TCTGAATACG GATTCGACGG AGATGAACTA     200
CCAGTAATCA AAGGTTCTGC TCTTAAAGCT CTTGAAGGAG ATGCAGATGC     250
AGAAAAAGCT ATCATCGAAT TAATGGAAAC AGTTGACGAA TACATCCCAA     300
CTCCAGAACG TGATAACGCT AAACCATTCA TGATGCCAGT TGAGGACGTA     350
```

TTCTCAATCA CAGGTCGTGG TACAGTTGCT ACTGGACGTG TTGAACGTGG 400
ACAAGTTAAA GTTGGAGACG TAGTAGAAAT CGTTGGATTA ACTGAAGAAC 450
CAGCTTCAAC TACTGTAACA GGTGTTGAAA TGTTCCGTAA ATTATTAGAT 500
TACGCTGAAG CAGGAGATAA CATCGGTGCA TTATTACGTG GTGTTGCTCG 550
TGAAGACATC GAACGTGGAC AAGTTTTAGC AGCTCCTAAA ACAATCACTC 600
CACACACTCA ATTCGTAGCT GACGTGTACG TATTATCTAA AGAAGAAGGT 650
GGACGTCACA CTCCATTCTT CACAAACTAC CGTCCTCAAT TCTACTTCCG 700
TACTACTGAC GTAACTGGTG TAGTTACTTT ACCAGAAGGT ACTGAAATGG 750
TAATGCCTGG GGATAACGTA TCAATCAACG TAGAACTTAT TTCTCCAATC 800
GCGATCGAAG AAGGAACTCG TTTCTCAA 828

2) INFORMATION FOR SEQ ID NO: 88

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Gemella morbillorum*
(B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

TCTTAGTAAT CGCTGCTACA GATGGTCCTA TGGCTCAAAC TCGTGAACAC 50
ATCCTATTAT CTCGTAACGT TGGAGTACCT AAAATTGTTG TATTCTTAAA 100
CAAATGTGAT ATGGTTGATG ACGAAGAGTT ATTAGAATTA GTAGAAATGG 150
AAGTTCGTGA ACTATTATCT GAATACGGAT TTGATGGAGA TGAACTACCA 200
GTAATCAAAG GTTCAGCTCT TAAAGCTCTT GAAGGAGATG CAGATGCTGA 250
AAAAGCTATC ATCGAATTAA TGGAAACAGT TGACGAGTAC ATCCCAACTC 300
CAGAACGTGA TAACGCTAAA CCATTTATGA TGCCAGTTGA GGACGTGTTC 350
TCAATCACAG GTCGTGGTAC AGTTGCTACT GGACGTGTTG AACGTGGACA 400
AGTTAAAGTT GGTGACGTAG TAGAAATCGT TGGATTAACT GAAGAACCAG 450
CTTCAACTAC TGTAACAGGT GTTGAAATGT TCCGTAAATT ATTAGATTAC 500
GCTGAAGCAG GAGATAACAT CGGTGCATTA TTACGTGGTG TTGCTCGTGA 550
AGATATCGAA CGTGGACAAG TTTTAGCAGC TCCTAAAACA ATCACTCCAC 600
ATACTCAATT CGTAGCTGAT GTGTACGTAT TATCTAAAGA AGAAGGTGGA 650
CGTCACACTC CATTCTTCAC AAACTACCGT CCACAATTCT ACTTCCGTAC 700
TACTGACGTA ACTGGTGTAG TTACTTTACC AGAAGGTACT GAAATGGTAA 750
TGCCTGGGGA CAACGTATCA ATCAACGTAG AACTTATTTC TCCAATCGCT 800
ATCGAAGAAG GAACTCGTTT CTC 823

2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus actinomycetemcomitans*
(B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

```
GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACTCGTGA      50
GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT     100
TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA     150
ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCGG GCGATGACAC     200
CCCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAAGGC GATGCCGCAT     250
GGGAAGAAAA AATCCTTGAA TTAGCAAACC ATTTAGATAC TTACATCCCG     300
GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCAA TTGAAGATGT     350
GTTCTCTATC TCCGGTCGTG GTACCGTAGT AACGGGTCGT GTTGAGCGCG     400
GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT     450
GCAAAAACCA CCGTAACCGG TGTTGAAATG TTCCGTAAAT TACTTGACGA     500
AGGTCGTGCG GGTGAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG     550
AAGAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG     600
CACACTGACT TCGAATCTGA AGTGTACGTA TTGTCCAAAG AAGAAGGTGG     650
TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA     700
CAACTGACGT AACCGGTACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT     750
ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC     800
GATGGACCAA GGTTTACGTT TCGCTATCG                            829
```

2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus aphrophilus*
(B) STRAIN: ATCC 33389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

```
TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCTTA CATCATCGTA     100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT     150
TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGATG     200
ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA     250
GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACTTAG ATACTTACAT     300
TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATTGAAG     350
ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGTTGAG     400
CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC     450
GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG     500
ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA     550
CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC     600
TCCGCACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC     700
CGTACAACTG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGGAAAT     750
GGTTATGCCT GGCGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA     800
TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG                       833
```

2) INFORMATION FOR SEQ ID NO: 91

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 815 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus ducreyi*
(B) STRAIN: DSM 8925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

```
CGGCGCTATC TTAGTTGTAG CAGCAACTGA TGGTCCTATG CCTCAAACTC      50
GTGAACACAT CTTATTAGGC CGCCAAGTTG GTGTTCCTTA CATCATCGTA     100
TTCTTAAATA AATGCGATAT GGTAGATGAT GAAGAATTAT TAGAATTAGT     150
TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGATTTC CCAGGTGACG     200
ATACTCCTAT CGTTCGTGGT TCAGCATTAC AAGCATTAAA TGGTGTGCCT     250
GAGTGGGAAG AAAAAATCAT TGAATTAGCA CAACACTTAG ATTCTTATAT     300
CCCTGAGCCT GAGCGTGCGA TTGATAAACC TTTCTTATTA CCAATCGAAG     350
ACGTATTCTC AATTTCAGGT CGTGGTACAG TAGTAACCGG TCGTGTTGAG     400
CGTGGTATCA TCAAATCAGG TGAAGAAGTT GAAATCGTAG GGATTAAAGA     450
AACGACAAAA ACAACAGTAA CCGGTGTTGA GATGTTCCGT AAACTATTAG     500
ACGAAGGTCG TGCGGGTGAA AACGTAGGTG CCTTATTACG TGGTACTAAA     550
CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTACAATTAC     600
ACCACACACT GATTTTGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ATCGTCCTCA GTTCTACTTC     700
CGYACAACGG ACGTAACAGG AACGATTGAA TTACCTGAAG ATGTTGAGAT     750
GGTAATGCCT GGTGATAATA TCAAGATGAC AGTAAGCTTA ATTCACCCTA     800
TCGCGATGGA CGAAG                                          815
```

2) INFORMATION FOR SEQ ID NO: 92

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus haemolyticus*
(B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

```
TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCAATG CCACAAACTC      50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCATA CATCATCGTA     100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT     150
AGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCAGGTGACG     200
ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCATTAAA TGGCGTAGCA     250
GAATGGGAAG AAAAAATCCT TGAGTTAGCA AACCACTTAG ATACTTACAT     300
CCCAGAACCA GAGCGTGCAA TTGACCAACC GTTCCTTCTT CCAATCGAAG     350
```

ATGTGTTCTC AATCTCAGGT CGTGGTACAG TAGTAACTGG TCGTGTAGAA 400
CGTGGTATCA TCCGTACTGG TGATGAAGTA GAAATCGTAG GTATCAAAGA 450
TACAGCAAAA ACTACTGTAA CGGGTGTTGA AATGTTCCGT AAATTACTTG 500
ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAAA 550
CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTTCAATCAC 600
GCCACACACT GACTTCGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG 650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC 700
CGTACAACTG ACGTAACTGG TACTATCGAG TTACCAGAAG GCGTAGAAAT 750
GGTAATGCCA GGCGATAACA TCAAGATGAC AGTAAGCTTA ATCCACCCAA 800
TCGCGATGGA CCAAGGTTTA CGTTTCGCAA 830

2) INFORMATION FOR SEQ ID NO: 93

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus parahaemolyticus*
(B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

TCTTAGTAGT AGCAGCAACA GACGGTCCAA TGCCACAAAC TCGTGAGCAC 50
ATCTTATTAG GTCGCCAAGT AGGTGTTCCA TACATCATCG TATTCTTAAA 100
CAAATGCGAT ATGGTTGACG ATGAAGAATT ATTAGAATTA GTTGAAATGG 150
AAGTGCGTGA ACTTCTTTCA CAATATGACT TCCCAGGTGA TGACACGCCA 200
GTAGTACGTG GTTCAGCGTT ACAAGCGTTA AACGGCGTAG CAGAGTGGGA 250
AGAAAAAATT CTTGAATTAG CAAACCACTT AGATACATAC ATCCCAGAGC 300
CAGAGCGTGC GATTGATAAA CCATTCTTAT TACCAATCGA AGACGTATTC 350
TCAATCTCAG GTCGTGGTAC AGTAGTAACA GGTCGTGTTG AGCGTGGTAT 400
CATCAAAGCG GGTGAAGAAG TTGAAATCGT AGGTATCAAA GACACTGCGA 450
AAACAACAGT AACTGGCGTG GAAATGTTCC GTAAATTATT AGACGAAGGT 500
CGTGCGGGTG AAAACGTTGG TGCATTATTA CGTGGTACAA AACGTGAAGA 550
AATCGAACGT GGTCAAGTGT TAGCGAAACC AGGTACAATT ACACCACACA 600
CAGACTTCGA ATCAGAAGTG TACGTATTAT CAAAAGAAGA AGGTGGTCGT 650
CACACTCCAT TCTTCAAAGG TTACCGTCCA CAATTCTACT TCCGTACAAC 700
TGACGTAACT GGTACTATTG AATTACCAGA AGGCGTAGAA ATGGTAATGC 750
CAGGCGATAA CATCAAAATG ACAGTATCAT TAATCCACCC AATCGCGATG 800
GACGAAGGTT TACGTTTTGC GATT 824

2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*
(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

```
TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCTTA CATCATCGTG     100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT     150
TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG     200
ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA     250
GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT     300
TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG     350
ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG     400
CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC     450
GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG     500
ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA     550
CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC     600
TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC     700
CGTACAACTG ACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAAT     750
GGTTATGCCT GGTGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA     800
TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG                       833
```

2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus paraphrophilus*
(B) STRAIN: ATCC 29241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

```
TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCTTA CATCATCGTA     100
TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT     150
TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG     200
ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA     250
GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACTTGG ATACTTACAT     300
TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG     350
ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG     400
CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC     450
GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG     500
ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAAA     550
CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC     600
TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC     700
CGTACAACTG ACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAAT     750
GGTAATGCCT GGCGATAACA TCAAAATGAC CGTATCCTTA ATCCACCCAA     800
TCGCGATGGA CCAAGGTTTA CGTT                                 824
```

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus segnis*
(B) STRAIN: ATCC 33393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

```
GCTATCTTAG TAGTAGCAGC AACTGATGGT CCTATGCCAC AAACTCGTGA      50
GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT     100
TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA     150
ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCAG GTGATGATAC     200
TCCAATCATT CGTGGTTCTG CATTACAAGC GTTAAACGGC GTAGCAGAAT     250
GGGAAGAAAA AATCCTTGAA TTAGCTCAAG CATTAGATAC TTACATTCCT     300
GAACCTGAGC GTGCAATCGA CCAACCGTTC CTTCTTCCAA TTGAAGACGT     350
GTTCTCAATC TCTGGTCGTG GTACTGTAGT AACAGGTCGT GTAGAGCGTG     400
GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTTGGTAT CAAACCAACT     450
GCGAAAACAA CCGTAACCGG TGTTGAAATG TTCCGTAAAT TACTTGACGA     500
AGGTCGTGCA GGTGAAAACA TCGGTGCATT ATTACGTGGT ACTAAACGTG     550
AAGAAATCGA ACGTGGTCAA GTATTAGCGA AACCGGGTTC AATCACTCCA     600
CACACTGACT TCGAATCTGA AGTGTACGTA TTATCTAAAG AAGAAGGTGG     650
TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA     700
CAACTGACGT AACCGGTACT ATCGAGTTAC CGGAAGGCGT GGAAATGGTT     750
ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATCC ACCCAATCGC     800
GATGGACCAA GGTTTACG                                       818
```

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 763 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Hafnia alvei*
(B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

```
CGGCGCTATC CTGGTTGTTG CTGCGACTGA CGGCCCTATG CCTCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTW CATCATCGTR     100
TTCCTGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT     150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCWGGYGATG     200
ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGYGMACCT     250
GAGTGGGAAG CTAAGATCGT AGAACTGGCT GAAACTCTGG ATTCTTACAT     300
YCCACARCCA GAACGTGCTA TCGAYAAGCC ATTCCTGCTG CCAATCGAAG     350
```

```
ACGTATTCTC TATCTCTGGC CGTGGTACWG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GARATCGTTG GTATCAAAGA      450
TACCGTTAAA TCAACTTGTA CCGGCGTTGA AATGTTCCGT AAACTGCTGG      500
ACGAAGGTCG TGCAGGCGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG      550
CGTGAAGACA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GYTCYATCAA      600
GCCACACACC AAGTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG      650
GCGGYCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAACTG ACGTGACCGG TACCATCGAA TTGCCAGAAG GCGTGGAAAT      750
GGTAATGCCA GGC                                             763
```

2) INFORMATION FOR SEQ ID NO: 98

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Kingella kingae*
- (B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

```
CGGCGCAATC TTGGTATGTT CAGCAGCTGA CGGTCCTATG CCACAAACTC       50
GCGAACACAT CTTGTTGGCT CGCCAAGTAG GTGTACCTTA TATCATCGTA      100
TTCATGAACA AATGCGACAT GGTCGATGAT GCTGAGTTGT TGGAATTGGT      150
TGAAATGGAA ATCCGTGACT TGTTGTCTAG CTACGATTTT CCAGGCGACG      200
ATTGCCCAAT CGTTCAAGGT TCTGCATTGC GYGCATTGGA AGGCGACGCT      250
GCATACAAAG AAAAAATCTT TGAATTGGCT GCTGCTTTGG ATAGCTACAT      300
TCCTACTCCA GAACGTGCTG TTGATAAACC ATTCTTGTTG CCAATCGAAG      350
ATGTATTCTC TATCTCTGGT CGTGGTACAG TAGTTACTGG TCGTGTAGAG      400
CGCGGTATCA TCAAAGTAGG CGAAGAGATT GAAATCGTTG GTTTGAAAGA      450
CACGCAAAAA ACCACTTGTA CTGGCGTGGA AATGTTCCGC AAATTGTTGG      500
ACGAAGGTCA AGCTGGTGAT AACGTTGGTG TATTATTGCG TGGTACGAAG      550
CGTGAAGACG TTGAACGTGG TCAGGTATTG GCTAAACCAG GTTCTATCAC      600
TCCGCACACT AAATTTGAAG CTGAAGTGTA TGTGTTGAGC AAAGAAGAAG      650
GTGGCCGTCA TACGCCATTC TTCGCTAACT ACCGCCCACA ATTCTACTTC      700
CGTACGACTG ACGTAACTGG TGCAGTTACT TTGTCTGAGG GTGTGGAAAT      750
GGTTATGCCA GGCGAAAACG TGAAAATCAC TGTTGAGTTG ATTGCACCTA      800
TCGCTAGGAA AACGGTTTGC GTTTTGCG                              828
```

2) INFORMATION FOR SEQ ID NO: 99

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

```
GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAGCTGGTT     150
GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA     200
CACGCCGATC GTTCGTGGTT CCGCTCTGAA AGCGCTGGAA GGCGAAGCAG     250
ACTGGGAAGC GAAAATCATC GAACTGGCTG GCTACCTGGA TTCTTACATC     300
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA     350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG     450
ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCTATCAAG     600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC     700
GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG     750
GTCATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TTCACCCGAT     800
CGCGATGGAC GATGGTCTGC GTTTCGCA                             828
```

2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 749 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

```
GATGCCGCAG ACTCGTGAGC ACATCCTGCT GGGTCGTCAG GTAGGCGTTC      50
CGTACATCAT CGTGTTCCTG AACAAGTGCG ACATGGTTGA TGACGAAGAG     100
CTGCTGGAAC TGGTTGAAAT GGAAGTTCGT GAACTTCTGT CTCAGTACGA     150
TTTCCCGGGC GACGACACTC CGATCGTTCG TGGTTCTGCT CTGAAAGCGC     200
TGGAAGGCGA CGCWGAGTGG GAAKCKAAAA TCATCGAACT GGCTGGCTTC     250
CTGGATTCTT ACATTCCGGA ACCAGAGCGT GCGATTGACA AGCCGTTCCT     300
GCTGCCGATC GAAGACGTAT TCTCCATCTC CGGTCGTGGT ACCGTTGTTA     350
CCGGTCGTGT AGAGCGCGGT ATCATCAAAG TTGGCGAAGA AGTTGAAATY     400
GTTGGTATYA AAGACACTGC TAAGTCTACC TGTACTGGCG TTGAAATGTT     450
CCGCAAACTG CTGGACGAAG GCCGYGCTGG TGAGAACGTT GGTGTTCTGC     500
TGCGTGGTAT CAAACGTGAA GAAATCGAAC GTGGTCAGGT ACTGGCTAAG     550
CCGGGCTCTA TCAAGCCGCA CACCAAGTTC GAATCTGAAG TTTATATCCT     600
GTCCAAAGAC GAAGGCGGCC GTCACACTCC GTTCTTCAAA GGCTACCGTC     650
CGCAGTTCTA CTTCCGTACA ACTGACGTGA CTGGCACCAT CGAACTGCCG     700
GAAGGCGTAG AGATGGTTAT GCCGGGCGAC AACATCAAAA TGGTTGTTA      749
```

2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella planticola*
(B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

```
TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
TGAAATGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG     200
ACACTCCGAT CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA     250
GACTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT     300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCTATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG     400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
TACTGCTAAR TCWACCTGTA CYGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA     600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG     650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATTCACCCRA     800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA                           830
```

2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
(B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

```
CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA      50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC     100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TTGAGATGGA     150
AGTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA     200
TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA     250
GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGGAACC     300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT     350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC     400
ATCAAAGTAG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AAACCGCGAA     450
AACCACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC     500
```

```
GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC      600
CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GGCGGCCGTC      650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT      700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC      750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG      800
ACGACG                                                     806
```

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 743 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
(B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

```
GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA       50
TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG      100
GAACTGGTTG AGATGGAAGT TCGTGAACTG CTGTCTCAGT ACGATTTCCC      150
GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG      200
GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGCTGG CCACCTGGAT      250
ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC      300
GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC      350
GTGTAGAGCG CGGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT      400
ATCAAAGAAA CCGCGAAAAC CACCTGTACT GGCGTTGAAA TGTTCCGCAA      450
ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG      500
GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC      550
ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGTACA TCCTGTCCAA      600
AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT      650
TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC      700
GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA             743
```

2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae* subsp. *rhinoscleromatis*
(B) STRAIN: ATCC 13884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC 50
CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA 100
ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT GAGATGGAAG 150
TTCGTGAACT RCTGTCTCAG TACGATTTCC CGGGCGACGA CACCCCGATC 200
GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC 250
GAAAATCATC GAACTGGCTG GCCACCTGGA TACCTATATC CCGGAACCAG 300
AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC 350
ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC GCGGTATCAT 400
CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAA ACCGCGAAAA 450
CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 500
GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT 550
CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC CCGCACACCA 600
AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG CGGCCGTCAC 650
ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA 700
CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG 750
GCGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCGAT CGCGATGGAC 800
GACGGTCTGC GTTTCGCAA 819

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Kluyvera ascorbata*
(B) STRAIN: ATCC 33433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

CGGCGCGATC CTGGTTGTTG CTGCGACTGA TGGCCCTATG CCACAGACTC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG 100
TTCCTGAACA AATGYGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG 200
ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGATGCA 250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
CCCAGAACCA GAACGTGCTA TCGATAAGCC GTTCCTGCTG CCAATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTTGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
CACCGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCTATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
CGTACTACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT 750
GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA 800
TCGCGATGGA CGACGGCCTG CGTTTCGCAA CC 832

2) INFORMATION FOR SEQ ID NO: 106

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Kluyvera cryocrescens*
(B) STRAIN: ATCC 33435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACTC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG 100
TTCCTGAACA AATGTGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG 200
ACACTCCTAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGACGCT 250
GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCGA TTGATAAGCC GTTCCTGCTG CCAATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA 450
CACTGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCCATCAA 600
GCCGCACACC AAATTCGAAT CTGAAGTTTA CATCCTGTCC AAAGACGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCAA 800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA 830

2) INFORMATION FOR SEQ ID NO: 107

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Kluyvera georgiana*
(B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

CGCGATCCTG GTTGTTGCTG CGACTGACGG CCCGATGCCG CAGACTCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCGTACAT CATCGTGTTC 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGACTTCCCG GGCGACGACA 200
CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCTGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCGGGC TTCCTGGATT CTTACATCCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACCGTTG TTACCGGTCG TGTAGAACGC 400
GGTATCATCA AAGTTGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGACAC 450
CGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550

GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGTT CTATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG 650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT 700
ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TTGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG 800
CGAAGGACGA AGGTCTGCGT TTCGCA 826

2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactobacillus casei* subsp. *casei*
(B) STRAIN: ATCC 393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

GCTGCTGATG GCCCAATGCC ACAAACTCGT GAACATATCT TACTTTCACG 50
TCAAGTTGGT GTTCCATACA TCGTTGTATT CATGAACAAA TGTGACATGG 100
TTGACGATGA AGAATTACTA GAATTAGTTG AAATGGAAAT TCGTGATCTA 150
TTAACTGAAT ATGAATTCCC TGGCGATGAC ATTCCTGTAA TCAAAGGTTC 200
AGCTCTTAAA GCACTTCAAG GTGAAGCTGA CTGGGAAGCT AAAATTGACG 250
AGTTAATGGA AGCTGTAGAT TCTTACATTC CAACTCCAGA ACGTGATACT 300
GACAAACCAT TCATGATGCC AGTTGAGGAT GTATTCTCAA TCACTGGTCG 350
TGGAACAGTT GCAACTGGAC GTGTTGAACG TGGACAAGTT AAAGTTGGTG 400
ACGAAGTAGA AGTTATCGGT ATTGAAGAAG AGAGCAAAAA AGTAGTAGTA 450
ACTGGAGTAG AAATGTTCCG TAAATYACTA GATTACGCTG AAGCTGGCGA 500
CAACATTGGC GCACTTCTAC GTGGTGTTGC TCGTGAAGAT ATCCAACGTG 550
GTCAAGTATT AGCTAAACCA GGTTCGATTA CTCCACACAC TAACTTCAAA 600
GCTGAAACTT ATGTTTTAAC TAAAGAAGAA GGTGGACGTC ACACTCCATT 650
CTTCAACAAC TACCGCCCAC AATTCTATTT CCGTACTACT GACGTAACTG 700
GTATTGTTAC ACTTCCAGAA GGTACTGAAA TGGTAATGCC TGGTGATAAC 750
ATTGAGCTTG CAGTTGANCT AATTGCACCA ATCGCTATCG AAGACGGTAC 800
TAA 803

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactococcus lactis* subsp. *lactis*
(B) STRAIN: ATCC 19435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

```
CGGTGCAATC CTCGTTGTTG CTGCAACTGA TGGACCAATG CCACAAACTC      50
GTGAACACAT CTTGCTTTCA CGTCAAGTTG GTGTTAAATA CCTTATCGTC     100
TTCCTTAACA AGGCTGACCT TGTTGATGAT GAAGAATTGA TGGAACTCGT     150
TGAAATGGAA GTTCGTGACC TCTTGAGCGA ATACGACTTC CCAGGTGACG     200
ATATTCCTGT AATCGCTGGT TCAGCACTTG GTGCTTTGAA CGGTGAACCA     250
CAATGGGTTG CTAAAGTTGA AGAATTGATG GACATCGTTG ATGAATACAT     300
CCCAACTCCA GAACGCGACA CTGACAAACC ACTCCTTCTT CCAGTCGAAG     350
ACGTATTCTC TATCACTGGT CGTGGTACAG TTGCTTCAGG ACGTATCGAA     400
CGTGGTACTG TTAAAGTTGG TGACGAAGTT GAAATCGTTG GTATCAAAGA     450
AGAAACTAAA AAAGCTGTTG TTACTGGTAT CGAAATGTTC CGTAAAACAC     500
TTACTGAAGG TCTTGCTGGT GATAACGTCG GTGCACTTCT CCGTGGTATC     550
CAACGTGACG AAATCGAACG TGGTCAAGTT ATTGCTAAAC CAGGTTCAAT     600
CACTCCACAC AAACTTTTCG AAGGTGAAGT TTACGTATTG AGCAAAGAAG     650
AAGGCGGACG TCACACTCCA TTCTTCGACA ACTACCGTCC TCAATTCTAC     700
TTCCACACAA CTGACGTTAC TGGTTCAGTT AAACTTCCAG AAGGAACTGA     750
AATGGTAATG CCTGGTGACA ACGTGCATAT CGACGTTGAA TTGATCCACC     800
CAGTTGCGAT CGAACAAGGT ACTAC                                825
```

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leclercia adecarboxylata*
- (B) STRAIN: ATCC 23216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

```
GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCAATGC CTCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTTC ATCATCGTGT     100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT     150
GAGATGGAAG TTCGTGAACT YCTGTCCCAG TACGACTTCC CGGGCGACGA     200
CACCCCAATC GTTCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG     250
AGTGGGAAGA GAAAATCATC GARCTGGCTG GCTACCTGGA TTCCTACATC     300
CCAGAGCCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA     350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAARGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAGGAC     450
ACTGCTAAGT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCCGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC     550
GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CTAAGCCAGG CTCYATCAAG     600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCYA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC     700
GTACKACTGA CGTGACCGGT ACCATCGARC TGCCAGAAGG CGTTGAGATG     750
GTAATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT     800
CGCAATGGAC GATGGTCTGC GTTC                                 824
```

2) INFORMATION FOR SEQ ID NO: 111

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Legionella micdadei*
(B) STRAIN: ATCC 33218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

```
CGGAGCGATA TTAGTAGTAT CAGCAGCGGA TGGCCCAATG CCTCAAACGA      50
GAGAGCACAT ACTYTTATCC CGSCAGGTAG GTGTTCCCTA TATAGTAGTG     100
TTCTTAAACA AAGCTGACAT GGTGGATGAT GCGGAGTTAT TAGAATTAGT     150
TGAAATGGAA GTACGCGAYT TGTTGAGCAG CTATGAATTT CCAGGAGATG     200
AGATCCCGAT TGTAGTTGGT TCAGCATTAA AAGCATTGGA AGGCGATACG     250
AGTGATATAG GTGTACCAGC GATTGAGAAG TTAGTTGAGA CGATGGATTC     300
TTATATACCT GAGCCGGTAA GAAACATCGA TAAAAGTTTC TTGTTACCGA     350
TCGAAGACGT GTTCTCAATA TCTGGACGAG GAACAGTAGT AACAGGACGT     400
ATCGAAAGCG GGATCATCAA AGTTGGTGAG GAAGTCGAGA TTGTTGGTAT     450
ACGTGACACT CAAAAGACGA CATGCACAGG CGTTGAAATG TTCCGTAAAT     500
TACTTGACGA AGGTCGAGCT GGAGACAACG TTGGTATATT GCTACGTGGT     550
ACGAAGCGGG ATGAAGTTGA ACGCGGACAA GTATTAGCTA AGCCGGGAAG     600
CATTAAACCG CATACTAAAT TTGAAGCTGA AGTGTATGTG TTGTCAAAAG     650
ATGAAGGTGG ACGTCATACC CCATTCTTTA ACGGATATCG GCCTCAATTT     700
TACTTCAGGA CCACAGACGT AACTGGTTCT TGTGATTTAC CTGARGGTAT     750
AGAAATGGTA ATGCCAGGTG ATAACGTCAA GCTGATTGTT AGCTTACACT     800
CACCGATTGC TATGGACGAA GGTTTGCGTT TTGCAATC                  838
```

2) INFORMATION FOR SEQ ID NO: 112

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
(B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

```
CGGAGCGATA CTGGTTGTAT CAGCAGCTGA TGGTCCTATG CCACAAACGA      50
GGGAACACAT TCTATTGTCT CGCCAGGTAG GTGTTCCATA TATTGTTGTG     100
TTCATGAACA AAGCGGATAT GGTTGATGAC CCTGAGTTAT TAGAGTTAGT     150
GGAAATGGAA GTGCGAGATT TATTAAGCAG TTACGATTTC CCAGGGGATG     200
ACATACCTAT TGTTGTTGGT TCAGCTTTGA AAGCATTGGA AGGTGAAGAC     250
AGTGATATAG GCGTTAAGGC TATTGAGAAA TTGGTTGAAA CAATGGATTC     300
ATACATTCCT GAGCCAGTTA GAAACATAGA CAAGCCATTT TTGTTGCCGA     350
TTGAAGACGT ATTTTCAATT TCTGGACGCG GAACAGTGGT AACTGGTCGT     400
GTAGAGAGTG GAATTGTTAA AGTTGGTGAG GAAGTTGAAA TTGTTGGAAT     450
AAGAGACACC CAAAAGACGA CTTGTACGGG TGTTGAGATG TTCCGTAAAT     500
TACTTGATGA AGGTCGAGCT GGTGATAACG TTGGTGTGTT ATTACGAGGT     550
```

ACGAAGCGAG ATGAAGTGGA GCGTGGACAG GTATTGGCGA AGCCAGGAAC 600
CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG 650
AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATACCG TCCACAATTC 700
TATTTCAGAA CCACTGACGT GACAGGTACT TGTGACTTGC CATCAGGAGT 750
TGAAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG 800
CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT 838

2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leminorella grimontii*
(B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

GTGCAATCCT GGTAGTAGCA GCGACTGACG GCCCGATGCC TCAGACTCGC 50
GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA TCATCGTATT 100
CCTGAACAAG TGCGATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG 150
ARATGGAAGT TCGCGAACTG CTGTCTCAGT ACGACTTCCC GGGCGACGAC 200
ACTCCGGTAG TCCGCGGTTC AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA 250
GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC 300
CAGAACCTGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC KATCGAAGAC 350
GTATTCTCTA TCTCCGGCCG TGGTACCGTT GTTACCGGTC GTGTAGAGCG 400
CGGCATCATC AAAGTCGGTG AAGAAGTGGA AATCGTCGGT ATCAAAGATA 450
CCACCAAGAC CACCTGTACC GGCGTTGAAA TGTTCCGTAA GCTGCTGGAC 500
GAAGGCCGTG CGGGCGAGAA CGTGGGCGTT CTGCTGCGCG GTACCAAGCG 550
TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC 600
CTCACACCCA GTTCGTGTCA GAAGTGTATA TCCTGAGCAA GGATGAAGGC 650
GGCCGTCATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG 700
TACGACTGAC GTGACAGGCA CCATCGAACT GCCGGAAGGC GTAGAGATGG 750
TAATGCCAGG CGACAACATT CAGATGACCG TAAGTCTGAT TGCGCCGATC 800
GCAATGGACG AAGGTCTGCG CTTCGCAA 828

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leminorella richardii*
(B) STRAIN: ATCC 33998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

GCTATCCTGG TTGTTGCTGC GACTGACGGC CCAATGCCTC AGACTCGTGA 50
GCACATCCTG CTGGGTCGCC AGGTAGGCGT TCCTTACATC ATCGTGTTCC 100
TGAACAAGTG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150
ATGGAAGTTC GTGAACTTCT GTCTCAATAC GACTTCCCGG GCGACGATAC 200
GCCGGTTGTT CGCGGTTCAG CGCTGAAAGC GCTGGAAGGT GACGCYGAGT 250
GGGAARCGAA AATCATTGAA CTGGCGGAAT CCTTRGATAC TTAYATTCCA 300
GAGCCAGAGC GTGCGATTGA CAAGCCGTTC CTGCTGCCTA TCGAAGACGT 350
TTTCTCTATC TCTGGCCGTG GTACTGTAGT CACCGGTCGT GTAGAGCGCG 400
GCATCATCAA AGTTGGTGAA GAAGTGGAAA TCGTGGGAAT CAAAGACACC 450
ACCAAGACCA CCTGTACTGG CGTTGAAATG TTCCGTAAGC TGCTGGACGA 500
AGGCCGTGCA GGTGAGAACG TTGGTGTTCT GCTGCGYGGT ACTAAGCGTG 550
ACGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCAGGCAC CATCACTCCT 600
CACACAGAAT TCGTGTCAGA AGTGTATATC CTGAGCAAGG ATGAAGGCGG 650
YCGTCATACT CCGTTCTTCA AAGGCTACCG TCCTCAGTTC TACTTCCGTA 700
CGACTGACGT GACCGGCACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA 750
ATGCCAGGCG ATAACATCCA GATGGTAGTT ACGCTGATTG CCCCAATCGC 800
GATGGACGAA GGTCTGCGCT TCGCAA 826

2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leptospira interrogans*
(B) STRAIN: ATCC 23581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

TGCGGCGATT CTTGTAGTAT CCGCAACTGA CGGACCTATG CCACAAACAA 50
AAGAACATAT CCTTCTTGCT CGTCAGGTAG GTGTTCCATA TGTAATTGTA 100
TTCATTAACA AAGCAGATAT GCTTGCTGCT GACGAAAGAG CAGAAATGAT 150
CGAAATGGTT GAGATGGACG TTCGTGAACT TCTCAATAAG TATAGCTTCC 200
CAGGAGATAC AACTCCTATC GTTCATGGTT CTGCGGTAAA AGCACTTGAG 250
GGCGATGAAT CTGAAATTGG GATGCCTGCA ATTCTCAAAT TGATGGAAGC 300
TCTGGATACT TTCGTTCCAA ATCCAAAACG TGTAATCGAC AAACCTTTCC 350
TTATGCCAGT AGAAGACGTT TTCTCGATCA CTGGTCGTGG AACTGTTGCA 400
ACTGGAAGAG TGGAACAAGG TGTTTTGAAA GTGAACGACG AAGTTGAAAT 450
TATCGGTATC CGCCCAACAA CAAAAACTGT TGTTACCGGT ATCGAAATGT 500
TCAGAAAACT TCTCGATCAA GCGGAAGCTG GCGACAACAT CGGCGCTCTT 550
CTTCGTGGAA CTAAAAAAGA AGAAATCGAA AGAGGGCAAG TTCTTGCGAA 600
GCCAGGTTCT ATCACTCCTC ACAAAAAGTT TGCCGCTGAG GTGTATGTAT 650
TAACTAAGGA TGAAGGCGGA CGTCATACTC CGTTTATCAA TAACTACCGT 700
CCTCAGTTTT ACTTTAGAAC AACTGACGTA ACCGGAGTTT GTAACCTTCC 750
TAATGGTGTC GAAATGGTTA TGCCTGGTGA TAACGTTTCT TTGACGGTTG 800
AATTGATTAG CCCGATCGCA ATGGACAAGG GTCTTAAGTT CGC 843

2) INFORMATION FOR SEQ ID NO: 116

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Megamonas hypermegale*
(B) STRAIN: ATCC 25560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

```
CGGTGCTATC CTCGTTGTTA GTGCTGCTGA TGGTCCTATG CCTCAGACTC      50
GTGAACACAT CCTTCTCGCT CGTCAGGTTG GTGTTCCAGC TATCGTTGTA     100
TTCCTCAACA AAGCTGACCA GGTTGATGAC CCTGAACTTC TCGAACTTGT     150
TGAAATGGAA GTTCGTGAAC TTCTTTCCAG CTATGACTTC CCAGGCGATG     200
ACGTTCCAGT AATCACTGGT TCCGCTCTTC AGGCTCTCGA AGGCGACGAA     250
GAAGCTAAAA AGAAAATTCT TGAATTAATG GATGCTGTTG ATGATTACAT     300
CCCAACTCCA ACACGTGACA CTGATAAACC TTTCTTAATG CCAGTTGAAG     350
ACGTATTCAC AATTACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
CGTGGCGAAC TTAAACTTGG TGACAGCGTT GAAATCGTTG GTCTTTCCGA     450
TGAAAAGAAA TCCACTACTG TAACTGGTAT CGAAATGTTC CGCAAAATGC     500
TTGATAGCGC TGTTGCTGGT GATAACATCG GTGCACTTCT TCGTGGTATT     550
GACCGTAAAG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CTGGCACAAT     600
TCATCCACAC AAAAAATTCA AAGCTCAGGT TTACGTATTA ACTAAAGAAG     650
AAGGTGGACG TCATACTCCA TTCTTCTCCA ACTATCGTCC ACAGTTCTAT     700
TTCCGTACTA CTGACGTTAC TGGTGTTGTA ACTCTTCCAG AAGGTACTGA     750
AATGGTTATG CCTGGCGATA ACATTGAAAT GAGCATCGAA CTCATCACTC     800
CAATCGCTAT TGAAAAAGGT CTTCGCTTCG CT                       832
```

2) INFORMATION FOR SEQ ID NO: 117

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 820 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mitsuokella multacida*
(B) STRAIN: ATCC 27723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

```
TGGTGCTATC CTCGTCGTTT CCGCTGCTGA TGGCCCGATG CCGCAGACGC      50
GTGAGCACAT CCTGCTCGCT CGCCAGGTCG GTGTTCCGGC AATCGTTGTC     100
TTCCTCAACA AGGTTGACCA GGTTGACGAT CCGGAGCTCC TCGAGCTCGT     150
CGAGATGGAA GTTCGCGAGC TGCTCTCCAG CTACGACTTC CCGGGCGATG     200
ACATCCCTGT AATCGCTGGT TCCGCTCTGA AGGCCCTCGA AGGCGACGAA     250
GAGCAGAAGA AGAACATCCT CAAGCTCATG GAAGCTGTCG ATGAGTACAT     300
CCCGACGCCG GTCCGCGACA ACGCTAAGCC GTTCCTGATG CCGGTCGAGG     350
ATGTCTTCAC GATCACGGGC CGTGGTACGG TTGCAACGGG CCGCGTTGAG     400
CGTGGTGAGC TCAAGATGAA CGATACGGTT GAGATCGTTG GTCTGCAGGA     450
CGAGCCGCGT CAGACGGTTG TCACGGGCAT CGAGATGTTC CGCAAGATGC     500
TTGATTTCGC TGAGGCTGGC GATAACATCG GTGCTCTGCT CCGTGGTATC     550
```

GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT 600
TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG 650
AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC 700
TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAACTGCCGG AAGGCACGGA 750
GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC 800
CGATCGCTAT CGAGAAGGGC 820

2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mobiluncus curtisii* subsp. *holmesii*
(B) STRAIN: ATCC 35242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA 50
AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC 100
GCTCTGAACA AGTGCGATTC TTCCGATGTG GACGAAGACA TGCTCGAAAT 150
CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG 200
ACTGCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC 250
GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTCG ATACCTACAT 300
TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG 350
ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA 400
CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTCGTCC 450
TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG 500
ACGAAGCCTA CGCCGGCGAG AACTGTGGTC TGTTGCTGCG TGGCACCAAG 550
CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCCTG GCTCCGTGAC 600
CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG 650
GTGGACGTCA CAAGTCGTTC TACGACGGCT ACCGCCCGCA GTTCTTCTTC 700
CGCACCACCG ACGTGACCGG TGTTATTCAC CTGCCCGAAG GCACCGAAAT 750
GGTTATGCCT GGCGACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA 800
TCGCTATGGA GGAAGGTCTC GGCTTCGCTA T 831

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moellerella wisconsensis*
(B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

```
GGTGCAATTC TGGTTGTTGC TGCAACTGAT GGCCCTATGC CACAGACTCG      50
TGAGCACATC CTGTTAGGTC GTCAGGTTGG CGTTCCATAC ATCATCGTTT     100
TCCTGAACAA ATGTGACATG GTAGACGACG AAGAGCTGTT AGAACTGGTT     150
GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGATTTCC CAGGCGATGA     200
CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCTCTGGAA GGCGAAGCTG     250
AGTGGGAAGC TAAAATCATT GAACTGGCAG AAGCACTGGA TTCTTATATC     300
CCAGAGCCAG AGCGTGACAT TGATAAGCCA TTCCTGTTAC CAATCGAAGA     350
CGTATTCTCA ATTTCAGGCC GTGGTACAGT TGTTACTGGT CGTGTTGAGC     400
GTGGTATCGT TAAAGTCGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT     450
ACCGTGAAAA CAACATGTAC TGGCGTTGAA ATGTTCCGTA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAAC     550
GTGATGATAT CGAACGTGGT CAAGTATTGG CTAAACCAGG TTCAATCACT     600
CCGCATACAA CTTTCGAATC AGAAGTTTAC ATCCTGAGCA AAGATGAAGG     650
TGGCCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAG TTCTACTTCC     700
GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG     750
GTAATGCCAG GTGATAACAT CAAAATGATC GTTACTCTGA TCCACCCAAT     800
TGCAATGGAT GCAGGTCTGC GTTTT                                825
```

2) INFORMATION FOR SEQ ID NO:120

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Branhamella catarrhalis*
- (B) STRAIN: ATCC 43628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

```
TGGTGCTATC TTGGTTGTTT CTGCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCATAT CCTACTATCT CGTCAGGTTG GTGTACCATA CATCATGGTA     100
TTCATGAACA AGTGCGATAT GGTTGATGAT GAAGAGCTAC TAGAATTGGT     150
TGAAATGGAA GTTCGTGAAC TTCTATCTGA CTATGATTTC CCTGGTGATG     200
ATACCCCAAT CATCAAAGGT TCAGCACTAG AAGCATTGAA TGGTTCTGAT     250
GGTAAATATG GCGAGCCTGC AGTTCTAGAA CTGCTAGACA CACTAGACAG     300
CTATATCCCA GAGCCTGAGC GTGATATCGA TAAGTCATTC TTGATGCCAA     350
TTGAAGATGT CTTCTCGATC TCAGGTCGTG GTACAGTTGT GACTGGTCGT     400
GTTGAATCAG GTATTATTAA AGTTGGTGAT GAAATTGAAA TCATCGGTAT     450
CAAACCAACT GCTAAAACCA CCTGTACTGG TGTTGAAATG TTCCGTAAAC     500
TGTTAGACGA AGGTCGTGCA GGTGAGAACT GTGGTATCTT GTTGCGTGGT     550
ACTAAGCGTG AAGAAGTTCA ACGCGGTCAA GTACTTGCAA AACCAGGTTC     600
AATCACCCCA CATACTAAGT TTGATGCTGA AGTTTATGTA CTGTCAAAAG     650
AAGAAGGTGG TCGTCACACC CCATTCTTAA ATGGCTATCG CCCACAGTTC     700
TACTTCCGTA CCACAGATGT GACTGGTGCC ATCACTCTAC AAGAAGGTAC     750
CGAAATGGTT ATGCCTGGTG ACAATGTTGA GATGAGTGTT GAGCTTATCC     800
ACCCAATCGC CAGGATAAAG GTCTACG                              827
```

2) INFORMATION FOR SEQ ID NO: 121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Morganella morganii* subsp. *morganii*
(B) STRAIN: ATCC 25830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

```
CGGCGCTATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACCC      50
GTGAGCACAT CCTGTTAGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA     100
TTCCTGAACA AATGTGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT     150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCTGGCGACG     200
ACACGCCAAT CGTTCGCGGT TCAGCGCTGA AAGCACTGGA AGGCGAGCCA     250
GAGTGGGAAG CTAARATCGT TGAACTGGCA GGTTTCCTGG ATTCTTACAT     300
CCCTGAGCCA GAGCGTGCAA TTGACAAGCC GTTCCTGCTG CCAATCGAAG     350
ACGTATTCTC AATCTCCGGC CGTGGTACCG TTGTTACCGG TCGTGTTGAG     400
CGCGGTATCA TCAAGGTTGG TGAGGAAGTT GAAATCGTGG GTATCAAAGA     450
TACTGCGAAA ACCACCTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCMGGTGAG AACGTCGGTG TTCTGCTGCG TGGTACCAAG     550
CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GTTCAATCAA     600
ACCACAYACC AAATTTGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGYT ACCGTCCACA GTTCTACTTC     700
CGTACCACAG ACGTAACAGG TACTATCGAA CTGCCGGAAG GCGTTGAAAT     750
GGTAATGCCG GGCGACAACA TCAAAATGAT CGTCACCCTG ATCCACCCAA     800
TCGCAA                                                    806
```

2) INFORMATION FOR SEQ ID NO: 122

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
(B) STRAIN: TB 299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

```
GGTGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCGATGC CCCAGACCCG      50
CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC ATCCTGGTAG     100
CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC     150
GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC     200
CCCGGTTGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT     250
GGGTTGCCTC TGTCGAGGAA CTGATGAACG CGGTCGACGA GTCGATTCCG     300
GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCGG TCGAGGACGT     350
CTTCACCATT ACCGGCCGCG GAACCGTGGT CACCGGACGT GTGGAGCGCG     400
GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG     450
ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA     500
CCAGGGCCAG GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GGCGTCAAGC     550
```

GCGAGGACGT CGAGCGTGGC CAGGTTGTCA CCAAGCCCGG CACCACCACG 600
CCGCACACCG AGTTCGAAGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG 650
CGGCCGGCAC ACGCCGTTCT TCAACAACTA CCGTCCGCAG TTCTACTTCC 700
GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG 750
GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT 800
CGCCATGGAC GAAGGTCTGC GTTTC 825

2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria cinerea*
(B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

CGGTGCGATC TTGGTATGTT CCGCAGCTGA CGGTCCTATG CCGCAAACTC 50
GCGAACACAT CCTGTTGGCC CGCCAAGTAG GTGTACCTTA CATCATCGTG 100
TTCATGAACA AATGCGACAT GGTTGACGAT GCCGAGCTGT TGGAGCTGGT 150
TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGTGACG 200
ACTGCCCGAT CGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGACGCA 250
GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT 300
CCCAACACCT GAGCGTGCAG TGGACAAACC TTTCTTGTTG CCTATCGAAG 350
ACGTATTCTC TATTTCCGGT CGCGGTACAG TAGTAACCGG TCGTGTAGAG 400
CGCGGTATCA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGTCA AGCTGGTGAC AACGTAGGTG TATTGCTGCG TGGTACTAAA 550
CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACTATCAC 600
TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG 650
GTGGTCGTCA CACTCCGTTC TTCGCTAACT ACCGTCCACA ATTCTACTTC 700
CGTACTACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTAGAAAT 750
GGTAATGCCG GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA 800
TCGCTA 806

2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria elongata* subsp. *elongata*
(B) STRAIN: ATCC 25295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

CGGCGCAATC TTGGTATGTT CCGCTGCYGA CGGTCCTATG CCGCAAACTC 50
GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG 100
TTCATGAATA AATGCGACAT GGTTGAYGAT GCCGAACTGC TGGAACTGGT 150
TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG 200
ACTGCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGACGCA 250
GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT 300
CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG 350
ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG 400
CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
AACCCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA 550
CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC 600
TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG 650
GTGGTCGTCA TACTCCGTTC TTCGCTAACT ACCGTCCACA ATTCTACTTC 700
CGTACTACCG ACGTAACCGG TGCGGTTACT TTGGAAGAAG GTGTAGAAAT 750
GGTTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAACTG ATTGCACCTA 800
TCGCTATGGA AGAAGGTCTG CG 822

2) INFORMATION FOR SEQ ID NO: 125

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 820 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria flavescens*
(B) STRAIN: ATCC 13120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

CGGCGCGACT TGGTATGTTC CGCAGCTGAC GGTCCTATGC CGCAAACCCG 50
CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT 100
TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAACTGGTT 150
GAAATGGAAA TTCGTGACTT GTTGTCAAGC TACGACTTCC CAGGCGACGA 200
CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG 250
CTTACGAAGA AAAAATCTTC GAATTGGCTG CTGCCTTGGA CAGCTACATC 300
CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA 350
CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC 400
GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA 450
ACTCAAAAAA CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC 550
GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT 600
CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG 650
TGGTCGTCAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC 700
GTACTACCGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG 750
GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCAAT 800
CGCTATGGAA GAAGTCTGCG 820

2) INFORMATION FOR SEQ ID NO: 126

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria gonorrhoeae*
(B) STRAIN: ATCC 49226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

```
GGTGCAATCC TGGTATGTTC TGCTGCCGAC GGCCCTATGC CGCAAACCCG      50
CGAACACATC CTGCTGGCCC GTCAAGTAGG CGTACCTTAC ATCATCGTGT     100
TCATGAACAA ATGCGACATG GTCGACGATG CCGAGCTGTT GGAACTGGTT     150
GAAATGGAAA TCCGCGACCT GCTGTCCAGC TACGACTTCC CCGGCGACGA     200
CTGCCCGATC GTACAAGGTT CCGCACTGAA AGCCTTGGAA GGCGATGCCG     250
CTTACGAAGA AAAAATCTTC GAACTGGCTA CCGCATTGGA CAGCTACATC     300
CCGACTCCCG AGCGTGCCGT GGACAAACCA TTCCTGCTGC CTATCGAAGA     350
CGTGTTCTCC ATTTCCGGCC GCGGTACCGT AGTCACCGGC CGTGTAGAGC     400
GAGGTATCAT CCACGTTGGT GACGAGATTG AAATCGTCGG TCTGAAAGAA     450
ACCCAAAAAA CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGTCAG GCGGGCGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC     550
GTGAAGACGT AGAACGCGGT CAGGTATTGG CCAAACCGGG TACTATCACT     600
CCTCACACCA AGTTCAAAGC AGAAGTGTAC GTATTGAGCA AAGAAGAGGG     650
CGGCCGCCAT ACCCCGTTTT TCGCCAACTA CCGTCCCCAA TTCTACTTCC     700
GTACCACTGA CGTAACCGGC GCGGTTACTT TGGAAAAAGG TGTGGAAATG     750
GTAATGCCGG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT     800
CGCTATGGAA GAAGGTCTGC GCTTTGCGAT                           830
```

2) INFORMATION FOR SEQ ID NO: 127

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria lactamica*
(B) STRAIN: ATCC 23970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

```
CGGCGCAATC TTGGTATGTT CCGCCGCCGA CGGCCCTATG CCGCAAACCC      50
GCGAACACAT TCTGTTGGCC CGCCAAGTAG GTGTACCTTA CATCATCGTA     100
TTCATGAACA AATGCGATAT GGTCGACGAT GCCGAGCTGT TGGAACTGGT     150
TGAAATGGAA ATCCGCGACC TGCTGTCAAG CTACGACTTC CCAGGCGACG     200
ACTGCCCAAT CGTACAAGGT TCCGCACTGA AAGCTTTGGA AGGCGATGCC     250
GCTTACGAAG AAAAAATCTT CGAACTGGCT GCCGCATTGG ACAGCTACAT     300
CCCGACTCCC GAGCGTGCCG TGGACAAACC GTTCCTGCTG CCTATCGAAG     350
ACGTATTCTC CATCTCCGGC CGCGGTACGG TAGTAACCGG CCGTGTAGAG     400
CGCGGTGTCA TCCACGTTGG CGACGAGATC GAAATCGTCG GTCTGAAAGA     450
AACCCAAAAA ACCACCTGTA CCGGTGTCGA GATGTTCCGC AAACTGCTGG     500
ACGAAGGTCA GGCAGGCGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA     550
```

```
CGTGAAGAAG TGGAACGCGG TCAGGTATTA GCCAAACCGG GTACCATCAC      600
TCCGCACACC AAGTTCAAAG CAGAAGTGTA TGTATTGAGC AAAGAAGAGG      650
GCGGTCGTCA CACTCCGTTC TTCGCCAACT ACCGTCCGCA ATTCTACTTC      700
CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GCGTGGAAAT      750
GGTAATGCCC GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA      800
TCGCTATGGA AGAAGG                                          816
```

2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: ATCC 13077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

```
CGGTGCAATC CTGGTATGTT CCGCAGCCGA CGGTCCTATG CCGCAAACCC       50
GCGAACACAT CCTGCTGGCC CGTCAAGTAG GCGTACCTTA CATCATCGTG      100
TTCATGAACA AATGCGACAT GGTCGACGAT GCCGAGCTGT TGGAACTGGT      150
TGAAATGGAA ATCCGCGACC TGCTGTCCAG CTACGACTTC CCCGGCGACG      200
ACTGCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGATGCC      250
GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT      300
CCCGACTCCC GAGCGTGCCG TGGACAAACC TTTCTTGTTG CCTATCGAAG      350
ACGTATTCTC TATTTCCGGT CGTGGTACAG TAGTAACCGG TCGTGTAGAG      400
CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTCG GTCTGAAAGA      450
AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG      500
ACGAAGGTCA AGCAGGCGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA      550
CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACAATCAC      600
TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG      650
GCGGCCGCCA TACCCCGTTC TTCGCCAACT ACCGTCCCCA ATTCTACTTC      700
CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTGGAAAT      750
GGTAATGCCG GGCGAGAACG TAACCATCAC CGTAGAACTG ATTGCGCCTA      800
TCGCTATGGA AGAAGGTTTG CGCTTTGCGA T                          831
```

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 815 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria mucosa*
(B) STRAIN: ATCC 19696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

```
CGGCGCAATC TTGGTATGTT CTGCTGCYGA CGGTCCTATG CCGCAAACCC      50
GYGAACACAT CCTGTTGGCC CGTCAAGTAG GYGTACCTTA CATCATCGTG     100
TTCATGAACA AATGCGACAT GGTTGACGAT GCCGAAYTGT TGGAACTGGT     150
TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCTGGYGACG     200
ACTGCCCGAT TGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGATGCC     250
GCTTACGAAG AAAAAATCTT CGAACTGGCT GCCGCATTGG ACAGCTACAT     300
CCCGACTCCC GAGCGTGCCG TAGACAAACC GTTCCTGTTG CCTATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACAG TAGTAACCGG CCGTGTAGAG     400
CGCGGTGTTA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA     450
AACCCAAAAA ACCACATGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGTCA AGCCGGTGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA     550
CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC     600
TCCGCACACC AAATTCAAAG CAGAAGTGTA CGTATTGAGC AAAGAAGAGG     650
GTGGTCGTCA TACTCCGTTC TTCGCTAACT ACCGTCCTCA ATTCTACTTC     700
CGTACTACCG ACGTAACCGG TGCGGTTACT TTGGAAGAAG GTGTAGAAAT     750
GGTTATGCCT GGTGAGAAYG TAGCCATYAC TGTAGAACTG ATTGCGCCTA     800
TYGCTATGGA AGAAG                                          815
```

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Neisseria sicca*
- (B) STRAIN: ATCC 9913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

```
GGCGCAATCT TGGTATGTTC CGCTGCTGAC GGTCCTATGC CGCAAACCCG      50
CGAACACATC CTGTTGGCCC GCCAAGTAGG CGTACCTTAC ATCATCGTGT     100
TCATGAACAA ATGCGACATG GTTGACGATG CCGAGCTGTT GGAACTGGTT     150
GAAATGGAAA TCCGTGACTT GCTGTCAAGC TACGACTTCC CTGGTGACGA     200
CTGCCCGATC GTACAAGGTT CTGCACTGAA AGCCTTGGAA GGCGACGCCG     250
CTTACGAAGA AAAAATCTTC GAACTGGCTG CTGCATTGGA CAGCTACATC     300
CCGACTCCTG AGCGTGCCGT GGACAAACCG TTCCTGTTGC CTATTGAAGA     350
CGTATTCTCC ATCTCCGGTC GCGGTACCGT AGTAACCGGC CGTGTAGAGC     400
GCGGTGTTAT CCACGTTGGT GACGAGATTG AAATCGTAGG TCTGAAAGAA     450
ACCCAAAAAA CCACTTGTAC CGGTGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGTCAA GCCGGTGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC     550
GTGAAGAAGT GGAACGCGGT CAAGTATTGG CTAAACCGGG TACCATCACT     600
CCTCACACTA AATTCAAAGC AGAAGTTTAC GTATTGAGTA AAGAAGAGGG     650
TGGTCGTCAT ACTCCGTTCT TCGCTAACTA CCGTCCTCAA TTCTACTTCC     700
GTACTACCGA CGTAACCGGC GCGGTTACTT TGGAAGAAGG TGTAGAAATG     750
GTTATGCCTG GTGAGAACGT AGCCATCACT GTAGAACTGA TTGCACCGAT     800
CGCTATGGAA GAAGGTCTGC GCTTTGCGA                            829
```

2) INFORMATION FOR SEQ ID NO: 131

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria subflava*
(B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

```
CGGCGCGACT TGGTATGTTC CGCAGCTGAT GGTCCTATGC CTCAAACTCG      50
CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT     100
TCATGAACAA ATGCGACATG GTTGACGATG CCGAGCTGTT GGAACTGGTT     150
GAAATGGAAA TCCGTGACCT GTTGTCAAGC TACGACTTCC CAGGCGACGA     200
CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGACGCTG     250
GTTACGAAGA GAAAATCTTC GAATTGGCTG CTGCTCTGGA CAGCTACATC     300
CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA     350
CGTATTCTCT ATCTCTGGCC GTGGTACAGT AGTAACTGGT CGTGTAGAGC     400
GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA     450
ACCCAAAAAA CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGTCAA GCTGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACCAAAC     550
GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATTACT     600
CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG     650
TGGTCGTCAC ACTCCATTCT TCGCTAACTA CCGTCCACAA TTCTACTTCC     700
GTACTACTGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG     750
GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT     800
CGCTATGGAA GAAG                                           814
```

2) INFORMATION FOR SEQ ID NO: 132

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

```
GCCATCTTGG TATGTTCTGC TGCTGACGGT CCTATGCCGC AAACCCGTGA      50
GCACATCCTG TTGGCTCGTC AAGTAGGTGT ACCCTACATC ATCGTATTCA     100
TGAACAAATG CGATATGGTT GATGATGCAG AGCTGCTGGA ATTGGTAGAA     150
ATGGAAATCC GTGATCTGCT GAGCAGCTAC GATTTCCCTG GCGATGATTG     200
YCCAATCGTG CAAGGTTCTG CTTTGAAAGC TTTGGAAGGT GATGCCGCTT     250
ACGAAGAAAA AATCTTTGAA TTAGCTGCTG CATTGGATAG CTATATTCCA     300
ACWCCTGAGC GYGCTGTTGA TAAACCATTC CTGTTGCCGA TTGAAGATGT     350
ATTCTCAATT TCAGGTCGTG GTACAGTAGT AACTGGTCGT GTAGAGCGCG     400
GTATTATTCA CGTAGGCGAT GAAATTGAAA TTGTAGGTTT GAAAGARACY     450
CAAAAAACTA CTTGTACCGG CGTTGAAATG TTCCGTAAAT TGCTGGATSA     500
AGGTCAGGCT GGTGATAACG TAGGCGTATT GTTGCGTGGT ACCAAACGTG     550
```

```
AAGACGTTGA GCGTGGTCAA GTATTGGCTA AGCCTGGTWC TATTACTCCG      600
CAYACCAAAT TCAAAGCAGA RGTKTATGTW TTGAGYAAGG AAGAAGGCGG      650
TCGTCATACT CCGTTCTTCG CTAACTATCG TCCGCAATTC TATTTCCGTA      700
CTACAGACGT TACCGGTGCK GTRACTTTAG AAGAAGGTGT GGAAATGGTA      750
ATGCCTGGTG AGAAYGTTGC CATTACTGTW GARYTGATYG CTCCGATTGC      800
KATGGAAGAA GGYTGCGT                                        818
```

2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 836 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Ochrobactrum anthropi*
- (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

```
CGGCGCAATT CTGGTTGTTT CGGCCGCTGA CGGCCCGATG CCGCAGACCC       50
GTGAGCACAT CCTGCTCGCT CGTCAGGTTG GCGTTCCGGC AATCGTCGTG      100
TTCCTGAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT      150
TGAACTGGAA GTTCGCGAAC TTCTGTCGAA ATACGATTTC CCGGGCGACG      200
AAGTTCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCG      250
AAGGAACTGG GCGAAGACGC CGTTCGTTCG CTGATGGCCG CTGTTGACGA      300
CTACATTCCG ACCCCGGAAC GTCCGATCGA CCAGCCGTTC CTGATGCCGA      350
TCGAAGACGT TTTCTCGATC TCGGGCCGTG GTACGGTTGT GACGGGTCGC      400
GTTGAGCGCG GTATCGTCAA GGTTGGTGAA GAAGTTGAAA TCGTCGGCAT      450
CAAGGCGACG GCGAAGACGA CGGTAACCGG CGTTGAAATG TTCCGCAAGC      500
TGCTCGAYCA GGGCCAGGCT GGCGACAACA TCGGCGCTCT GATCCGCGGC      550
GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTC      600
TGTGAAGCCG CACACCAAGT TCAAGGCAGA AGCCTACATT CTGACCAAGG      650
ACGAAGGTGG CCGTCATACG CCGTTCTTTA CGAACTACCG TCCGCAGTTC      700
TACTTCCGCA CGACGGACGT GACCGGTGTT GTCACGCTGC CGGAAGGCAC      750
GGAAATGGTT ATGCCTGGCG ACAACGTCGC TATGGACGTC ACCCTGATCG      800
TGCCGATCGC CATGGAAGAG AAGCTCCGCT TCGCTA                     836
```

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 805 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Pantoea agglomerans*
- (B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

```
CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA      50
TCCTGCTGGG TCGTCAGGTT GGCGTTCCTT ACATCATCGT GTTCCTGAAC     100
AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAACTGG TAGAGATGGA     150
AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA     200
TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA     250
GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCCGGATCC     300
AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT     350
CAATCTCTGG CCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGCATC     400
GTTAAAGTCG GCGACGAAGT TGAAATCGTG GGTATCAAAG ATACTGCGAA     450
ATCAACCTGT ACCGGTGTTG AGATGTTCCG TAAGCTGCTG GACCAGGGTC     500
AGGCAGGCGA AAACTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC     550
ATCCAGCGTG GCCAGGTTCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC     600
CCAGTTCGAG TCAGAAGTTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC     650
ATACTCCGTT CTTCAAAGGC TATCGTCCAC AGTTCTACTT CCGTACAACT     700
GATGTAACCG GTTCAGTAGA GCTGCCAGAA GGCGTTGAGA TGGTCATGCC     750
AGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG     800
ACGAA                                                     805
```

2) INFORMATION FOR SEQ ID NO: 135

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Pantoea dispersa*
- (B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

```
CGCGATCCTG GTTGTTGCTG CGACTGATGG CCCAATGCCT CAGACCCGTG      50
AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC     100
CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA     150
GATGGAAGTT CGCGATCTGC TGTCTCAGTA CGACTTCCCA GGCGACGATA     200
CCCCAATCGT ACGCGGTTCT GCGCTGAAAG CGCTGGAAGG CGACGCTGAG     250
TGGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC     300
AGATCCAGTA CGTGCTATCG ATCTGCCGTT CCTGCTGCCA ATCGAAGACG     350
TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCG TGTTGAGCGC     400
GGCATCGTGA AAGTGGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC     450
TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAAA CTGCTGGACC     500
AGGGTCAGGC AGGCGAGAAC TGTGGTGTTC TGCTGCGCGG TATCAAGCGT     550
GAAGAGATCC AGCGTGGTCA GGTTCTGGCT AAGCCAGGCA CCATCAAGCC     600
ACACACCAAG TTCGTATCAG AAGTGTACGT ACTGTCTAAA GACGAAGGCG     650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT     700
ACYACTGATG TGACCGGCAM CATMGAACTG CCAGAAGGCG TTGAGATGGT     750
AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG     800
CGATGGACCA GGGTCTGCGT TTCGC                                825
```

2) INFORMATION FOR SEQ ID NO: 136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pasteurella multocida*
(B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

```
CACAAACACG TGAGCACATC CTTTTAGGTC GCCAAGTAGG CGTTCCTTAC      50
ATCATCGTAT TCTTAAACAA ATGCGACATG GTGGATGATG AAGAATTATT     100
AGAATTAGTT GAAATGGAAG TGCGTGAACT TCTTTCTCAA TATGATTTCC     150
CAGGTGATGA TACACCAATC GTACGTGGTT CAGCGTTACA AGCGTTAAAC     200
GGYGTAGCTG AGTGGGAAGA GAAAATTCTT GAGTTAGCCA ACCACTTAGA     250
TACTTACATT CCAGAGCCAC AACGTGCAAT CGACCAACCG TTCCTTCTTC     300
CGATTGAAGA CGTGTTCTCA ATTTCTGGTC GTGGTACAGT AGTAACAGGT     350
CGTGTTGAGC GTGGTATCAT CCGTACAGGT GAAGAGGTTG AAATTGTTGG     400
TATTAAAGCG ACAACGAAGA CCACAGTAAC AGGTGTTGAG ATGTTCCGTA     450
AATTATTAGA CGAAGGTCGT GCGGGTGAGA ACGTTGGTGC TTTATTACGT     500
GGTACTAARC GTGAAGAAAT CGAACGTGGT CAAGTGTTAG CGAAACCGGG     550
TTCAATYACG CCACACACTG ATTTTGAATC AGAAGTTTAC GTGTTATCAA     600
AAGAAGAAGG TGGTCGTCAT ACACCATTCT TCAAAGGTTA CCGTCCACAG     650
TTCTACTTCC GTACAACGGA CGTAACAGGT ACAATCGAAT TACCGGAAGG     700
TGTTGAGATG GTGATGCCTG GTGATAACAT CAAGATGACT GTAAGTTTGA     750
TTCACCCAAT CG                                             762
```

2) INFORMATION FOR SEQ ID NO: 137

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Peptostreptococcus anaerobius*
(B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

```
TGGAGCTATC TTAGTTGTAT CAGCAGCGGA TGGACCAATG CCACAAACAA      50
GAGAACACAT CTTATTATCA AGACAAGTAG GAGTACCATA TATCGTAGTA     100
TATTTGAATA AAGCAGATAT GGTAGAAGAT GAAGAATTAT TAGAATTAGT     150
AGAAATGGAA GTAAGAGAAT TACTATCTGA ATATGGATTC CCAGGAGATG     200
AAATTCCAAT CATAACAGGA TCATCCTTAG GAGCATTAAA TGGAGAACAA     250
AAATGGATAG ATCAAATCAT GGCATTGATG AAAGCCGTAG ATGAATATAT     300
TCCAACACCG GAAAGAGCAG TAGATCAACC ATTCTTGATG CCAATCGAAG     350
ACGTATTTAC AATTACAGGA AGAGGAACTG TAGTAACAGG AAGAGTTGAA     400
AGAGGAGTTG TAAAAGTWGG AGAAGAAGTT GAAATCGTAG GAATCAAAGC     450
GACAACAAAG ACAACTTGTA CYGGAGTAGA AATGTTCCGA AAATTATTGG     500
ATCAAGGACA AGCAGGAGAT AACATCGGAG CTTTATTRAG AGGAACCAAG     550
AAAGAAGATG TAGAAAGAGG ACAAGTATTG GCAAAACCAG GAACAATTCA     600
```

TCCTCATACA AACTTCAGTG GAGAAGTATA TGTATTGACA AAAGAAGAAG 650
GAGGAAGACA TACTCCATTC TTCTCAGGAT ACAGACCACA ATTTTACTTT 700
AGAACCACAG ATATTACAGG AGCAGTAACA TTACCAGAAG GAGTAGAAAT 750
GGTAATGCCR GGAGATAATA TCACAATGAC AGTAGAATTG ATTCACCCAA 800
TTGCAATGGA AACAGGATTA CGATTTGCAA TT 832

2) INFORMATION FOR SEQ ID NO: 138

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Peptostreptococcus asaccharolyticus*
(B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

TAGTATGTTC AGCAGCAGAY GGTCCAATGC CACAAACAAG AGAACACATT 50
CTACTAGCAA GACAAGTTGG TGTACCAAAG ATAGTAGTAT TCCTAAACAA 100
AGAAGACCAA GTAGACGATC CAGAACTAAT TGAATTAGTA GAGATGGAAA 150
TCAGAGACCT ACTATCAGAA TATGACTTCG AYGGAGACAA CACACCAATC 200
GTAGTAGGAT CAGCATTAAA AGCCCTAGAC GATCCAGACG GAGAATGGGG 250
AGACAAAATC GTAAAACTAA TGGAAGMAGT AGACGAATAC ATCCCAACAC 300
CAGTAAGAGA TACAGAACAC CCATTCCTAA TGCCAATCGA AGACRTATTC 350
TCAATYACAG GAAGAGGAAC AGTAGCAACA GGAAGAGTAG AACAAGGTGT 400
AGTAAAAGTA GGMGACACAG TAGAACTAGT AGGCTTAACA GACGAAAGCA 450
GACAAGTAGT AGTAACAGGT GTAGAAATGT TTAGAAAACA ACTAGACCTA 500
GCAGAAGCMG GAGACAACAT TGGAGCCCTA CTAAGAGGAG TACAAAGAGA 550
AGAAATCCAA AGAGGACAAG TACTAGCAGC ACCAGGAACA ATCAAACCAC 600
ACACAAAATT TGAAGCAGAA GTATACGTAC TAACAAAAGA AGAAGGTGGA 650
AGACACACAC CATTCTTTAA CGGATACAGA CCACAATTCT ACTTCAGAAC 700
AACAGACGTA ACAGGAGACA TCCAACTAGC AGACGGAGTA GAAATGGTAA 750
TGCCAGGAGA CAACTCAACA TTTACAGTAA CACTAATCAC ACCAATCGCA 800
ATGGACGAAG GACTAAGATT CGC 823

2) INFORMATION FOR SEQ ID NO: 139

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Peptostreptococcus prevotii*
(B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

CTATCATCGT AGTATCTGCA GCAGACGGTC CAATGCCCAA ACAGAGAGAA 50
CACATCCTAC TAGCAAGACA AGTAGGCGTT CCAAAAATCG CAGTATTCCT 100
AAACAAAGAA GACCAAGTAG ACGATCCAGA ACTAATCGAA TTAGTAGAAA 150
TGGAAATCAG AGACCTACTT TCAGAATACG ACTTCGATGG AGACAACGCT 200
CCAGTAGTAG TAGGATCTGC TCTTAAATCA CTAGAAGAAG GCGGAGAAGG 250
CCCATGGTCA GACAAAATCC TTGACCTAAT GGCACAAGTA GACGAATACT 300
TCGACATCCC AGAAAGAGAC AACGACCAAC CATTCCTAAT GCCAGTAGAA 350
GACGTAATGA CAATCTCAGG ACGTGGAACA GTAGCAACAG GAAGAGTTGA 400
AAGAGGAACA CTAAAAGTTG GTGATACAGT AGAAATCGTA GGACTAACAG 450
AAGATACAAA AGAAACAGTA GTAACTGGAG TAGAAATGTT CCACAAATCM 500
CTAGACCAAG CAGAATCTGG AGATAACGTA GGACTACTAC TAAGAGGAGT 550
AACAAGAGAT CAAATCTCAA GAGGACAAGT ACTAGCAAAA CCAGGWTCAG 600
TAAACCCACA CACAGAATTC GAAGGTCAAG TATACGTACT AACAAAAGAA 650
GAAGGTGGAC GTCACACACC ATTCTTCAGT GGATATAGAC CACAATTCTT 700
CTTTAGAACA ACAGACGTAA CAGGAGACAT CGAACTAGAA GAAGGCGTAG 750
AAATGGTAAT GCCAGGAGAC AACGCAACAT TCAAAATCAC ACTCCAAAAA 800
CCAATCGCTC TAGAAGAAGG ACTAAGATTC GC 832

2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas asaccharolytica*
(B) STRAIN: ATCC 25260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

CGGTGCTATC ATCGTAGTTG CTGCAACTGA TGGTCCTATG CCTCAGACGC 50
GTGAGCACAT CCTACTAGCA CGTCAGGTCA ACGTACCTCG TCTAGTTGTC 100
TTTATGAACA AGTGCGACCT TGTTGATGAC GAGGAGATGC TCGAGCTCGT 150
AGAGATGGAT ATGCGTGAGC TACTAAGCTT CTATGACTTT GACGGCGACA 200
ACACTCCTGT CATCCGTGGT TCTGCTCTTG GTGCTCTCAA TGGTGAGCCT 250
AAGTGGGTAG AGAAGGTTAT GGAGCTCATG GAGGCTGTAG ACACTTGGAT 300
CCCACTACCT GAGCGCGACA TCGACAAGCC TTTCCTAATG CCTGTAGAGG 350
ACGTATTCTC TATCACAGGT CGTGGTACTG TCGCTACTGG TCGTATCGAG 400
ACTGGTGTCG TTAAGGTCAA CGATGAGGTT CAGATCATCG GTCTAGGTGC 450
TGAGGGTAAG AAGAGCGTCG TAACTGGCGT GGAAATGTTC CGCAAGATCC 500
TTGATGAGGG TGAAGCTGGT GATAACGTAG GTCTCCTACT CCGTGGTATC 550
GACAAGGACG AGATCAAGCG CGGTATGGTC CTAGCACACC CAGGTCAGGT 600
CAAGCCTCAC GATCACTTCA AGGCTGAGGT CTATATCCTG AAGAAGGAAG 650
AGGGTGGTCG TCACACACCA TTCCACAACA AGTACCGTCC TCAGTTCTAC 700
ATCCGTACGC TAGACGTAAC GGGCGAGATC ACACTCCCAG AGGGTGTAGA 750
GATGGTTATG CCTGGTGATA ACGTCACCAT CGATGTCAAG CTCATCTCTC 800
CAGTAGCTTG TAGCGTAGGT CTACGCTTCG C 831

2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*
(B) STRAIN: ATCC 33277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

```
CGGTGCTATA ATCGTTGTAG CAGCTACAGA CGGTCCTATG CCTCAGACTC      50
GCGAGCACAT CCTTTTGGCT CGCCAGGTAA ACGTTCCTCG TCTGGTTGTT     100
TTCATGAACA AATGTGACAT GGTAGACGAT GAAGAGATGC TCGAGCTTGT     150
TGAAATGGAC ATGCGCGAAC TCCTTTCTTT CTACGATTTC GATGGTGACA     200
ATACCCCTAT CATCCGTGGT TCTGCTCTGG GCGCTTTGAA TGGAGAGCCT     250
CAGTGGGAAG ACAAGGTGAT GGAGCTTATG GAAGCTGTTG ACAACTGGGT     300
TCCCCTGCCT GAGCGCGATA TCGACAAACC GTTCTTGATG CCGGTTGAAG     350
ACGTGTTCTC TATCACGGGT CGTGGTACGG TCGCTACAGG ACGTATCGAA     400
ACCGGTATTG TGAAGACCGG TGACGAAGTT CAAATCATCG GCCTCGGTGC     450
AGAAGGAATG AAGTCGGTTG TTACGGGTGT TGAAATGTTC CGTAAGATTC     500
TTGACGAAGG TCAGGCTGGT GACAACGTTG GTCTCCTCCT GCGTGGTATC     550
GATAAGGATC AGATCAAGCG TGGTATGGTT ATCTCTCACC CGGGTAAGAT     600
TACTCCTCAC AAGAGATTTA AGGCCGAGGT TTATATCTTG AAGAAAGAAG     650
AAGGTGGTCG CCACACTCCT TTCCACAACA AATATCGTCC GCAGTTCTAC     700
ATCCGTACGC TTGACGTGAC CGGTGAAATC ACTCTTCCCG AAGGAACAGA     750
AATGGTTATG CCCGGTGACA ACGTAACGAT CACTGTAGAA CTCATCTACC     800
CGGTTGCATG TAATGTAG                                       818
```

2) INFORMATION FOR SEQ ID NO: 142

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pragia fontium*
(B) STRAIN: ATCC 49100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

```
CGGCGCTATT CTGGTTGTTG CTGCAACTGA TGGTCCTATG CCTCAAACTC      50
GTGAGCACAT CCTGTTAGGY CGCCAGGTTG GCGTACCATA CATCATTGTG     100
TTCCTGAACA AGTGTGACAT GGTTGAYGAT GAAGAGCTGT TAGAACTGGT     150
TGAAATGGAA GTTCGTGAGC TTCTGTCTCA GTACGATTTC CCAGGTGATG     200
ATACTCCAGT TGTTCGTGGT TCTGCGCTGA AAGCGTTRGA AGGCGAAGCT     250
GAGTGGGAAG CTAAAATCAT TGAATTGGCT GACTCCCTGG AYAGCTACAT     300
TCCACAGCCA GAGCGTGCAA TTGATAAGCC GTTCCTGCTG CCAATCGAAG     350
ACGTTTTCTC AATCTCTGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG     400
CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
TACTGTGAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AARTTACTGG     500
ATGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAG     550
CGTGATGAAA TCGAACGTGG TCAAGTATTA GCAAAACCAG GTTCAATCAA     600
```

CCCGCATACT AACTTCGTAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG 650
GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTYTACTTC 700
CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCA GGTGATAACA TTCAGATGAC TGTAACTCTG ATTGCCCCAA 800
TCGCGATGGA CGAAGGTTTA CGCTTCGCTA 830

2) INFORMATION FOR SEQ ID NO: 143

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Prevotella melaninogenica*
(B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

TGGTGCTATC TTGGTTGTAG CTGCTACTGA TGGTCCTATG CCTCAGACTC 50
GTGAGCACGT ATTGCTCGCT CGTCAGGTAA ACGTACCTCG CTTGGTTGTA 100
TTCTTGAACA AGTGTGATAT GGTTGACGAT GCTGAGATGC TTGACCTCGT 150
TGAGATGGAG GTTCGTGAGA TCCTCGAGCA GTACGGTTAT GAGGAGGATA 200
CTCCTATTAT TCGTGGTTCT GCACTCGGTG CTTTGAACGG TGTTGAGAAG 250
TGGGTAGACT CTGTAATGGA GCTCATGGAT ACTGTTGACA CTTGGATTGA 300
AGAGCCAGAG CGTGAGATTG ACAAGCCATT CTTGATGCCT GTTGAGGACG 350
TATTCTCTAT CACAGGTCGT GGTACTGTAG CTACTGGTCG TATCGAGACT 400
GGTATCTGTA AGGTAGGTGA TGAGGTTCAG TTGCTCGGTC TCGGTGAGGA 450
CAAGAAGTCT GTTATCACTG GTGTTGAGAT GTTCCGTAAG AACCTTCCAA 500
CAGGTCAGGC TGGTGACAAC GTAGGTCTCC TCCTTCGTGG TATCGATAAG 550
GCTGAGGTTA AGCGTGGTAT GGTTGTTGTG CACCCAGGTG CTATTACTCC 600
TCACGATCAC TTCAAGGCAT CTATCTATGT ATTGAAGAAG GAAGAGGGTG 650
GTCGTCATAC TCCATTCGGT AACAAGTATC GTCCACAGTT CTACCTCCGT 700
ACAATGGACT GTACAGGTGA AATCCACCTC CCAGAGGGCG TTGAGATGGT 750
TATGCCAGGT GACAACGTAG AGATTGAAGT TGTATTGATC TATAAGGTTG 800
CTTTGAACGA GGGTCTTCGT T 821

2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Prevotella oralis*
(B) STRAIN: ATCC 33269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

```
TGGTGCTATT CTTGTAGTAG CTGCTACTGA CGGTCCTATG CCTCAAACTC      50
GTGAACACGT GCTTCTTGCT CGTCAGGTGA ACGTACCTCG TTTGGTCGTT     100
TTCTTGAACA AGTGCGATAT GGTTGACGAT GAAGAAATGC TTGAGCTCGT     150
AGAAATGGAG CTTCATGAAC TTCTCGAGCA GTATGAATAT GAGGAGGATA     200
CTCCTATTGT TCGTGGTTCG GCACTTGGCG CTCTGAATGG AGTAGAGAAG     250
TGGGTTGACA GCGTGATGAA GTTGATGGAT ACCGTTGATG AATGGATACA     300
GGAACCACCG CGTGATCTTG ATAAGCCTTT CTTGATGCCG GTAGAGGATG     350
TATTTTCTAT TACTGGTCGT GGAACGGTTG TTACAGGCCG TATTGAAACT     400
GGTAAGGTTA AGGTGGGCGA TGAAGTTCAA CTTCTTGGTC TCGGTGAAGA     450
TAAGAAGTCC GTTGTGACAG GCGTTGAGAT GTTCCGTAAG ATTCTTGACG     500
AAGGTGAAGC TGGTGATAAT GTAGGCTTGC TGCTTCGTGG TATCGATAAG     550
ACGGAAGTAA AGCGTGGTAT GGTTGTCGTA CATCCGGGGG CTATTACTCC     600
TCACGATCAT TTCAAGGCTT CAGTTTACGT ATTGAAGAAA GAAGAAGGCG     650
GTCGCCATAC TCCGTTTGGT AMCAAGTATC GTCCACAGTT CTATCTTCGT     700
ACCATGGACT GTACTGGTGA AATTACTCTT CCGGAAGGAG TTGAGATGGT     750
AATGCCGGGT GATAACGTCG AAATTGAAGT TAAGTTGATC TATCCGGTAG     800
CTTTGAACGA GGGACTTCGT TTCGCTA                              827
```

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Propionibacterium acnes*
(B) STRAIN: ATCC 6919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

```
CGGCGCCATC CTCGTGGTTG CTGCTACCGA CGGCCCGATG CCTCAGACTC      50
GCGAGCACGT TCTGCTCGCT CGTCAGGTGG GCGTGCCCGC CATCGTCGTC     100
GCCCTCAACA AGTGCGACAT GGTTGACGAT GAGGAGCTCA TTGAGCTCGT     150
CGAGATGGAG GTCCGCGAGC TGCTGACCTC GCAGGAGTTC GACGGCGACA     200
ACTGCCCTGT CGTTCGCATC TCCGCCTTCC AGGCCCTCCA GGGTGATGAG     250
AAGTGGACCC AGTCGATCCT CGACCTCATG GACGCCGTGG ACGAGTACAT     300
CCCGCAGCCT GAGCGCGATC TCGACAAGCC CTTCCTTATG CCGATCGAGG     350
ACGTCTTCAC CATCACCGGC CGTGGCACCG TTGTCACCGG TCGTGTCGAG     400
CGCGGCGTCG TCAAGACTGG CGAAGAGGTC GAGATCGTCG GTATCCACGA     450
GAAGACCCAG AAGACCACCG TTACCGGTGT CGAGATGTTC CGCAAGATCC     500
TCGACGAGGG CCGCGCTGGT GAGAACGTCG GCGTTCTGCT CCGTGGCACC     550
AAGAAGGAGG ATGTCGTTCG CGGCATGGTC CTCTCCAAGC CTGGTTCCAC     600
CACCCCCCAC ACCGACTTCG AGGGCCAGGT CTACGTCCTC AAGAAGGATG     650
AGGGTGGCCG CCACAAGCCG TTCTTCTCCC ACTACAGCCC CCAGTTCTAC     700
TTCCGTACCA CGGACGTGAC TGGCACTGTT GAGCTCCCCG AGGGCACCGA     750
GATGGTCATG CCTGGCGACA ACACCGACAT GACTGTGCAC CTGATTCACC     800
CGGTTGCCAT GGAGGATCAG CTCAAGTTCG CTA                       833
```

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*
(B) STRAIN: ATCC 35659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

CACAAACTCG TGAGCACATC CTGTTAGGTC GTCAGGTTGG TGTTCCTTAC 50
ATCATCGTAT TCCTGAACAA ATGTGACATG GTAGATGATG AAGAGCTGTT 100
AGAATTAGTT GAAATGGAAG TTCGTGAACT TCTGTCTCAA TACGATTTCC 150
CAGGTGATGA CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCACTGGAA 200
GGCGAAGCAG AGTGGGAAGC AAAAATTGTT GAATTAGCAG AAGCACTGGA 250
TTCTTATATC CCAGAGCCAG AGCGTGCAAT TGACAAACCA TTCCTGTTAC 300
CAATCGAAGA TGTATTCTCA ATCTCAGGCC GTGGTACAGT AGTTACTGGT 350
CGTGTAGAGC GTGGTATCAT CAAAGTAGGT GATGAAGTTG AGATTGTTGG 400
TATCAAAGAA ACCGCCAAAA CAACTTGTAC TGGCGTTGAA ATGTTCCGTA 450
AATTACTTGA CGAAGGTCGT GCAGGTGAGA ACGTAGGTGT TCTGCTGCGT 500
GGTACAAAAC GTGAAGAAAT CGAACGTGGA CAAGTACTGG CRAAACCAGG 550
CTCAATCAAC CCACACAACA AATTTGAATC AGAAGTTTAT ATTCTGAGCA 600
AAGATGAAGG TGGTCGTCAC ACTCCATTCT TCAAAGGCTA CCGTCCACAG 650
TTCTACTTCC GTACAACTGA CGTAACTGGT ACTATCGAAT TACCAGAAGG 700
CGTAGAAATG GTAATGCCAG GCGACAACGT GAACATGATC GTTGA 745

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus penneri*
(B) STRAIN: ATCC 33519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

GGAGCTATCC TGGTTGTTGC TGCGACAGAT GGCCCAATGC CACAAACTCG 50
TGAGCACATC CTGTTAGGTC GTCAGGTTGG TGTTCCTTAC ATCATCGTAT 100
TCCTGAACAA ATGTGACATG GTAGATGATG AAGAGTTACT GGAATTAGTM 150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC CAGGTGATGA 200
CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCACTGGAA GGCGAAGCAG 250
AGTGGGAAGC AAAAATTGTT GAATTAGCAG AAGCACTGGA TTCATACATC 300
CCAGARCCAG AGCGTGCAAT TGACAAACCA TTCCTGTTAC CAATTGAAGA 350
CGTATTCTCA ATTTCAGGCC GTGGTACAGT AGTAACAGGT CGTGTTGAGC 400
GTGGCGTAAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATTAAACCA 450
ACAGCGAAAA CAACTTGTAC TGGCGTTGAA ATGTTCCGTA AATTACTTGA 500
CGAAGGTCGT GCAGGTGAGA ACGTAGGTGT TCTTCTGCGT GGTACTAAAC 550
GTGAAGAAAT CGAACGTGGA CAAGTACTGG CGAAACCAGG TTCAATCAAC 600
CCACACACTA AATTTGAATC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG 650
TGGTCGTCAT ACTCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700

GTACAACTGA CGTAACTGGT ACTATCGAAT TACCAGAAGG CGTAGAAATG 750
GTAATGCCAG GTGACAACAT CAACATGATC GTTGAACTGA TTCACCCAAT 800
CGCGATGGAC GACGGTTTAC GTTTCGCTA 829

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus vulgaris*
(B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC 50
GTGAGCACAT CCTGTTAGGT CGCCAGGTTG GTGTACCTTA CATCATCGTA 100
TTCCTGAACA AATGTGACAT GGTTGATGAT GAAGAACTGC TGGAATTAGT 150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG 200
ACACTCCAGT AATCCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT 250
GAGTGGGAAG CAAAAATTGT TGAATTAGCA GAAGCACTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCTATCGAAG 350
ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTAGAG 400
CGTGGTGTTG TTAAAGTTGG TGAAGAAGTT GAGATTGTTG GTATTAAAGA 450
CACAGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAATTACTTG 500
ACGAAGGTCG TGCAGGTGAG AACGTAGGTG TTCTTCTGCG TGGTACTAAA 550
CGTGAAGAAA TCGAACGTGG ACAAGTACTG GCTAAACCAG GTTCAATCAA 600
GCCACACACT AAATTCGAAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG 650
GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
CGTACAACTG ACGTAACTGG TACTATCGAA TTACCAGAAG GCGTAGAAAT 750
GGTAATGCCA GGTGACAACA TCAACATGAT CGTTGAACTG ATTCACCCTA 800
TCGCGTAGGA CGACGGTTTA CGTT 824

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia alcalifaciens*
(B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

CACAAACTCG TGAGCACATC CTGTTAGGTC GCCAAGTAGG TGTTCCTTAC 50
ATCATCGTTT TCCTGAACAA ATGTGACATG GTAGACGACG AAGAACTGTT 100

AGAATTAGTT GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC 150
CAGGCGATGA CACTCCAGTT GTTCGCGGTT CAGCACTGAA AGCGCTGGAA 200
GGCAACCCAG AGTGGGAAGC AAAAATTGTT GAATTAGCAG GTTACCTGGA 250
TTCTTACATC CCAGAACCAG AGCGTGCAAT TGACAAGCCA TTCCTGCTGC 300
CAATCGAAGA CGTATTCTCA ATCTCTGGTC GTGGTACAGT AGTAACAGGC 350
CGTGTTGAGC GTGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG 400
TATTCAAGCG ACTGCGAAAA CAACTTGTAC TGGCGTTGAA ATGTTCCGTA 450
AACTGCTGGA TGAAGGTCGT GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT 500
GGTACTAAAC GTGAAGAAAT TCAACGTGGT CAAGTACTGG CTAAACCAGG 550
TTCAATCAAG CCACACACTC AATTCGAATC AGAAGTATAT ATTCTGAGCA 600
AAGATGAAGG TGGTCGTCAT ACTCCATTCT TCAAAGGCTA CCGTCCACAG 650
TTCTACTTCC GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG 700
CGTAGAGATG GTAATGCCAG GCGACAACAT CAACATGATC GTGAC 745

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia rettgeri*
(B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

CGGTGCAATC CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC 50
GTGAGCACAT CCTGTTAGGY CGCCAAGTAG GTGTWCCTTA CATCATCGTT 100
TTCCTGAACA AATGTGACAT GGTAGACGAC GAAGAACTGT TAGAATTAGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA ATACGATTTC CCAGGCGACG 200
ACACTCCAGT TGTCCGTGGT TCAGCTCTGA AAGCGCTGGA AGGCAACCCA 250
GAGTGGGAAG CGAAAATTGT TGAATTAGCA GGTCACTTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCAATCGAAG 350
ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTTGAG 400
CGTGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCCAAGA 450
CACGGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAACTGCTGG 500
ACGAAGGTCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAA 550
CGTGAAGAAA TTCAACGTGG TCAAGTACTG GCAAAACCAG GTTCAATCAA 600
GCCACACACT AAATTCGAAT CAGAAGTCTA TATTCTGAGC AAAGATGAAG 650
GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
CGTACAACTG ACGTAACAGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCA GGTGATAACA TCAACATGAT CGTTACCCTG ATCCACCCAA 800
TCGCGATGGA CGACGGTTTA CGTTTCGCAA 830

2) INFORMATION FOR SEQ ID NO: 151

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia rustigianii*
(B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

```
CGGTGCAATC CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC      50
GTGAGCACAT CCTGTTAGGT CGCCAAGTAG GTGTTCCTTA CATCATCGTT     100
TTCCTGAACA AATGTGACAT GGTTGACGAC GAAGAACTGT TAGAATTAGT     150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG     200
ACACTCCAGT TGTTCGYGGT TCAGCACTGA AAGCGCTGGA AGGTATCCCT     250
GAGTGGGAAG CGAAAATTGT TGAATTAGCC GGTTACCTGG ACAGCTACAT     300
CCCAGAACCA GAGCGCGCAA TTGACCGTCC ATTCCTGCTG CCAATCGAAG     350
ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG SCGTGTTGAG     400
CGTGGTATCG TTAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCCAAGA     450
CACRGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAACTGCTTG     500
ACGAAGGTCG TGCTGGTGAG AACGTTGGTG TTTTACTGCG TGGTACTAAG     550
CGTGAAGAAA TTCAACGTGG TCAAGTACTG GCTAAACCAG GTTCAATCAA     600
GCCACACACT ACTTTTGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC     700
CGTACAACTG ACGTAACCGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT     750
GGTAATGCCA GGCGACAACA TCAACATGAT CGTGACACTG ATTCACCCAA     800
TCGCGATGGA TGATGGTTTA CGTTTC                               826
```

2) INFORMATION FOR SEQ ID NO: 152

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia stuartii*
(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

```
CGGTGCAATC CTAGTTGTTG CGGCAACAGA TGGCCCAATG CCACAAACTC      50
GTGAGCACAT CCTGTTAGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTG     100
TTCCTGAACA AATGTGACAT GGTAGACGAC GAAGAGCTGC TGGAACTGGT     150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA ATACGATTTC CCAGGTGATG     200
ACACTCCAGT TATCCGTGGT TCAGCGCTGA AAGCGTTGGA AGGCAACCCA     250
GAGTGGGAAG CGAAAATCGT TGAACTAGCA GAAGCACTGG ACAGCTACAT     300
CCCAGAGCCA GAGCGTGCAA TTGACAAGCC ATTCCTGCTG CCAATCGAAG     350
ACGTATTCTC AATCTCAGGT CGTGGTACAG TAGTCACAGG CCGTGTTGAG     400
CGTGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTAG GTATCAAAGA     450
GACTGCGAAA ACCACTTGTA CTGGCGTTGA AATGTTCCGT AAACTGCTGG     500
ACGAAGGCCG TGCGGGTGAG AACGTAGGTG TTCTGCTGCG TGGTACTAAG     550
CGTGAAGAAA TCGAACGTGG TCAAGTTCTG GCGAAACCAG GTTCAATCAA     600
GCCACACACA ACTTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG     650
GTGGTCGTCA CACGCCATTC TTCAAAGGYT ACCGTCCACA GTTCTACTTC     700
CGTACAACTG ACGTAACAGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT     750
GGTAATGCCA GGCGACAACG TGAACATGAA AGTAACTCTG ATTCACCCAA     800
```

TCGCGATGGA CGATGGTTTG CGTTTCGCAA

2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: ATCC 35554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

```
CCTGGTTTGC TCGGCTGCCG ACGGCCCCAT GCCGCAGACC CGCGAGCACA      50
TCCTGCTGTC CCGCCAGGTA GGCGTTCCCT ACATCGTCGT GTTCCTGAAC     100
AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAACTGG TCGAGATGGA     150
AGTTCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GACACTCCGA     200
TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC     250
ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCCTGG ACTCCTACAT     300
TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG     350
ACGTGTTCTC GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAGAG     400
CGCGGCATCA TCAAGGTCCA GGAAGAAGTG GAAATCGTCG GCATCAAGGC     450
GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG     500
ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACCAAG     550
CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA     600
GCCGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG     650
GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAGATGGT TGTCACCCTG ATCGCTCCGA     800
TCGCCATGGA AGATGGCTGC GTTCGCG                              827
```

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas fluorescens*
(B) STRAIN: ATCC 13525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

```
CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC      50
GTGAACACAT CCTGCTGTCC CGTCAGGTTG GCGTTCCGTA CATCGTGGTT     100
TACCTGAACA AGGCTGACCT GGTAGACGAC GCTGAGCTGC TGGAACTGGT     150
TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG     200
```

ACACTCCGAT CATCATCGGT TCTGCTCGTA TGGCTCTGGA AGGCAAAGAC 250
GACAACGAAA TGGGCACCAC GTCCGTTCGT AAACTGGTTG AAACTCTGGA 300
CAGCTACATC CCAGATCCAG TTCGTGTTAT CGACAAGCCG TTCCTGATGC 350
CAATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGTACTGT TGTGACTGGT 400
CGTATCGAGC GCGGTATCGT TAAGGTTCAA GATCCACTGG AAATCGTTGG 450
TCTGCGTGAC ACTACCGTCA CCACCTGCAC CGGTGTTGAA ATGTTCCGTA 500
AGCTGCTCGA CGAAGGTCGT GCTGGCGAGA ACTGCGGCGT TCTGCTGCGT 550
GGTACCAAGC GTGACGACGT TGAGCGTGGC CAGGTTCTGG TTAAGCCAGG 600
TTCGGTTAAG CCGCACACCA AGTTCGAAGC TGAAGTCTAC GTACTGAGCA 650
AAGAAGAAGG CGGTCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCACAG 700
TTCTACTTCC GTACTACTGA CGTGACTGGT AACTGCGAGC TGCCGGAAGG 750
CGTTGAAATG GTTATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA 800
TCAAAACCAT CGCAATGGAA GACGGTCTGC GTTTCGCTAT T 841

2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas stutzeri*
(B) STRAIN: ATCC 17588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

CGGCGCGATC CTGGTCTGCT CGGCTGCTGA CGGCCCCATG CCGCAGACTC 50
GCGAGCACAT CCTGCTGTCC CGTCAGGTTG GTGTTCCGTA CATCGTCGTG 100
TTCCTGAACA AGGCCGACAT GGTTGATGAC GCCGAGCTGC TCGAGCTGGT 150
CGAGATGGAA GTTCGYGACC TGCTGTCGAC CTACGACTTC CCGGGTGAYG 200
ACACTCCGAT CATCATCGGC TCCGCGCTGA TGGCGCTGAA CGGCGAAGAC 250
GACAACGAGC TCGGCACCAC TGCGGTGAAG AAGCTGGTCG AGACCCTGGA 300
CAGCTACATT CCCGAGCCGG TTCGTGCCAT CGACAAGCCG TTCCTGATGC 350
CGATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGCACSGT GGTAACCGGT 400
CGCGTAGAGC GCGGCATCGT CAAGGTTCAG GAAGAGATCG AGATCGTCGG 450
TCTGCGTCCG ACCACCAAGA CTACCTGCAC CGGCGTTGAG ATGTTCCGCA 500
AGCTGCTCGA YGARGGTCGT GCTGGCGAGA ACTGCGGYGT GCTGCTGCGT 550
GGCACCAAGC GTGACGAAGT GGAGCGTGGT CAGGTTCTGG CCAAGCCGGG 600
CACCATCAAG CCGCACACCA AGTTCGAAGC CGAAGTGTAC GTGCTGTCCA 650
AGGAAGAAGG TGGTCGTCAC ACCCCGTTCT TYAAGGGCTA CCGTCCKCAG 700
TTCTACTTCC GTACCACTGA YGTGACYGGW TCGTGCGARC TGCCGGAAGG 750
CGTCGAGATG GTAATGCCGG GCGACAACGT GAAGATGGTT GTCACCCTGA 800
TCAAGCCGAT CGCCATGGAA GACGGCCTGC GCTTCGCGAT T 841

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Psychrobacter phenylpyruvicus*
(B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

GCTATTCTAG TAGTATCAGC AACTGACGGT CCAATGCCAC AAACACGTGA 50
GCACATTCTA TTATCACGTC AGGTTGGTGT ACCATACATC ATCGTATTCA 100
TGAACAAATG TGACATGGTA GATGACGAAG AGTTACTAGA GCTAGTAGAA 150
ATGGAAGTGC GTGAATTACT TTCAGACTAC GACTTCCCAG GTGATGACAC 200
TCCAATCATC AAAGGTTCAG CTTTAGAAGC GTTAAATGGT AACGACGGTA 250
AGTACGGTGA GCCAGCAGTT ATCGAACTAC TAAACACTCT AGACACTTAC 300
ATTCCAGAGC CAGAGCGTGA CATCGATAAG CCATTCCTAA TGCCAATCGA 350
AGACGTATTC TCAATCTCAG GTCGTGGTAC AGTAGTAACA GGCCGTGTTG 400
AATCTGGTAT CATCAAAGTT GGTGACGAAA TCGAAATCGT TGGTATCAAA 450
GACACAGTTA AAACAACTTG TACTGGTATC GAGATGTTCC GTAAGTTACT 500
AGACGAAGGT CGTGCTGGTG AGAACTGTGG TGTACTATTA CGTGGTACTA 550
AGCGTGAAGA CGTACAACGT GGTCAAGTAC TTGCTAAGCC AGGTTCAATC 600
ACTCCACACA CCAACTTCGA CGCAGAAGTA TACGTACTAT CAAAAGAAGA 650
AGGTGGTCGT CACACTCCAT TCTTAAATGG TTACCGTCCA CAGTTCTACT 700
TCCGTACTAC TGACGTAACA GGTGCAATCA CGTTACAAGA AGGTACTGAA 750
ATGGTAATGC CAGGCGATAA CGTTGAGATG AGCGTAGAGC TAATCCACCC 800
AATCGCTAGG ACAAAGGTTT ACGTTTCGCA ATC 833

2) INFORMATION FOR SEQ ID NO: 157

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Rahnella aquatilis*
(B) STRAIN: ATCC 33071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACTCG 50
TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCATAC ATGATCGTGT 100
TCATGAACAA ATGCGACATG GTAGATGACG AAGAGCTGCT GGAACTGGTA 150
GAAATGGAAG TTCGCGAACT TCTGTCTGCT TACGAATTCC CAGGCGACGA 200
CATCCCGGTC ATCAAAGGTT CAGCGCTGAA AGCACTGGAA GGCGATGCTA 250
CTTGGGAAGC GAAAATCATC GAACTGGCAG AAGCACTGGA CAGCTACATT 300
CCATTGCCAG AGCGTGCTAT CGATAAGCCA TTCCTGCTGC CAATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACAGT GGTTACCGGT CGTGTAGAGC 400
GCGGTATCGT TAAAGTGGGC GAAGAAGTTG AAATCGTCGG TATCAAGGAC 450
ACTGTTAAGT CTACTTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAGC 550
GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA 600
CCACACACCA AGTTTGATTC CGAAGTGTAC ATCCTGAGCA AAGATGAAGG 650
TGGTCGTCAC ACTCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700
GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG 750
GTTATGCCTG GTGACAACGT GAACATGGTT GTTACCCTGA TCCACCCAAT 800
CGCGATGGAT GACGGTCTGC GTTTC 825

2) INFORMATION FOR SEQ ID NO: 158

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
(B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ATACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT 300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTGGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA 830

2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Choleraesuis
(B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200

ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGTGACGCA 250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTGGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGTTGG 500
ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
(B) STRAIN: ATCC 43973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATTATCGT GTTCCTGAAC 100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TAGAAATGGA 150
AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCAA 200
TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250
GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAARCTGCTG GACGAAGGCC 500
GTGCWGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ATATTCTGTC CAAAGATGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Heidelberg
(B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

```
CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG     200
ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA     250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT     300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA     400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA     600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG     650
GCGGCCGTCA YACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACTACTG ACGTGACTGG CACCATCGAA TTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA     800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC                        832
```

2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

```
CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA      50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC     100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TAGAAATGGA     150
AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACGCCGA     200
TCGTGCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAATGGGAA     250
GCGAAAATCA TCGAACTGGC TGGCTACCTG GATTCTTACA TCCCGGAACC     300
AGAGCGTGCG ATTGACAAAC CGTTCCTGCT GCCGATCGAA GACGTATTCT     350
CTATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC     400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA     450
GTCGACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC     500
GTGCTGGCGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA     550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC     600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC     650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AATTCTACTT CCGTACGACT     700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGGTAATGCC     750
```

GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTTGCTG CGACTGACGG CCCGATGCCG CAGACCCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
AATGGAAGTT CGTGAACTTC TGTCTCAGTA CGACTTCCCG GGTGACGACA 200
CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTCG TGTAGAGCGC 400
GGTATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
TCAGAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
AAGGCCGTGC CGGTGAGAAC GTAGGTGTTC TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GATGAAGGCG 650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT 700
ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TAGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800
CRATGGACGA CGGTCTGCGT TTCGCAA 827

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC 100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TAGAAATGGA 150

AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCGA 200
TCGTGCGTGG TTCCGCTCTG AAAGCGCTGG AAGGCGAMGC TGAGTGGGAA 250
GMGAAAATCA TCGAACTGGC TGGCTWCCTG GATTCTTACA TTCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
GTGCCGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

2) INFORMATION FOR SEQ ID NO: 165

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Typhi
(B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCNGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACY AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

2) INFORMATION FOR SEQ ID NO: 166

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia fonticola*
(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

```
CGGCGCTATC CTGGTTGTAG CTGCGACTGA CGGCCCTATG CCTCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA     100
TTCATGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT     150
AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTATGACTTC CCTGGTGATG     200
ACCTGCCGGT TGTTCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT     250
GAGTGGGAAG CTAAAATCAT CGAGCTGGCC GGTCACCTGG ATTCCTACAT     300
CCCAGAACCA GAGCGTGCTA TCGATCAGCC GTTCCTGCTG CCAATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TAGTTACCGG TCGTGTTGAG     400
CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
CACCGTTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG     550
CGTGAAGACA TCGAACGTGG TCAGGTACTG GCTAAACCAG GTTCCATCAA     600
GCCGCACACT CAGTTCGATT CAGAAGTGTA TATCCTGAGC AAAGAAGAAG     650
GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC     700
CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT     750
GGTAATGCCA GGCGATAACG TGAACATGGT TGTTACCCTG ATCCACCCAA     800
TCGCTATGGA CCAAGGC                                        817
```

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia liquefaciens*
(B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

```
GCTGCGACTG ACGGCCCAAT GCCTCAGACC CGTGAGCACA TCCTGCTGGG      50
TCGTCAGGTT GGCGTTCCTT TCATCATCGT ATTCATGAAC AAATGCGACA     100
TGGTTGATGA TGAAGAGCTG CTGGAACTGG TAGAAATGGA AGTTCGTGAA     150
CTTCTGTCTG CTTACGACTT CCCTGGTGAT GACCTGCCGG TTGTTCGTGG     200
TTCAGCGCTG AAAGCACTGG AAGGCGAAGC TGAGTGGGAA GCTAAAATCA     250
TCGAGCTGGC CGGTTACCTG GATTCTTACA TCCCAGAACC AGAGCGTGCT     300
ATCGACAAGC CGTTCCTGCT GCCAATCGAA GACGTCTTCT CCATCTCCGG     350
TCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGTATC GTTAAAGTTG     400
GCGAAGAAGT TGAAATCGTT GGTATCAAAG ACACCGTTAA GTCTACCTGT     450
ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC GTGCTGGTGA     500
GAACGTTGGT GTTCTGCTGC GTGGTATCAA GCGTGAAGAC ATCGAACGTG     550
GTCAGGTACT GGCTAAACCA GGTTCAATCA AGCCACACAC CAAGTTCGAC     600
TCAGAAGTGT ACATCCTGAG CAAAGAAGAA GGTGGTCGTC ATACTCCATT     650
CTTCAAAGGC TACCGTCCAC AGTTCTACTT CCGTACAACT GACGTGACCG     700
```

GTACCATCGA ACTGCCAGAA GGCGTTGAAA TGGTAATGCC AGGTGACAAC 750
GTGAACATGG TTGTTACCCT GATCCACCCA ATCGCGA 787

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 745 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia marcescens*
(B) STRAIN: ATCC 13880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GGCGTTCCTT 50
TCATCATCGT ATTCATGAAC AAATGCGACA TGGTTGATGA TGAAGAGCTG 100
YTGGAACTGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150
CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCCGCGCTG AAAGCGCTGG 200
AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250
GACAGCTACA TCCCAGAGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300
GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350
GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400
GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450
CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500
GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTACT GGCTAAGCCA 550
GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600
CAAAGATGAA GGTGGTCGTC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650
AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700
GGCGTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia odorifera*
(B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

GGCGCAATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG 50
TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100
TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTA 150
GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTCC CTGGCGACGA 200
CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG 250

AGTGGGAAGC TAAGATTGTA GAACTGGCTG AAGCGCTGGA TTCTTACATC 300
CCAGAACCAG AGCGTGCTAT CGACAAGCCG TTCCTGCTGC CAATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTTGAGC 400
GCGGTATCAT CAAAGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAC 450
ACCGTTAAGT CTACCTGTAC CGGTGTAGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC 550
GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCTATCAAG 600
CCGCACACCA AATTCGACTC AGAAGTGTAC ATCCTGAGCA AAGAAGAAGG 650
TGGTCGTCAC ACGCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700
GTACTACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG 750
GTAATGCCAG GCGATAACGT GAACATGGTT GTTACCCTGA TTCACCCAAT 800
CGCAATGGAC GACGGTCTGC GTTTCGCAA 829

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia plymuthica*
(B) STRAIN: DSM 4540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

CGGCGCAATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTT CATCATCGTA 100
TTCATGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT 150
AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTACGACTTC CCTGGTGATG 200
ACCTGCCGGT TGTTCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAACCA 250
GAGTGGGAAG CTAAAATCAT CGAGCTGGCT GGTTTCCTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCTA TCGACAAGCC GTTCCTGCTG CCAATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTTGAG 400
CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTGG GTATCAAAGA 450
CACCGTTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTGGGTG TTCTGCTGCG TGGTATCAAG 550
CGCGAAGATA TCGAACGTGG TCAGGTCCTG GCTAAACCAG GTTCAATCAA 600
GCCACACACC AAGTTTGACT CAGAAGTGTA CATCCTGAGC AAAGAAGAAG 650
GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCA GGTGACAACG TGAACATGGT TGTAACCCTG ATCCACCCAA 800
TCGCGATGGA CGACGGCCTG CGTTTCGCAA 830

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia rubidaea*
(B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

```
GGCGCAATCC TGGTAGTAGC AGCGACTGAC GGCCCAATGC CTCAGACCCG      50
TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTACCTTAC ATCATCGTAT     100
TCATGAACAA ATGCGACATG GTAGATGATG AAGAGCTGCT GGAACTGGTA     150
GAGATGGAAG TTCGCGAACT GCTGTCTGCT TACGACTTCC CAGGCGACGA     200
CCTGCCGGTA ATCCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCCG     250
AGTGGGAAGC GAAAATCGTT GAGCTGGCAG AAGCGCTGGA CAGCTACATC     300
CCAGAGCCAG AGCGTGCTGT AGACAAGCCG TTCCTGCTGC CAATCGAAGA     350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC     400
GCGGTATCAT CAAAGTTGGT GAAGAAGTAG AAATCGTAGG TATCAAAGAC     450
ACCGTTAAGT CTACCTGTAC TGGCGTAGAA ATGTTCCGCA AACTGCTGGA     500
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAGC     550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CGAAGCCAGG TTCAATCAAG     600
CCGCACACCC AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC     700
GTACAACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG     750
GTAATGCCAG GCGACAACGT GAACATGAAA GTTACTCTGA TTCACCCAAT     800
CGCAATGGAC GACGGTCTGC GTTTCGCAA                            829
```

2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella boydii*
(B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

```
CGGCGCGATC YTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG     200
ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA     250
GAGTGGGAAG CGAAAATCCT GGAACTGGCT GGCTTCCTGG ATTCTTACAT     300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA     400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA     600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG     650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA     800
TCGCGATGGA CGACGGTCTG CGTTTC                               826
```

2) INFORMATION FOR SEQ ID NO: 173

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella dysenteriae*
(B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

TGGTAGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC 50
CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA 100
ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT GAAATGGAAG 150
TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC 200
GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC 250
GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCYTAYATT CCGGAACCAG 300
AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC 350
ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC GCGGTATCAT 400
CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACYCAGAAGT 450
CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 500
GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT 550
CGAACGTGGT CAGGTACTGG CGAAGCCRGG CACCATCAAG CCGCACACCA 600
AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT 650
ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA 700
CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG 750
GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC 800
GACGGTCTGC GTTTCGCA 818

2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella flexneri*
(B) STRAIN: ATCC 12022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

CCTGGTAGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC 100
AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TTGAAATGGA 150
AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACTCCGA 200
TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250

GCGAAAATCC TGGAACTGGC TGGCTTCCTG GATTCTTACA TTCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA ACGCGGTATC 400
ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGMCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
GACGTGACTG GTACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACG 806

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella sonnei*
(B) STRAIN: ATCC 29930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
GAGTGGGAAG CGAAAATCCT GGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGYCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC 832

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: ATCC 13301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

```
TCTGCTGCTG ACGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC      50
ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC AAAGTTGACA     100
TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC     150
TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG TAATCGCTGG     200
TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA GAAAAAATCT     250
TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACTCC AGAACGTGAT     300
TCTGACAAAC CATTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG     350
TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG     400
GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA AACAACTGTT     450
ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG AAGCTGGTGA     500
CAACATTGGT GCATTATTAC GTGGTGTTGC TCGTGAAGAC GTACAACGTG     550
GTCAAGTATT AGCTGCTCCT GGTTCAATTA CACCACATAC TGAATTCAAA     600
GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC ACACTCCATT     650
CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT GACGTAACTG     700
GTGTTGTTCA CTTACC                                         716
```

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 719 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: ATCC 29247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

```
TTCTTTTATC ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC      50
AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA     100
AGTTCGTGAC TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG     150
TAATCGCTGG TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA     200
GAAAAAATCT TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACTCC     250
AGAACGTGAT TCTGACAAAC CATTCATGAT GCCAGTTGAG GACGTATTCT     300
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA     350
ATCAAAGTTG GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA     400
AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG     450
AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTGC TCGTGAAGAC     500
GTACAACGTG GTCAAGTATT AGCTGCTCCT GGTTCAATTA CACCACATAC     550
TGAATTCAAA GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC     600
ACACTCCATT CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT     650
GACGTAACTG GTGTTGTTCA CTTACCAGAA GGTMCTGAAA TGGTAATGCC     700
TGGTGATAAC GTTGAAATG                                      719
```

2) INFORMATION FOR SEQ ID NO: 178

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 625 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: ATCC 33591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

```
GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      50
TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT     100
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG     150
ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT     200
CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT     250
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG     300
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA     350
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA     400
CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG     450
ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTTGCT     500
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC     550
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG     600
GTGGACGTCA CACTCCATTC TTCTC                                625
```

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 704 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: ATCC 43300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

```
GTTGGTGTAC CAGCATTAGT AGTATTCTTA AACAAAGTTG ACATGGTTGA      50
CGATGAAGAA TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAA     100
GCGAATATGA CTTCCCAGGT GACGATGTAC CTGTAATCGC TGGTTCAGCA     150
TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA TCTTAGAATT     200
AATGGAAGCT GTAGATACTT ACATTCCAAC TCCAGAACGT GATTCTGACA     250
AACCATTCAT GATGCCAGTT GAGGACGTAT TCTCAATCAC TGGTCGTGGT     300
ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG TTGGTGAAGA     350
AGTTGAAATC ATCGGTTTAC ATGACACATC TAAAACAACT GTTACAGGTG     400
TTGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG TGACAACATT     450
GGTGCATTAT TACGTGGTGT TGCTCGTGAA GACGTACAAC GTGGTCAAGT     500
ATTAGCTGCT CCTGGTTCAA TTACACCACA TACTGAATTC AAAGCAGAAG     550
TATACGTATT ATCAAAAGAC GAAGGTGGAC GTCACACTCC ATTCTTCTCA     600
AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA CTGGTGTTGT     650
```

TCACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA 700
TGAC 704

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 730 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
(B) STRAIN: ATCC 6538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 50
TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT 100
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 150
ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 200
CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT 250
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 300
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 350
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 400
CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG 450
ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTTGCT 500
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 550
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG 600
GTGGACGTCA CACTCCATTC TTCTCAAACT ATCGTCCACA ATTCTATTTC 650
CGTACTACTG ACGTAACTGG TGTTGTTCAC TTACCAGAAG GTACTGAAAT 700
GGTAATGCCT GGTGATAACG TTGAAATGAC 730

2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus auricularis*
(B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

CGGTGCGATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACCA AGTTGACGAC GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATACGACTAC CCAGGTGACG 200
ATGTACCTGT AATCTCTGGT TCTGCGTTGA AAGCATTAGA AGGCGACAAA 250

GAATACGAAC AAAAAATCTT AGACTTAATG CAACAAGTTG ACGATTACAT 300
TCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGAAAGA 450
CGGTTCACAA AAAACAACAG TTACTGGTGT AGAAATGTTC CGTAAATTAT 500
TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTATT 550
TCACGTGAAG AAGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT 600
TACACCACAC ACTAAATTCA CTGCAGAAGT TTACGTATTA TCTAAAGATG 650
AAGGTGGACG TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAT 700
TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACAGA 750
AATGGTAATG CCTGGCGATA ACGTTAAAAT GGAAGTTGAA TTAATTTCTC 800
CAATCGCTAT CGAAGACGGT ACTCGTTTCT CAAT 834

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
(B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGATG 200
ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 250
CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTACAT 300
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATCCACGA 450
AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTTGCT 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATCAC 600
ACCACACACT AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC 700
CGTACTACTG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACTGAAAT 750
GGTTATGCCT GGCGACAACG TTGAAATGAC AGTTGAATTA ATCGCTCCTA 800
TCGCTATTGA AGACGGTACT CGTTTCTCAA TCGGA 835

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Macrococcus caseolyticus*
(B) STRAIN: ATCC 13548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

```
GTATCTTAGT AGTATCTGCT GCTGACGGTC CAATGCCACA AACTCGTGAA      50
CACATCCTTT TATCACGTAA CGTTGGTGTA CCAGCATTAG TAGTATTCTT     100
GAACAAAGTT GACATGGTTG ACGATGAAGA ATTATTAGAA TTAGTTGAAA     150
TGGAAGTTCG TGACTTATTA TCTGAATATG ACTTCCCTGG TGACGATGTA     200
CCTGTAATCG CTGGATCTGC TTTAAAAGCA TTAGAAGGCG TTGAAGAATA     250
CGAAGACAAA ATCATGGAAT TAATGGACGC AGTTGATGAG TACATCCCAA     300
CTCCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT TGAGGACGTA     350
TTCTCAATCA CTGGTCGTGG TACAGTTGCA ACTGGACGTG TTGAGCGTGG     400
ACAAGTTAAA GTTGGTGAAG AAGTTGAAAT CATTGGTTTA ACTGAAGAAC     450
CAGCAAAAAC TACAGTTACA GGTGTAGAAA TGTTCCGTAA ATTATTAGAT     500
TACGCTGAAG CTGGAGATAA CATCGGTGCT TTATTACGTG GTGTTTCTCG     550
TGAAGACGTA CAACGTGGAC AAGTATTAGC TAAACCAGGT TCAATTACTC     600
CACATACTAA ATTCAAAGCT GAAGTTTACG TATTATCTAA AGAAGAAGGT     650
GGACGTCATA CTCCATTCTT CACTAACTAC CGCCCTCAGT TCTACTTCCG     700
TACAACTGAC GTAACTGGTG TAGTTAACTT ACCAGAAGGT ACTGAAATGG     750
TAATGCCTGG AGATAACATC GAAATGAACG TTGAATTAAT TTCTCCAATC     800
GCGA                                                      804
```

2) INFORMATION FOR SEQ ID NO: 184

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus cohnii*
(B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

```
CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC      50
GTGAACATAT CCTTTTATCA CGTAACGTTG GTGTTCCAGC ATTAGTTGTA     100
TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT     150
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG     200
ATGTACCTGT AATCTCTGGT TCAGCATTAA AAGCTCTTGA AGGCGACGCT     250
GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTTCAT     300
TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG GCGTGTTGAA     400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGCAAGA     450
AGATTCAAGC AAAACAACTG TTACTGGTGT AGAAATGTTC CGTAAATTAT     500
TAGACTACGC TGAAGCTGGT GACAACATTG GTGCGTTATT ACGTGGTGTT     550
GCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT     600
TACACCACAC ACAAACTTTA AAGCGGAAGT TTACGTTTTA TCAAAAGATG     650
AAGGTGGCCG TCATACGCCA TTCTTCAGTA ACTATCGCCC ACAATTCTAT     700
TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACTGA     750
AATGGTTATG CCTGGCGACA ACGTAGAAAT GGAAGTTGAA CTAATTTCTC     800
CAATCGCTAT CGAAGACGGT ACACGTTTCT CT                        832
```

2) INFORMATION FOR SEQ ID NO: 185

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 699 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: CSG 269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

```
ATCTGCTGCT GACGGTCCAA TGCCACAAAC TCGTGAACAC ATCTTATTAT      50
CACGTAACGT TGGTGTACCA GCATTAGTTG TATTCTTAAA CAAAGTTGAC     100
ATGGTAGACG ACGAAGAATT ATTAGAATTA GTTGAAATGG AAGTTCGTGA     150
CTTATTAAGC GAATATGACT TCCCAGGTGA CGATGTACCT GTAATCGCTG     200
GTTCTGCATT AAAAGCATTA GAAGGCGATG CTGAATACGA ACAAAAAATC     250
TTAGACTTAA TGCAAGCAGT TGATGATTAC ATTCCAACTC CAGAACGTGA     300
TTCTGACAAA CCATTCATGA TGCCAGTTGA GGACGTATTC TCAATCACTG     350
GTCGTGGTAC TGTTGCTACA GGCCGTGTTG AACGTGGTCA AATCAAAGTT     400
GGTGAAGAAG TTGAAATCAT CGGTATGCAC GAAACTTCTA AAACAACTGT     450
TACTGGTGTA GAAATGTTCC GTAAATTATT AGACTACGCT GAAGCTGGTG     500
ACAACATCGG TGCTTTATTA CGTGGTGTTG CACGTGAAGA CGTACAACGT     550
GGTCAAGTAT TAGCTGCTCC TGGTTCTATT ACACCACACA CAAAATTCAA     600
AGCTGAAGTA TACGTATTAT CTAAAGATGA AGGTGGACGT CACACTCCAT     650
TCTTCACTAA CTATCGCCCA CAATTCTATT TCCGTACTAC TGACGTAAC      699
```

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

```
CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC      50
GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA     100
TTCTTAAATA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT     150
TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG     200
ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT     250
CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT     300
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
```

CGTGGGCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATTG GTATCCATGA 450
CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CATTATTACG TGGTGTTGCT 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATCAC 600
ACCTCACACA AAATTTAAAG CAGACGTATA CGTTTTATCT AAAGACGAAG 650
GTGGACGTCA CACTCCATTC TTCACAAACT ATCGTCCACA ATTCTATTTC 700
CGTACTACTG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACTGAAAT 750
GGTTATGCCT GGCGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
TCGCGATTGA AGACGGTACT CGTTTCTCA 829

2) INFORMATION FOR SEQ ID NO: 187

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus warneri*
(B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

CACAAACTCG TGAACACATT CTTTTATCAC GTAACGTTGG TGTACCAGCT 50
TTAGTTGTAT TCTTAAACAA AGTTGATATG GTAGACGACG AAGAATTATT 100
AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCTGAA TATGACTTCC 150
CAGGTGACGA CGTACCTGTA ATCGCTGGTT CAGCATTAAA AGCTTTAGAA 200
GGCGACGAAA AATACGAAGA AAAAATCTTA GAATTAATGC AAGCAGTTGA 250
TGACTACATT CCAACTCCAG AACGTGATTC TGACAAACCA TTCATGATGC 300
CAGTTGAGGA CGTATTCTCA ATCACTGGTC GTGGTACTGT TGCTACAGGC 350
CGTGTTGAAC GTGGTCAAAT CAAAGTTGGT GAAGAAGTTG AAATCATCGG 400
TTTACATGAC ACTTCTAAAA CAACTGTTAC TGGTGTAGAA ATGTTCCGTA 450
AGTTATTAGA CTACGCTGAA GCTGGTGACA ACATCGGTGC TTTATTACGT 500
GGTGTTGCTC GTGAAGACGT ACAACGTGGT CAAGTATTAG CTGCTCCTGG 550
TTCAATTACA CCACATACAA AATTCAAAGC GGAAGTTTAC GTTTTATCTA 600
AAGACGAAGG TGGACGTCAC ACTCCATTCT TCAGTAACTA CCGCCCACAA 650
TTCTATTTCC GTACTACTGA CGTAACTGGC GTTGTTCAAT TACCAGAAGG 700
TACTG 705

2) INFORMATION FOR SEQ ID NO: 188

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 678 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: CSG 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
TTTTATCACG TAACGTTGGT GTACCAGCAT TAGTAGTATT CTTAAACAAA      50
GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTTG AAATGGAAGT     100
ACGTGACTTA TTATCTGAAT ACGACTTCCC AGGTGACGAC GTACCTGTAA     150
TCGCTGGTTC AGCTTTAAAA GCTTTAGAAG GCGATGCTCA ATACGAAGAA     200
AAAATCTTAG AATTAATGCA AGCAGTTGAT GATTACATTC CAACTCCAGA     250
ACGTGACTCT GATAAACCAT TCATGATGCC AGTTGAGGAC GTATTCTCAA     300
TCACTGGTCG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGTCAAATC     350
AAAGTTGGTG AAGAAGTTGA AATTATTGGT ATCAAAGAAA CTTCTAAAAC     400
AACTGTTACT GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG     450
CTGGTGACAA CATCGGTGCT TTATTACGTG GTGTTGCTCG TGAAGATGTA     500
CAACGTGGTC AAGTATTAGC TGCTCCAGGT TCAATTACAC CTCACACAAA     550
ATTCAAAGCA GACGTATACG TTTTATCAAA AGATGAAGGT GGACGTCATA     600
CTCCATTCTT CACTAACTAT CGTCCACAAT TCTATTTCCG TACTACTGAC     650
GTAACTGGTG TTGTTAACTT ACCAGAAG                             678
```

2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 668 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: CSG 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

```
ACCAGCATTA GTAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC     100
GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC     150
TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG     200
CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTC     250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC     300
TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA     350
TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG     400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT     450
ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG     500
CTCCAGGTTC AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT     550
TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAAACTATCG     600
TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC     650
CAGAAGGTAC TGAAATGG                                       668
```

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 593 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: CSG 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

```
AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TTGAAATGGA      50
AGTACGTGAC TTATTATCTG AATACGACTT CCCAGGTGAC GATGTACCTG     100
TAATCGCTGG TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA     150
GAAAAAATCT TAGAATTAAT GCAAGCAGTT GATGATTACA TTCCAACTCC     200
AGAACGTGAT TCTGACAAAC CATTCATGAT GCCAGTTGAG GACGTATTCT     250
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA     300
ATCAAAGTTG GTGAAGAAGT TGAAATCATT GGTATCCATG ACACTTCTAA     350
AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG     400
AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTGC TCGTGAAGAC     450
GTACAACGTG GTCAAGTATT AGCTGCTCCA GGTTCAATCA CACCTCACAC     500
AAAATTTAAA GCAGACGTAT ACGTTTTATC TAAAGACGAA GGTGGACGTC     550
ACACTCCATT CTTCACAAAC TATCGTCCAC AATTCTATTT CCG            593
```

2) INFORMATION FOR SEQ ID NO: 191

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
(B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

```
CGGCGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC      50
GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA     100
TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT     150
TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG     200
ACGTACCTGT AATCGCTGGT TCAGCTTTAA AAGCTTTAGA AGGCGATGCT     250
CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTATAT     300
TCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATTATTG GTATCAAAGA     450
AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG     500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTTGCT     550
CGTGAAGATG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATTAC     600
ACCTCACACA AAATTCAAAG CAGACGTATA CGTTTTATCA AAAGATGAAG     650
GTGGACGTCA TACTCCATTC TTCTCTAACT ATCGTCCACA ATTCTATTTC     700
CGTACTACTG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACTGAAAT     750
GGTAATGCCT GGTGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA     800
TCGCGATTGA AGACGGTACT CGTTTCTC                             828
```

2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus warneri*
(B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

ATGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC ACGTAACGTT 50
GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA 100
CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG 150
AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATTA 200
AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT 250
GCAAGCAGTT GATGACTACA TTCCAACTCC AGAACGTGAT TCTGACAAAC 300
CATTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT 350
GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT 400
TGAAATCATC GGTTTACATG ACACTTCTAA AACAACTGTT ACTGGTGTAG 450
AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT 500
GCTTTATTAC GTGGTGTTGC TCGTGAAGAC GTACAACGTG GTCAAGTATT 550
AGCTGCTCCT GGTTCAATTA CACCACATAC AAAATTCAAA GCGGAAGTTT 600
ACGTTTTATC TAAAGACGAA 620

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 692 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus hominis*
(B) STRAIN: CSG 170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA 50
ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGACTTATTA TCTGAATACG 100
ACTTCCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTTAAAAGCT 150
TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC 200
AGTTGATGAT TATATTCCAA CTCCAGAACG TGACTCTGAT AAACCATTCA 250
TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT 300
ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT 350
TATTGGTATC AAAGAAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT 400
TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CGGTGCTTTA 450
TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC 500
TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT 550
TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT 600
CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTTG TTAACTTACC 650

AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT

2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 684 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus hominis*
(B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

```
CATTCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA      50
ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG     100
GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC     150
TGTAATCGCT GGTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG     200
AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAACT     250
CCAGAACGTG ACTCTGATAA ACCATTCATG ATGCCAGTTG AGGACGTATT     300
CTCAATCACT GGTCGTGGTA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC     350
AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAAACTTCT     400
AAAACAACTG TTACTGGTGT AGAAATGTTC CGTAAATTAT TAGACTACGC     450
TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTT GCTCGTGAAG     500
ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC     550
ACAAAATTCA AAGCAGACGT ATACGTTTTA TCAAAAGATG AAGGTGGACG     600
TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA     650
CTGACGTAAC TGGTGTTGTT AACTTACCAG AAGG                      684
```

2) INFORMATION FOR SEQ ID NO: 195

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus hominis*
(B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

```
ACCAGCATTA GTAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG      50
AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC     100
GACTTCCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAAGC     150
TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG     200
CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC     250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC     300
TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA     350
```

```
TTATTGGTAT CAAAGAAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG    400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT    450
ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG    500
CTCCAGGTTC AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT    550
TTATCAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAACTATCG    600
TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC    650
CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC                   685
```

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 611 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus hominis*
(B) STRAIN: CSG 62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

```
GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC     50
TGGTTCAGCT TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA    100
TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT    150
GACTCTGATA AACCATTCAT GATGCCAGTT GAGGACGTAT TCTCAATCAC    200
TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG    250
TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAACT    300
GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG    350
TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC    400
GTGGTCAAGT ATTAGCTGCT CCAGGTTCAA TCACACCTCA CACAAAATTC    450
AAAGCAGACG TATATGTTTT ATCAAAAGAT GAAGGTGGAC GTCATACTCC    500
ATTCTTCACT AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA    550
CTGGTGTTGT TAACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC    600
AACGTTGAAA T                                             611
```

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus lugdunensis*
(B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

```
CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAAACTC     50
GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTGCCAGC ATTAGTAGTA    100
```

TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGATT TATTAACTGA ATATGACTTC CCAGGTGACG 200
ATGTGCCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA 250
AAATACGAAG CTAAAATCTT AGAATTAATG GATGCAGTTG ATAACTACAT 300
TCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATTATTG GTATCCACGA 450
TACTACTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CGTTATTACG TGGTGTTGCT 550
CGTGAAGATG TACAACGTGG ACAAGTATTA GCTGCTCCAG GTTCAATTAC 600
ACCTCACACT AAATTTAAAG CTGACGTATA TGTTTTATCT AAAGATGAAG 650
GTGGACGTCA TACACCATTC TTCTCAAACT ACCGCCCACA ATTCTATTTC 700
CGTACTACAG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACAGAAAT 750
GGTTATGCCT GGCGACAACG TTGAAATGAC AGTTGAATTA ATCGCTCCAA 800
TCGCTATCGA AGACGGAACT CGTTTCTC 828

2) INFORMATION FOR SEQ ID NO: 198

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 690 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

AGTAGTATCT GCTGCTGATG GCCCAATGCC ACAAACTCGT GAACACATTC 50
TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT CTTAAACAAA 100
GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG AAATGGAAGT 150
TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT GTACCTGTAA 200
TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA CTATGAGCAA 250
AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC CAACACCAGA 300
ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC GTATTCTCAA 350
TCACTGGTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTCAAATC 400
AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG AATCAAGCAA 450
AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG 500
AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTTC ACGTGATGAC 550
GTACAACGTG GTCAAGTTTT AGCTGCTCCT GGTACTATTA CACCACATAC 600
AAAATTCAAA GCGGATGTTT ACGTTTTATC TAAAGATGAA GGTGGTCGTC 650
ATACACCATT CTTCACTAAC TACCGCCCAC AATTCTATTT 690

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 723 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: CSG 83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

```
GCATTAGTTG TATTCTTAAA CAAAGTTGAC ATGGTTGACG ATGAAGAATT      50
ATTAGAATTA GTAGAAATGG AAGTTCGTGA TTTATTAAGC GAATATGACT     100
TCCCAGGTGA CGATGTACCT GTAATCTCTG GTTCTGCATT AAAAGCTTTA     150
GAAGGCGACG CTGACTATGA GCAAAAAATC TTAGACTTAA TGCAAGCTGT     200
TGATGACTTC ATTCCAACAC CAGAACGTGA TTCTGACAAA CCATTCATGA     250
TGCCAGTTGA GGACGTATTC TCAATCACTG GTCGTGGTAC TGTTGCTACA     300
GGCCGTGTTG AACGTGGTCA AATCAAAGTC GGTGAAGAAA TCGAAATCAT     350
CGGTATGCAA GAAGAATCAA GCAAAACAAC TGTTACTGGT GTAGAAATGT     400
TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT TGGTGCATTA     450
TTACGTGGTG TTTCACGTGA TGACGTACAA CGTGGTCAAG TTTTAGCTGC     500
TCCTGGTACT ATTACACCAC ATACAAAATT CAAAGCGGAT GTTTACGTTT     550
TATCTAAAGA TGAAGGTGGT CGTCATACAC CATTCTTCAC TAACTACCGC     600
CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTTG TTAACTTACC     650
AGAAGGTACT GAAATGGTTA TGCCTGGCGA TAACGTTGAA ATGGATGTTG     700
AATTAATTTC TCCAATCGCT ATT                                  723
```

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 697 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: CSsa 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

```
CGTTGGTGTT CCAGCATTAG TTGTATTCTT AAACAAAGTT GACATGGTTG      50
ACGATGAAGA ATTATTAGAA TTAGTAGAAA TGGAAGTTCG TGACTTATTA     100
AGCGAATATG ACTTCCCAGG TGACGATGTA CCTGTAATCT CTGGTTCTGC     150
ATTAAAAGCT TTAGAAGGCG ACGCTGACTA TGAGCAAAAA ATCTTAGACT     200
TAATGCAAGC TGTTGATGAC TTCATTCCAA CACCAGAACG TGATTCTGAC     250
AAACCATTCA TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG     300
TACTGTTGCT ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTCGGTGAAG     350
AAATCGAAAT CATCGGTATG CAAGAAGAAT CAAGCAAAAC AACTGTTACT     400
GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG CTGGTGACAA     450
CATTGGTGCA TTATTACGTG GTGTTTCACG TGATGACGTA CAACGTGGTC     500
AAGTTTTAGC TGCTCCTGGT ACTATTACAC CACATACAAA ATTCAAAGCG     550
GATGTTTACG TTTTATCTAA AGATGAAGGT GGTCGTCATA CACCATTCTT     600
CACTAACTAC CGCCCACAAT TCTATTTCCG TACTACTGAC GTAACTGGTG     650
TTGTTAACTT ACCAGAAGGT ACTGAAATGG TTATGCCTGG CGATAAC       697
```

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
(B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```
CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACTC      50
GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCCTGC ATTAGTAGTA     100
TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT     150
TGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG     200
ACGTTCCTGT AATTGCTGGT TCAGCATTAA AAGCATTAGA AGGCGACGAA     250
GCTTACGAAG ACAAAATCAT GGAATTAATG GATGCTGTTG ATACATTCAT     300
CCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA     450
AGAATCTTCT AAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTAT     500
TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGTT     550
GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT     600
CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG     650
AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT     700
TTCCGTACTA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA     750
AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTCAC     800
CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA                     835
```

2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus warneri*
(B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```
CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC      50
GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA     100
TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT     150
AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG     200
ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA     250
AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT     300
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA     450
CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG     500
```

```
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTTGCT     550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC     600
ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG     650
GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC     700
CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT     750
GGTTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA     800
TCGCGATTGA AGACGGTACT CGTTTCTCAA C                         831
```

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus warneri*
(B) STRAIN: CSG 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

```
CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC      50
GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA     100
TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT     150
AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG     200
ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA     250
AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT     300
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG     350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA     450
CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG     500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTTGCT     550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC     600
ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG     650
GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC     700
CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT     750
GGTTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA     800
TCGCGATTGA AGACGGTACT CGTTTCTCA                            829
```

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bifidobacterium longum*
(B) STRAIN: ATCC 15707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

```
TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCCCAGACTC      50
GCGAGCACGT GCTGCTCGCC CGTCAGGTTG GCGTTCCGAA GATCCTCGTC     100
GCCCTGAACA AGTGCGACAT GGTCGACGAT GAAGAGCTCA TCGAGCTCGT     150
CGAAGAAGAG GTCCGCGACC TCCTCGACGA GAACGGCTTC GACCGTGACT     200
GCCCGGTCAT CCACACCTCC GCTTACGGTG CTCTGCACGA CGACGCTCCG     250
GACCACGAGA AGTGGGTCCA GTCCGTTAAG GACCTCATGG ACGCTGTCGA     300
CGACTACATC CCGACCCCGG TTCACGACCT GGACAAGCCG TTCCTGATGC     350
CGATCGAGGA CGTCTTCACC ATCTCCGGCC GTGGTACCGT TGTCACCGGT     400
CGTGTCGAGC GTGGCCAGCT GGCCGTCAAC ACCCCGGTCG AGATCGTTGG     450
TATCCGTCCG ACCCAGCAGA CCACCGTCAC CTCCATCGAG ACCTTCCACA     500
AGACCATGGA CGCCTGCGAG GCTGGCGACA ACACCGGTCT GCTTCTGCGT     550
GGTCTCGGCC GTGACGATGT CGAGCGTGGC CAGGTTGTGG CCAAGCCGGG     600
CTCCGTCACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA     650
AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG     700
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCGAGC TGCCGGAAGG     750
CGTCGAGATG GTTCAGCCGG GCGACCACGC TACCTTCACC GTTGAGCTGA     800
TTCAGCCCAT CGCTATGGAG GAAGGCCTGA CCTTCGCTG                 839
```

2) INFORMATION FOR SEQ ID NO: 205

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stenotrophomonas maltophilia*
(B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

```
CGGCGCGATC CTGGTGTGCT CGGCCGCTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGTCG CGCCAGGTCG GCGTGCCGTA CATCGTCGTG     100
TTCCTGAACA AGGCCGACAT GGTCGACGAC GCCGAGCTGC TCGAGCTGGT     150
CGAGATGGAA GTGCGCGAAC TGCTGAGCAA GTACGAGTTC CCGGGCGACG     200
ACACCCCGAT CATCGCCGGT TCGGCCCGCC TGGCGCTGGA AGGCGACCAG     250
AGCGACATCG GCGTGCCGGC CATCCTGAAG CTGGTCGACG CGCTGGACAG     300
CTGGATTCCG GAGCCGGAGC GTGCGATCGA CAAGCCGTTC CTGATGCCGG     350
TGGAAGACGT GTTCTCGATC TCGGGCCGCG GCACCGTGGT GACCGGTCGT     400
ATCGAGCGCG GCGTGATCAA GGTTGGCGAC GAAATCGAAA TCGTCGGCAT     450
CCGTCCGGTG CAGAAGACCA CCGTGACCGG CGTTGAAATG TTCCGCAAGC     500
TGCTGGACCA GGGTCAGGCA GGCGACAACG CTGGCCTGCT GCTGCGCGGC     550
ACCAAGCGTG ATGACGTCGA GCGTGGCCAG GTGCTGGCCA AGCCGGGCAC     600
GATCAAGCCG CACACCAAGT TCGAAGGCGA AGTGTACGTC CTGTCGAAGG     650
ACGAGGGCGG CCGCCACACC CCGTTCTTCA ACGGCTACCG TCCGCAGTTC     700
TACTTCCGCA CCACCGACAT CACCGGCGCC GCTGCACTGC CGGAAGGCGT     750
CGAA                                                      754
```

2) INFORMATION FOR SEQ ID NO: 206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus acidominimus*
(B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

```
TGGTGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAAAA CCTTATCGTT     100
TTCATGAACA AAGTTGACCT TGTTGATGAT GAAGAATTGC TTGAATTGGT     150
TGAAATGGAA ATCCGTGACC TTCTTTCAGA ATACGATTTC CCAGGTGATG     200
ATCTTCCAGT TGTTCAAGGT TCAGCTCTTA AAGCGCTTGA AGGTGATTCA     250
GCACAAGAAG ATGTTATCAT GGAATTGATG TCAATCGTTG ACACATACAT     300
TCCAGAACCA GAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCGAGG     350
ATGTATTCTC AATCACTGGA CGTGGTACTG TTGCTTCAGG ACGTATCGAC     400
CGTGGTACTG TTAAAGTTAA TGACGAAGTT GAAATCGTTG GTATCAAAGA     450
CGAAATCTCT AAAGCAGTTG TTACTGGTGT TGAAATGTTC CGTAAACAAC     500
TTGACGAAGG TCTTGCTGGA GATAACGTTG GTGTTCTTCT TCGTGGTGTA     550
CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT     600
CAACCCACAC ACTAAATTCA AAGGTGAAGT TTACGTTCTT TCTAAAGAAG     650
AAGGTGGACG TCACACTCCA TTCTTCGATA ACTACCGTCC TCAGTTCTAC     700
TTCCGTACAA CTGACGTAAC TGGTTCAATC AAATTGCCAG AAGGTACTGA     750
AATGGTAATG CCTGGTGATA ACGTAACTAT CGAAGTTGAG TTGATCCACC     800
CAATCGCCGT TGAACAAGGT ACTACTTTCT CTATC                     835
```

2) INFORMATION FOR SEQ ID NO: 207

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

```
CTATCCTTGT AGTTGCTTCA ACTGATGGAC CAATGCCACA AACTCGTGAG      50
CACATCCTTC TTTCACGTCA AGTTGGTGTT AAACACCTTA TCGTATTCAT     100
GAACAAAGTT GACCTTGTTG ATGATGAAGA ATTGCTTGAA TTGGTTGAAA     150
TGGAAATTCG TGACCTTCTT TCAGAATACG ACTTCCCAGG TGATGACCTT     200
CCAGTTATCC AAGGTTCAGC TCTTAAAGCA CTTGAAGGCG ACGAAAAATA     250
CGAAGACATC ATCATGGAAT TGATGAGCAC TGTTGATGAG TACATTCCAG     300
AACCAGAACG TGATACTGAC AAACCTTTAC TTCTTCCAGT TGAAGATGTA     350
TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG     400
TACTGTTCGT GTCAACGACG AAGTTGAAAT CGTTGGTATT AAAGAAGATA     450
TCCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC     500
GAAGGTCTTG CAGGGGACAA CGTTGGTGTT CTTCTTCGTG GTGTTCAACG     550
```

```
TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC      600
CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT      650
GGACGTCATA CTCCATTCTT CAACAACTAC CGTCCACAAT TCTACTTCCG      700
TACAACTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG      750
TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC      800
GCCGTAGAAC AAGGTACTA                                       819
```

2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

```
CTATCCTTGT AGTTGCTTCA ACTGATGGAC CAATGCCACA AACTCGTGAG       50
CACATCCTTC TTTCACGTCA AGTTGGTGTT AAACACCTTA TCGTATTCAT      100
GAACAAAGTT GACCTTGTTG ATGATGAAGA ATTGCTTGAA TTGGTTGAAA      150
TGGAAATTCG TGACCTTCTT TCAGAATACG ACTTCCCAGG TGATGACCTT      200
CCAGTTATCC AAGGTTCAGC TCTTAAAGCA CTTGAAGGCG ATGAAAAATA      250
CGAAGACATC ATCATGGAAT TGATGAGCAC TGTTGATGAG TACATTCCAG      300
AACCAGAACG TGATACTGAC AAACCTTTAC TTCTTCCAGT CGAAGATGTA      350
TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
TACTGTTCGT GTCAACGACG AAGTTGAAAT CGTTGGTATT AAAGAAGATA      450
TCCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC      500
GAAGGTCTTG CAGGGGACAA CGTTGGTGTT CTTCTTCGTG GTGTTCAACG      550
TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC      600
CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT      650
GGACGTCATA CTCCATTCTT CAACAACTAC CGTCCACAAT TCTACTTCCG      700
TACAACTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG      750
TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC      800
GCCGTAGAAC AAGGTACTA                                       819
```

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG 50
AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC 100
ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA 150
AATGGAAATT CGTGACCTTC TTTCAGAATA CGACTTCCCA GGTGATGACC 200
TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA 250
TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC 300
AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG 350
TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT 400
GGTACTGTTC GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA 450
TATCCAAAAA GCAGTTGTTA CTGGTGTTGA AATGTTCCGT AAACAACTTG 500
ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCAA 550
CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA 600
CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG 650
GTGGACGTCA TACTCCATTC TTCAACAACT ACCGTCCACA ATTCTACTTC 700
CGTACAACTG ACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT 750
GGTTATGCCT GGTGATAACG TTACTATCGA AGTTGAATTG ATTCACCCAA 800
TCGCCGTAGA ACAAGGTACT AC 822

2) INFORMATION FOR SEQ ID NO: 210

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: CDCss-1073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC 50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA 100
TTCATGAACA AAGTTGACCT TGTTGATGAT GAAGAATTGC TTGAATTGGT 150
TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG 200
ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA 250
AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT 300
TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG 350
ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC 400
CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA 450
AGATATCCAA AAAGCAGTTG TTACTGGTGT TGAAATGTTC CGTAAACAAC 500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT 550
CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC 700
TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA 750
AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTCACC 800
CAATCGCCGT AGAACAAGGT ACTAC 825

2) INFORMATION FOR SEQ ID NO: 211

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus anginosus*
(B) STRAIN: ATCC 33397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CTCAAACTCG 50
TGAACACATC CTTCTTTCAC GCCAAGTAGG TGTTAAATAC CTTATCGTCT 100
TCATGAATAA AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT 150
GAAATGGAAA TCCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA 200
AATCCCAGTT ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATGAAA 250
AATATGAAGA CATCATCATG GAATTGATGG ATACTGTTGA TGAATACATT 300
CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTTGAAGA 350
TGTATTCTCA ATTACTGGAC GTGGTACTGT TGCTTCAGGA CGTATCGACC 400
GTGGTACTGT TAAAGTCAAC GACGAAGTTG AAATCGTTGG TATCCGTGAT 450
GAAATCCAAA AAGCAGTTGT TACTGGTGTT GAAATGTTCC GTAAACAATT 500
GGACGAAGGT CTTGCTGGAG ATAACGTAGG GGTTCTTCTT CGTGGTATCC 550
AACGTGACGA AATCGAACGT GGACAAGTTC TTGCTAAACC AGGTTCAATT 600
CATCCACACA CTAAATTCAA AGGTGAAGTT TACATCCTTA CTAAAGAAGA 650
AGGTGGACGT CATACTCCAT TCTTCAACAA CTACCGTCCT CAATTCTACT 700
TCCGTACTAC AGACGTTACA GGTTCAATCG AACTTCCTGC AGGTACTGAA 750
ATGGTAATGC CTGGTGATAA CGTAACAATC GACGTTGAAT TGATCCACCC 800
AATTGCCGTA GAACAAGGAA CTACAT 826

2) INFORMATION FOR SEQ ID NO: 212

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus bovis*
(B) STRAIN: ATCC 33317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

TGGTGCTATC CTTGTAGTAG CTTCTACAGA TGGTCCAATG CCACAAACAC 50
GTGAACACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTC 100
TTCATGAACA AAGTTGACCT TGTTGATGAC GAAGAATTGC TTGAATTGGT 150
TGAAATGGAA ATCCGTGACC TTCTTTCAGA ATATGATTTC CCAGGTGATG 200
AAATCCCTGT AATCCAAGGT TCAGCTCTTA AAGCCCTTGA AGGTGACACT 250
CACTACGAAG ACATCATCAT GGAATTGATG AACACTGTAG ATGAATACAT 300
TCCAGAACCA AAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCATCAGG ACGTATCGAC 400
CGTGGTACTG TTAAAGTCAA CGACGAAGTT GAAATCGTTG GTATCCGTGA 450
CGACATCCAA AAAGCTGTTG TTACTGGTGT TGAAATGTTC CGTAAACAAC 500
TTGATGAAGG TATCGCAGGG GATAACGTTG GTGTTCTTCT TCGTGGTATC 550

```
CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG      650
AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC      700
TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA      750
AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTCACC      800
CAATCGCCGT TGAACAAGGT ACTACAT                               827
```

2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus anginosus* (deposited as *Streptococcus constellatus*)
(B) STRAIN: ATCC 27823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

```
GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACTCGTGA       50
ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA      100
TGAACAAAGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA      150
ATGGAAATCC GTGACCTTCT TCAGAATAC GATTTCCCAG GTGATGAAAT       200
CCCAGTTATC CAAGGTTCAG CTCTTAAAGC TCTTGAAGGT GATGAAAAAT      250
ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA      300
GAACCAGAAC GTGACACTGA CAAACCACTT CTTCTTCCAG TCGAAGATGT      350
ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG      400
GTACTGTTAA AGTCAATGAT GAAGTTGAAA TTGTTGGTAT TCGTGACGAA      450
ATCCAAAAAG CAGTTGTTAC TGGTGTTGAA ATGTTCCGTA AACAATTGGA      500
CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC      550
GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTCAT      600
CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG      650
TGGACGTCAT ACTCCATTCT TCAACAACTA CCGTCCTCAA TTCTACTTCC      700
GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG      750
GTAATGCCTG GTGATAACGT AACAATTGAT GTTGAGTTGA TCCACCCAAT      800
TGCCGTAGAA CAAGGAACTA C                                     821
```

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus cricetus*
(B) STRAIN: ATCC 19642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

```
GCTATCCTTG TAGTAGCTTC TACAGACGGA CCAATGCCAC AAACTCGTGA      50
ACACATCTTG CTTTCACGCC AAGTTGGTGT TAAGAGCCTT ATCGTCTTCA     100
TGAACAAGGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA     150
ATGGAAATCC GTGATCTTCT TTCAGAATAC GATTTCCCAG GTGATGATAT     200
CCCTGTTGTT CAAGGTTCAG CTCTTAAAGC CCTTGAAGGT GATACAGCTG     250
CCGAAGACAA GATCATGGAA TTGATGGACA TCGTTGATGA CTACATTCCA     300
GAACCAAAAC GTGATACTGA TAAGCCATTG CTTCTTCCAG TCGAAGACGT     350
ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG     400
GTACTGTTAA GGTCAATGAC GAAGTTGAAA TCGTTGGTAT CAAGGACGAA     450
ATCCAAAAAG CGGTTGTTAC CGGAGTTGAA ATGTTCCGTA AACAATTGGA     500
TGAAGGTCTT GCAGGGGATA ACGTTGGTGT GCTTCTTCGT GGTATCCAAC     550
GTGATGAAAT CGAACGTGGT CAAGTATTGG CTGCACCTGG TTCAATCCAT     600
CCACACACTA AATTCAAGGG TGAAGTTTAC ATCCTTTCTA AAGATGAAGG     650
TGGACGTCAC ACTCCATTCT TCAACAACTA CCGTCCACAG TTCTACTTCC     700
GTACAACTGA CGTAACTGGT TCAATCGAAT TGCCAGCAGG TACTGAAATG     750
GTTATGCCTG GTGATAACGT TACTATCGAC GTTGAATTGA TCCACCCAAT     800
CGCTGTTGAA AAAGGTACTA C                                    821
```

2) INFORMATION FOR SEQ ID NO: 215

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus cristatus*
- (B) STRAIN: ATCC 51100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

```
TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG     100
AACAAGATCG ACTTGGTTGA TGACGAAGAA TTGCTTGAAT TGGTTGAAAT     150
GGAAATCCGT GACCTCTTGT CAGAATACGA CTTCCCAGGT GACGATCTTC     200
CAGTTATCCA AGGTTCAGCT CTTAAAGCTC TTGAAGGTGA TACTAAGTAC     250
GAAGACATCA TCATGGAATT GATGAACACT GTTGATGAGT ACATCCCAGA     300
ACCAGAACGT GATACTGACA AACCTCTTCT TCTTCCAGTC GAAGACGTAT     350
TCTCAATCAC TGGTCGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT     400
ACTGTTCGTG TCAACGATGA AATCGAAATC GTTGGTATCA AAGAAGAAAT     450
CCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAGCTTGACG     500
AAGGTCTTGC AGGGGACAAC GTAGGTGTAC TTCTTCGTGG TATCCAACGT     550
GATGAAATCG AACGTGGTCA AGTTATCGCT AAACCAGGTT CAATCAACCC     600
ACACACTAAA TTCAAGGGTG AAGTTTACAT CCTTACTAAA GAAGAAGGTG     650
GACGTCACAC TCCATTCTTC AACAACTACC GTCCACAGTT CTACTTCCGT     700
ACAACTGACG TTACAGGTTC AATCGAACTT CCAGCAGGTA CTGAAATGGT     750
AATGCCTGGT GATAACGTAA CTATCGACGT TGAGTTGATC CACCCAATCG     800
CCGTTGAACA AGGTACTCCT T                                    821
```

2) INFORMATION FOR SEQ ID NO: 216

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 792 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus downei*
(B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

```
AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC      50
TTTCACGTCA GGTTGGTGTT AAGAACCTTA TCGTCTTCAT GAACAAGGTT     100
GACTTGGTTG ACGATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG     150
TGACCTGCTT TCAGAATACG ATTTCCCAGG TGATGATATC CCTGTTGTTC     200
AAGGTTCAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG     250
ATCATGGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG     300
TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA     350
CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTTAAG     400
GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAAGC     450
AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG     500
CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC     550
GAACGTGGTC AAGTGTTGGC TGCGCCTGGT TCGATTCACC CACACACTAA     600
GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA     650
CTCCATTCTT TAACAACTAC CGTCCACAGT TCTACTTCCG TACAACTGAC     700
GTAACTGGTT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG     750
TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC             792
```

2) INFORMATION FOR SEQ ID NO: 217

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus dysgalactiae*
(B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

```
GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT      50
CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTTC ATGAACAAAA     100
TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC     150
CGTGACCTTC TTTCAGAATA CGATTTCCCA GGTGATGACC TTCCAGTTAT     200
CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA     250
TCATCATGGA ATTGATGGAT ACTGTTGATT CATACATTCC AGAACCAGAA     300
CGTGACACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG TATTCTCAAT     350
CACAGGTCGT GGTACAGTTG CTTCAGGACG TATCGACCGT GGTACTGTTC     400
GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA     450
GCTGTTGTTA CTGGTGTTGA AATGTTCCGT AAACAACTTG ACGAAGGTCT     500
TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTCAA CGTGACGAAA     550
```

TCGAACGTGG TCAAGTTATT GCTAAACCAG GTTCAATCAA CCCACACACT 600
AAATTCAAAG GTGAAGTATA TATCCTTTCT AAAGACGAAG GTGGACGTCA 650
CACTCCATTC TTCAACAACT ATCGTCCACA ATTCTACTTC CGTACAACTG 700
ACGTAACAGG TTCAATCGAA CTTCCAGCTG GTACAGAAAT GGTTATGCCT 750
GGTGATAACG TGACAATCAA CGTTGAGTTG ATCCACCCAA TCGCC 795

2) INFORMATION FOR SEQ ID NO: 218

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus equi* subsp. *equi*
(B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

CGGAGCTATC CTTGTAGTTG CTTCAACTGA CGGACCAATG CCACAAACTC 50
GTGAGCACAT CCTTCTTTCA CGTCAGGTTG GTGTTAAGCA CCTTATCGTG 100
TTCATGAACA AGGTTGACCT TGTTGACGAT GAAGAATTGC TTGAGCTTGT 150
TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATATGATTTC CCAGGTGATG 200
ACCTTCCAGT TATCCAAGGT TCAGCGCTTA AGGCTCTTGA AGGCGACAGC 250
AAATACGAAG ATATCATCAT GGAATTGATG GATACTGTTG ATTCATACAT 300
TCCAGAACCA GAACGTGACA CAGACAAGCC ATTGCTTCTT CCAGTCGAGG 350
ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTTCAGG ACGTATCGAC 400
CGCGGTACTG TTCGTGTTAA CGACGAAATC GAAATCGTTG GTATCAGAGA 450
CGAGATCAAA AAAGCAGTTG TTACTGGTGT CGAAATGTTC CGTAAACAGC 500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTA 550
CAACGTGATG AAATCGAACG TGGTCAAGTT ATTGCTAAGC CAGGTTCTAT 600
CAACCCACAC ACTAAATTTA AAGGTGAAGT ATATATCCTT ACTAAAGAAG 650
AAGGTGGACG TCACACACCA TTCTTCAACA ACTATCGTCC ACAATTCTAC 700
TTCCGTACTA CTGACGTAAC AGGTTCAATC GAGCTTCCAG CAGGTACAGA 750
AATGGTTATG CCTGGTGATA ACGTGACTAT TGACGTTGAG TTGATCCACC 800
CAATCGCCGT AGAACAAGGT ACTACATT 828

2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus ferus*
(B) STRAIN: ATCC 33477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

CGGTGCAATC CTTGTAGTAG CTTCTACAGA TGGACCAATG CCACAAACTC 50
GTGAGCACAT CCTTCTTTCA CGTCAGGTAG GTGTTAAACA CCTTATCGTC 100
TTCATGAACA AAGTTGACTT GGTTGACGAT GAAGAATTGC TTGAATTGGT 150
TGAAATGGAA ATCCGTGACC TGCTTTCAGA ATATGATTTC CCAGGTGATG 200
ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCGCTTGA AGGTGATACT 250
GCTCAAGAAG ATGTTATCAT GGAATTGATG AAAACCGTTG ATGAGTACAT 300
CCCAGAACCA GAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCGAAG 350
ATGTATTCTC AATCACAGGT CGTGGTACTG TAGCTTCAGG ACGTATCGAT 400
CGTGGTACTG TAAGAGTCAA CGATGAAGTT GAAATCGTTG GTATCAAAGA 450
CGAAATCACT AAAGCAGTTG TTACCGGTGT TGAAATGTTC CGTAAACAAT 500
TGGACGAAGG TCTTGCTGGT GATAACGTTG GTGTGCTTCT CCGTGGTGTG 550
CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTAAAC CAGGTTCAAT 600
CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
AAGGTGGACG TCATACACCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTTCAATC GAATTGCCAG CAGGTACTGA 750
AATGGTTATG CCTGGTGATA ACGTGACTAT CGACGTTGAA TTGATCCACC 800
CAATCGCCGT TGAACAAGGT ACTAC 825

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus gordonii*
(B) STRAIN: ATCC 10558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

CGGAGCTATC CTTGTAGTAG CTTCAACTGA TGGTCCTATG CCACAAACTC 50
GTGAGCACAT CCTTCTCTCA CGCCAAGTTG GTGTTAAACA CTTGATCGTG 100
TTCATGAACA AAGTTGACTT GGTTGACGAT GAAGAATTGC TTGAGTTGGT 150
TGAAATGGAA ATCCGTGACC TCTTGTCAGA ATACGACTTC CCAGGTGACG 200
ATCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA AGGTGACTCT 250
AAATATGAAG ATATCATCAT GGAATTGATG AACACTGTTG ATGAGTACAT 300
CCCAGAACCA GAACGCGACA CTGACAAACC ATTGCTTCTT CCAGTCGAAG 350
ACGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC 400
CGTGGTATCG TTAAAGTCAA TGACGAAATC GAAATCGTTG GTATCAAAGA 450
AGAAATCCAA AAAGCAGTTG TTACTGGTGT TGAAATGTTC CGTAAACAGC 500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTGCTTCT TCGTGGTATC 550
CAACGTGATG AAATCGAACG TGGACAAGTT ATTGCTAAAC CAGGTTCAAT 600
CAACCCACAC ACTAAATTCA AAGGTGAAGT TTATATCCTT ACTAAAGAAG 650
AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC 700
TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
AATGGTAATG CCTGGTGATA ACGTAACTAT CGACGTTGAG TTGATCCACC 800
CAATCGCCGT TGAACAAGGT ACTACT 826

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus anginosus*
(B) STRAIN: ATCC 27335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

```
TGTAGTAGCT TCAACTGACG GACCAATGCC TCAAACTCGT GAACATATCC      50
TTCTTTCACG TCAAGTAGGT GTTAAATACC TTATTGTCTT CATGAACAAA     100
GTTGACTTGG TTGACGATGA AGAATTGCTT GAATTGGTTG AAATGGAAAT     150
CCGTGATCTT CTTTCAGAAT ACGATTTCCC AGGTGATGAT ATTCCAGTAA     200
TCCAAGGTTC AGCACTTAAA GCTCTTGAAG GTGATGAAAA ATATGAAGAC     250
ATCATCATGG AATTGATGAA TACTGTTGAT GAATATATTC CAGAACCAGA     300
ACGTGATACT GACAAACCAT TGCTTCTTCC AGTCGAAGAT GTATTCTCAA     350
TCACTGGACG TGGTACTGTT GCTTCAGGAC GTATCGACCG TGGTACTGTT     400
AAAGTCAACG ATGAAGTTGA AATCGTTGGT ATCCGCGAGG AAATCCAAAA     450
AGCAGTTGTT ACTGGTGTTG AAATGTTCCG TAAACAATTG GACGAAGGTC     500
TTGCTGGAGA TAACGTAGGG GTTCTTCTTC GTGGTATCCA ACGTGACGAA     550
ATTGAACGTG GACAAGTTCT TGCTAAACCA GGTTCAATTC ATCCACACAC     600
TAAATTCAAA GGTGAAGTTT ACATCCTTAC TAAAGAAGAA GGTGGACGTC     650
ATACTCCATT CTTCAACAAC TACCGTCCTC AATTCTACTT CCGTACTACA     700
GACGTTACAG GTTCAATCGA ACTTCCTGCA GGTACTGAAA TGGTAATGCC     750
TGGTGATAAC GTAACAATTG ATGTTGAGTT GATCCACCCA ATTGCCGTA      799
```

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus macacae*
(B) STRAIN: ATCC 35911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

```
TGGTGCTATT CTTGTAGTAG CTTCAACTGA CGGTCCAATG CCTCAAACGC      50
GTGAACATAT CCTTCTTTCA CGCCAAGTAG GTGTTAAAAA CCTTATTGTT     100
TTCATGAATA AAGTTGACTT AGTTGATGAT GAAGAATTGC TTGAATTGGT     150
TGAAATGGAA ATCCGTGATC TTCTTACAGA ATATGATTTC CCAGGCGATG     200
AACTTCCAGT TATCCAAGGT TCAGCACTTA AAGCTCTTGA AGGTGATACT     250
AAGTACGAAG ATATTATCAT GGAATTGTTG GATACTGTAG ATGATTACAT     300
CCCAGAACCA CAACGTGATA CTGACAAGCC ATTGCTTCTT CCAGTCGAAG     350
ATGTTTTCTC TATTACTGGA CGTGGTACTG TTGCTTCAGG ACGTATTGAC     400
CGTGGTACTG TTAAGGTTAA TGATGAAGTT GAAATCGTTG GTATTCGTGA     450
CGATATTCAA AAAGCAGTTG TTACTGGTGT TGAAATGTTC CGTAAACAGC     500
TTGACGAAGG TCTTGCTGGT GATAACGTCG GTGTCCTTCT TCGTGGTATC     550
CAACGTGATG AAATTGAACG CGGTCAAGTT CTTGCTAAAC CAGGATCAAT     600
TCATCCACAT ACTAAATTCA AAGGTGAAGT TTATATTCTT ACTAAAGAAG     650
```

AAGGTGGACG TCATACTCCA TTCTTTAACA ACTACCGTCC ACAGTTCTAC 700
TTCCGTACAA CTGATGTAAC TGGTTCAATT GATTTGCCAG CAGGTACTGA 750
AATGGTTATG CCTGGTGATA ATGTTACGAT TGATGTTGAA CTGATCCACC 800
CAATCGCTGT TGAACAAGGT ACAAC 825

2) INFORMATION FOR SEQ ID NO: 223

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus gordonii* (deposited as *Streptococcus mitis*)
(B) STRAIN: ATCC 33399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG 50
CACATCCTTC TTTCACGTCA GGTTGGTGTT AAACACCTTA TCGTCTTCAT 100
GAACAAAGTT GACTTGGTTG ACGACGAAGA ATTGCTTGAA TTGGTTGAAA 150
TGGAAATCCG TGACCTATTG TCAGAATACG ACTTCCCAGG TGACGATCTT 200
CCAGTTATCC AAGGTTCAGC TCTTAAAGCC CTTGAAGGTG ACACTAAATA 250
CGAAGACATC GTTATGGAAT TGATGAACAC AGTTGATGAG TACATCCCAG 300
AACCAGAACG TGACACTGAC AAACCATTGC TTCTTCCAGT CGAAGACGTA 350
TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400
TATCGTTAAA GTCAACGACG AAATCGAAAT CGTTGGTATC AAAGAAGAAA 450
CTCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC 500
GAAGGTCTTG CCGGAGATAA TGTAGGTGTC CTTCTTCGTG GTGTTCAACG 550
TGATGAAATC GAACGTGGAC AAGTTATTGC TAAACCAGGT TCAATCAACC 600
CACACACTAA ATTCAAAGGT GAAGTTTACA TCCTTACTAA AGAAGAAGGT 650
GGACGTCACA CTCCATTCTT CAACAACTAC CGTCCACAAT TCTACTTCCG 700
TACTACTGAC GTTACAGGTT CAATCGAACT TCCAGCAGGT ACTGAAATGG 750
TAATGCCTGG TGATAACGTG ACAATCGACG TTGAGTTGAT CCACCCAATC 800
GCCGTAGAAC AAGGTACTAC AT 822

2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus mutans*
(B) STRAIN: ATCC 25175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

CCCTGGTGCT ATCCTTGTAG TAGCTTCAAC TGATGGACCA ATGCCACAAA 50
CTCGTGAACA CATTCTTCTT TCACGTCAAG TTGGTGTTAA ATACCTCATT 100
GTCTTCATGA ATAAAGTTGA TTTGGTTGAC GATGAAGAAT TGCTTGAATT 150
GGTTGAAATG GAAATCCGTG ATCTTCTTTC AGAATATGAT TTCCCAGGTG 200
ATGATATTCC AGTTATTCAA GGTTCAGCTC TTAAAGCTCT TGAAGGCGAT 250
ACTGCTCAAG AAGATATCAT CATGGAATTA ATGCATACTG TTGATGACTA 300
CATTCCAGAT CCAGAACGTG ATACTGACAA GCCGCTCCTT CTTCCAGTCG 350
AAGATGTTTT CTCAATCACT GGTCGTGGTA CTGTTGCTTC AGGACGTATT 400
GATCGTGGTA CTGTTAAAGT TAACGATGAA GTTGAAATCG TTGGTATCCG 450
TGATGACATT CAAAAAGCTG TTGTTACTGG TGTTGAAATG TTCCGTAAAC 500
AATTGGATGA AGGTATTGCA GGGGATAATG TTGGTGTTCT CCTTCGTGGT 550
ATCCAACGTG ATGAAATCGA ACGTGGTCAA GTTCTTGCTA AACCAGGTTC 600
AATTCACCCA CATACTAAAT TCAAAGGTGA AGTTTATATC CTTACTAAAG 650
AGGAAGGTGG ACGTCATACA CCATTCTTCA ATAACTATCG TCCACAATTC 700
TACTTCCGTA CAACTGACGT AACTGGTTCA ATTGAGTTGC CAGCAGGTAC 750
TGAAATGGTT ATGCCTGGTG ATAACGTTAC TATTGACGTT GAATTGATCC 800
ATCCAATCGC TGTTGAACAA GGTACTA 827

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus parasanguinis*
(B) STRAIN: ATCC 15912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

AGCTATCCTT GTAGTAGCTT CAACTGACGG ACCAATGCCA CAAACACGTG 50
AACACATCCT TCTTTCACGT CAGGTTGGTG TTAAACACTT GATCGTCTTC 100
ATGAACAAAG TTGACTTGGT TGATGATGAA GAATTGCTTG AATTGGTTGA 150
AATGGAAATC CGTGACCTTC TTTCAGAATA CGATTTCCCA GGTGATGACC 200
TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG TGACTCTAAA 250
TATGAAGATA TCATCATGGA ATTGATGGAT ACTGTTGATG AGTACATCCC 300
AGAACCAGAA CGCGATACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG 350
TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT 400
GGTGTTGTTC GTGTCAATGA TGAAATCGAA ATCGTTGGTA TCAAAGAAGA 450
AATCCAAAAA GCAGTTGTTA CTGGTGTTGA AATGTTCCGT AAACAACTTG 500
ACGAAGGTCT TGCAGGGGAT AACGTTGGTG TGCTTCTTCG TGGTATCCAA 550
CGTGATGAAA TCGAACGTGG ACAAGTTATC GCTAAACCAG GTTCAATCAA 600
CCCACACACT AAATTCAAAG GTGAAGTTTA CATCCTTACT AAAGAAGAAG 650
GTGGACGTCA TACTCCATTC TTCAACAACT ACCGTCCACA GTTCTACTTC 700
CGTACAACTG ACGTAACTGG ATCTATCGAA CTTCCACCAG GAACTGAAAT 750
GGTAATGCCT GGTGATAACG TGACTATCGA CGTTGAGTTG ATCCACCCAA 800
TCGCCGTTGA ACAAGGTACT ACAT 824

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus ratti*
(B) STRAIN: ATCC 19645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

TGGTGCTATC CTTGTAGTAG CTTCAACTGA TGGACCAATG CCGCAAACTC 50
GTGAACACAT CTTGCTTTCA CGTCAAGTTG GTGTTAAATA CCTTATCGTC 100
TTCATGAACA AGGTTGACTT GGTTGATGAT GAAGAATTGC TTGAATTGGT 150
TGAAATGGAA ATCCGTGATC TTCTTTCAGA ATACGATTTC CCAGGTGATG 200
ACATTCCAGT TATCCAAGGT TCAGCCCTTA AAGCTCTTGA AGGTGACACT 250
GAACAAGAAG ATGTTATCAT GGAATTGATG AAAACAGTTG ATGAGTACAT 300
CCCAGATCCA GAACGCGATA CTGATAAGCC ATTGCTTCTT CCAGTCGAAG 350
ACGTGTTCTC AATCACTGGA CGTGGTACTG TTGCATCAGG ACGTATCGAC 400
CGTGGTACTG TTAAAGTCAA TGACGAAGTT GAAATCGTTG GTATCCGTGA 450
TGACATCCAA AAAGCTGTTG TTACTGGTGT TGAAATGTTC CGTAAACAGC 500
TTGACGAAGG TCTTGCTGGT GATAACGTTG GTGTACTTCT TCGTGGTATC 550
CAACGTGATG AAATCGAACG CGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
TCATCCGCAT ACTAAATTTA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
AAGGCGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTTCAATC GAATTGCCAG CAGGTACTGA 750
AATGGTTATG CCTGGTGATA ACGTGACTAT CGACGTTGAA TTGATCCACC 800
CAATCGCTGT TGAACAAGGT ACTA 824

2) INFORMATION FOR SEQ ID NO: 227

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus sanguinis*
(B) STRAIN: ATCC 10556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

TGTAGTAGCT TCAACTGACG GACCAATGCC ACAAACTCGT GAGCACATCT 50
TGCTTTCACG TCAGGTTGGT GTTAAACACT TGATCGTCTT CATGAACAAA 100
GTTGACTTGG TTGACGATGA AGAATTGCTT GAATTGGTTG AAATGGAAAT 150
CCGTGACCTC TTGTCAGAAT ACGACTTCCC AGGTGACGAT CTTCCAGTTA 200
TCCAAGGTTC AGCTCTTAAA GCTCTTGAAG GTGACTCTAA ATATGAAGAC 250
ATCATCATGG AATTGATGGA CACTGTTGAT GAGTACATCC CAGAACCAGA 300
ACGCGATACT GACAAGCCAT TGCTTCTTCC AGTCGAAGAC GTATTCTCAA 350
TCACTGGTCG TGGTACAGTT GCTTCAGGAC GTATCGACCG TGGTATCGTT 400
AAAGTCAACG ACGAAATCGA AATCGTTGGT ATCAAAGAAG AAATCCAAAA 450
AGCAGTTGTT ACTGGTGTTG AAATGTTCCG TAAACAGCTT GACGAAGGTC 500
TTGCAGGGGA CAACGTAGGT GTGCTTCTCC GTGGTATCCA ACGTGATGAA 550
ATCGAACGTG GACAAGTTAT CGCTAAACCA GGTTCAATCA ACCCACACAC 600

TAAATTCAAG GGTGAAGTTT ATATCCTTAC TAAAGAAGAA GGCGGACGTC 650
ACACTCCATT CTTCAACAAC TACCGTCCAC AGTTCTACTT CCGTACAACT 700
GACGTTACAG GTTCAATCGA ACTTCCAGCA GGTACTGAAA TGGTAATGCC 750
TGGTGATAAC GTAACAATCG ACGTTGAGTT GATCCACCCA ATCGC 795

2) INFORMATION FOR SEQ ID NO: 228

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus sobrinus*
(B) STRAIN: ATCC 33478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TGTAGTAGCT TCTACTGACG GACCAATGCC ACAAACTCGT GAACACATCT 50
TGCTTTCACG CCAAGTTGGT GTTAAGAACC TCATCGTCTT CATGAACAAG 100
GTTGACTTGG TTGATGATGA AGAATTGCTT GAATTGGTTG AAATGGAAAT 150
CCGTGATCTT CTTTCAGAAT ACGATTTCCC AGGTGACGAC ATTCCTGTTG 200
TTCAAGGTTC AGCTCTTAAG GCTCTTGAAG GTGATACAGC TGCCGAAGAC 250
AAGATTATGG AATTGATGGA CATCGTTGAT GATTACATTC CAGAACCAAA 300
ACGCGATACT GATAAGCCAT TGCTTCTCCC AGTCGAAGAC GTATTCTCAA 350
TCACTGGTCG TGGTACTGTT GCTTCAGGAC GTATTGACCG TGGTACTGTT 400
AAGGTTAACG ACGAAGTTGA AATCGTTGGT ATCCGTGACG ATATCCAAAA 450
AGCAGTTGTT ACTGGAGTTG AAATGTTCCG TAAGCAATTG GACGAAGGTC 500
TTGCTGGAGA TAACGTTGGT GTGCTTCTTC GTGGTATCCA ACGTGATGAA 550
ATTGAACGTG GTCAAGTATT GGCTGCACCT GGTTCAATCC ACCCACACAC 600
TAAGTTCAAG GGTGAAGTTT ACATCCTTTC TAAAGATGAA GGTGGACGTC 650
ACACTCCATT CTTCAACAAC TACCGTCCAC AGTTCTACTT CCGTACAACT 700
GACGTAACTG GTTCAATCGA ATTGCCAGCA GGTACTGAAA TGGTTATGCC 750
TGGTGATAAC GTTACTATCG ACGTTGAATT GATCCACCCA ATCGC 795

2) INFORMATION FOR SEQ ID NO: 229

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus suis*
(B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

TGTAGTAGCT TCAACTGACG GTCCAATGCC ACAAACTCGT GAGCACATCC 50
TTCTTTCACG TCAGGTTGGT GTTAAACACC TTATCGTCTT CATGAACAAA 100

```
GTTGACTTGG TTGACGATGA AGAATTGCTT GAGTTGGTTG AAATGGAAAT      150
CCGTGACCTT CTTTCAGAAT ACGATTTCCC AGGTGATGAT CTTCCAGTTA      200
TCCAAGGTTC AGCTCTTAAA GCTCTTGAAG GTGACTCTAA GTACGAAGAC      250
ATCGTTATGG AATTGATGAA CACTGTTGAT GAGTACATTC CAGAACCAGA      300
ACGCGACACT GACAAACCAT TGTTGCTTCC AGTCGAGGAC GTATTCTCAA      350
TCACTGGTCG TGGTACTGTA GCTTCAGGAC GTATCGACCG TGGTACTGTT      400
CGTGTCAACG ACGAAATCGA AATCGTTGGT CTTCAAGAAG AAAAATCTAA      450
AGCAGTTGTT ACTGGTGTTG AAATGTTCCG TAAACAACTT GACGAAGGTC      500
TTGCCGGCGA TAACGTTGGT GTGCTTCTTC GTGGTGTACA ACGTGATGAA      550
ATCGAACGTG GTCAAGTTAT CTCTAAACCA GGTTCTATCA ACCCACACAC      600
TAAATTCAAA GGTGAAGTTT ACATCCTTAC TAAAGAAGAA GGTGGACGTC      650
ACACTCCATT CTTCGACAAC TACCGTCCAC AGTTCTACTT CCGTACAACT      700
GACGTAACTG GTTCAATCAA ATTGCCAGAA GGTACTGAAA TGGTAATGCC      750
TGGTGATAAC GTTACTATCG ACGTTGAATT GATCCACCCA ATCGCCG         797
```

2) INFORMATION FOR SEQ ID NO: 230

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 793 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus uberis*
- (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

```
TTGTTGTTGC ATCAACTGAT GGACCAATGC CACAAACTCG TGAGCACATC       50
CTTCTTTCAC GCCAAGTTGG TGTTAAACAC CTTATCGTTT TCATGAACAA      100
AATCGACCTT GTTGACGATG AAGAATTGCT TGAATTAGTT GAAATGGAAA      150
TCCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA CCTACCAGTT      200
ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA      250
CATCATCATG GAATTGATGA AAACTGTTGA TGAGTATATT CCAGAACCAG      300
AACGTGATAC AGACAAACCA TTACTTCTTC CAGTCGAAGA CGTATTCTCA      350
ATCACAGGTC GTGGTACTGT AGCTTCAGGA CGTATCGATC GTGGTACTGT      400
TCGTGTCAAC GACGAAATTG AAATCGTTGG TATCAAAGAA GAAACTAAAA      450
AAGCAGTTGT TACTGGTGTT GAAATGTTCC GTAAACAACT TGACGAAGGT      500
CTTGCAGGAG ATAACGTAGG TATCCTTCTT CGTGGTGTTC AACGTGACGA      550
AATCGAACGT GGACAAGTTA TTGCTAAACC AGGTTCAATC AACCCACACA      600
CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGATGA AGGTGGACGT      650
CATACTCCAT TCTTCAACAA CTACCGTCCT CAATTCTATT TCCGTACAAC      700
TGACGTAACA GGTTCAATCG AACTTCCAGC TGGTACTGAA ATGGTAATGC      750
CTGGTGATAA CGTGACAATC AGCGTTGAGT TGATCCACCC AAT             793
```

2) INFORMATION FOR SEQ ID NO: 231

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus vestibularis*
(B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

```
TTGTAGTAGC ATCTACTGAC GGACCAATGC CACAAACTCG TGAGCACATC      50
CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA     100
AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT GAAATGGAAA     150
TCCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA TATTCCAGTT     200
ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA     250
CATCATCATG GACTTGATGA ACACTGTTGA CGAATACATT CCAGAACCAG     300
AACGTGACAC TGACAAACCA TTGTTGCTTC CAGTCGAAGA CGTATTCTCA     350
ATCACTGGTC GTGGTACTGT TGCTTCAGGA CGTATCGACC GTGGTGTTGT     400
TCGTGTTAAT GACGAAGTTG AAATCGTTGG TCTTAAAGAA GAAATCCAAA     450
AAGCAGTTGT TACTGGTGTA GAAATGTTCC GTAAACAACT TGACGAAGGT     500
ATTGCCGGAG ATAACGTCGG TGTCCTTCTT CGTGGTATCC AACGTGATGA     550
AATTGAACGT GGTCAAGTAT TGGCTGCACC TGGTTCAATC AACCCACACA     600
CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGAAGA AGGTGGACGT     650
CACACTCCAT TCTTCAACAA CTACCGTCCA CAGTTCTACT TCCGTACAAC     700
TGACGTAACA GGTTCAATCG AACTTCCTGC AGGTACTGAA ATGGTTATGC     750
CTGGTGATAA CGTGACTATC GACGTTGAGT TGATCCACCC AATCGCCG       798
```

2) INFORMATION FOR SEQ ID NO: 232

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Tatumella ptyseos*
(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

```
GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACCCG      50
TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTTCCTTAC ATCATCGTGT     100
TCCTGAACAA ATGTGACATG GTTGATGATG AAGAGCTGCT GGAACTGGTA     150
GAAATGGAAG TCCGTGACCT GCTGTCACAG TACGACTTCC CGGGTGACGA     200
CACGCCAATC GTTCGCGGTT CAGCGCTGAA AGCACTGGAA GGTGAAGGCG     250
AGTGGGAAGA GAAGATTCTG GAGCTGGCTG GCTTCCTGGA TTCTTACATC     300
CCTGAGCCAG AGCGTGCTAT CGATCAGCCG TTCCTGCTGC CAATCGAAGA     350
CGTATTCTCA ATCTCCGGTC GTGGTACAGT TGTTACCGGT CGTGTAGAGC     400
GCGGGATCAT CAAAGTCGGT GAAGAAGTTG AGATCGTTGG TATCAAAGAT     450
ACTGCGAAAT CAACCTGTAC CGGTGTTGAA ATGTTCCGTA AACTGCTGGA     500
CCAGGGTCAG GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC     550
GTGAAGAGAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA     600
CCACACACCC AGTTCGAGTC AGAAGTTTAT ATTCTGTCTA AAGACGAAGG     650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC     700
GTACAACTGA CGTGACCGGA ACCATCGAAC TGCCGGAAGG CGTAGAGATG     750
GTAATGCCTG GTGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCAAT     800
CGCGATGGAC GATGGTCTGC GTTTCGCAA                            829
```

2) INFORMATION FOR SEQ ID NO: 233

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trabulsiella guamensis*
(B) STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

GGCGCAATCC TGGTAGTAGC AGCGACTGAC GGCCCGATGC CGCAGACTCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTA 150
GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CGGGCGATGA 200
CACGCCGATC GTACGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
AGTGGGAAGC GAAAATCATC GAACTGGCAG GTTTCCTGGA TTCTTACATT 300
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCC ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
GCGGTATCAT CAAAGTGGGT GAAGAAGTAG AAATCGTTGG TATCAAAGAG 450
ACTGCGAAGT CAACCTGTAC TGGCGTAGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC 600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG 650
CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCGATGGAC GACGGTCTGC GTTTCGCAA 829

2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Veillonella parvula*
(B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

CGGCGCTATC TTGGTTGTAT CCGCAGCTGA CGGCCCTATG CCTCAAACTC 50
GCGAACACAT CTTGTTGGCT CGCCAAGTTG GTGTTCCTGC AATCGTAGTA 100
TTCTTGAACA AAGCTGACAT GGTTGACGAT GAAGAATTGA TCGAATTGGT 150
AGAAATGGAA GTTCGTGAAC TTCTTTCTTC CTACGAATTC CCTGGCGACG 200
AAGTACCTAT CGTTGTAGGT TCCGCGTTGA AAGCTTTGGA AGGCGATGCT 250

CAATATGTAG CTAAAATTGA CGAATTGATG GACGCTGTAG ACTCCTACAT 300
CCCAACACCA GTTCGTGACA CTGATAAACC ATTCTTGATG CCTGTGGAAG 350
ATGTTTTCAC AATCACTGGT CGTGGTACAG TAGCAACTGG CCGTGTTGAA 400
CGTGGTCAAG TAAACGTTGG TGATACTGTT GAAGTAGTAG GCTTGAAAGA 450
AAAAGCTGAA CAATACGTAG TAACAGGTCT TGAAATGTTC CGTAAAGTGT 500
TGGATTCTGC AGTAGCAGGT GACAACGTAG GTGCATTGCT TCGTGGTGTT 550
GATCGTAAAG ACATYGAACG TGGTCAAGTA TTGGCTAAAC CAGGTTCCAT 600
CAACCCACAY ACAAAATTCA AAGCAGAAGT ATACGTATTG ACTAAAGAAG 650
AAGGTGGTCG TCATACTCCA TTCTTCTCCA ACTACCGTCC ACAATTCTAC 700
TTCCGTACAA CAGACGTAAC AGGTGTTGTA AACCTTCCTG AAGGTGTAGA 750
AATGTGTATG CCTGGCGATA ACGTAACAAT GGAAATCGAA TTGATTACTC 800
CAATCGCTAT CGAAGAAGGT CTTCG 825

2) INFORMATION FOR SEQ ID NO: 235

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia enterocolitica*
(B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

CGCTATCCTG GTTGTTGCTG CAACTGATGG CCCAATGCCA CAGACTCGTG 50
AGCACATCCT GTTGGGTCGT CAGGTTGGTG TTCCTTACAT CATCGTATTC 100
ATGAACAAAT GTGACATGGT TGACGATGAA GAGCTGCTAG AACTGGTAGA 150
AATGGAAGTG CGCGATCTTC TGTCTACCTA CGATTTCCCA GGCGATGATA 200
CGCCAGTTGT TCGTGGTTCC GCGCTGAAAG CATTGGAAGG CGAACCTGAG 250
TGGGAAGCAA AAATTATCGA ACTGGCTGGC TACCTGGATT CTTACATCCC 300
AGAACCAGAG CGTGCTATCG ATAAGCCGTT CCTGCTGCCA ATCGAAGACG 350
TATTCTCTAT CTCTGGTCGT GGTACTGTTG TAACGGGTCG TGTAGAGCGC 400
GGTATCGTTA AAGTTGGTGA AGAAGTCGAA ATTGTTGGCC TGAAAGATAC 450
CGTTAAATCT ACTTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGATG 500
AAGGCCGTGC AGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAGCGT 550
GAAGATATCG AACGTGGTCA AGTTCTTGCT AAACCAGGTT CGATTAAACC 600
ACACACCAAA TTTGAATCAG AAGTTTATAT TCTGAGCAAA GATGAAGGTG 650
GTCGCCATAC TCCGTTCTTC AAAGGCTACC GTCCTCAGTT CTACTTCCGT 700
ACAACTGATG TAACCGGTAC TATTGAACTG CCAGAAGGCG TTGAGATGGT 750
GATGCCAGGT GATAACATTC AAATGATTGT TAACCTGATT GCTCCTATCG 800
CAATGGATGA CGGCTTGCGC TTTGC 825

2) INFORMATION FOR SEQ ID NO: 236

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DN A

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia frederiksenii*
(B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

```
GGCGCGATCC TGGTTGTTGC TGCCACTGAT GGCCCGATGC CACAGACTCG       50
CGAGCACATT CTGTTAGGGC GTCAGGTGGG TGTTCCTTAC ATCCTGGTCT      100
TCCTGAACAA ATGTGACATG GTTGACGACG AAGAGCTGCT GGAACTGGTA      150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC CTGGCGACGA      200
CACTCCAGTT ATCCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCTG      250
AGTGGGAAGC AAAAATCATC GAATTGGCTG AGGCGCTGGA TAGCTATATT      300
CCACAGCCAG AGCGTGCGAT TGATAAACCA TTCCTGCTGC CAATCGAAGA      350
CGTATTCTCA ATCTCTGGCC GTGGTACTGT TGTCACCGGT CGTGTAGAGC      400
GCGGTATCGT TAAAGTCGGC GAAGAAGTCG AAATCGTTGG TATCATTGAT      450
ACCATCAAGA CTACCTGTAC TGGTGTTGAA ATGTTCCGCA AATTGCTGGA      500
CGAAGGCCGT GCGGGTGAGA ACGTTGGTGT TCTGCTACGT GGTACTAAAC      550
GTGATGACGT ACAACGTGGT CAGGTATTGG CAAAACCAGG TTCTATCAAG      600
CCACACACCA AATTTGAATC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG      650
TGGTCGCCAT ACTCCGTTCT TCAAAGGTTA TCGTCCTCAG TTCTACTTCC      700
GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
GTGATGCCAG GTGATAACAT TCAAATGATT GTTAACCTGA TTGCTCCTAT      800
CGCAATGGAT GACGGTCTGC GCTTTGCG                              828
```

2) INFORMATION FOR SEQ ID NO: 237

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia intermedia*
(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

```
CTTGGTTGTC GCTGCAACTG ATGGTCCTAT GCCACAGACT CGCGAGCACA       50
TCCTGCTAGG TCGTCAGGTG GGTGTTCCTT ACATCCTGGT CTTCCTGAAC      100
AAGTGTGACA TGGTTGACGA TGAGGAGTTG CTGGAATTGG TAGAAATGGA      150
AGTCCGCGAA CTTCTGTCTC AATATGATTT CCCTGGCGAT GATACTCCTG      200
TTATCCGTGG TTCAGCGCTG AAGGCGTTGG AAGGCGAGCC TGAATGGGAA      250
GCAAAAATTA TCGAATTAGC TGAGGCGCTG GATAGTTATA TTCCACAGCC      300
AGAGCGCGCG ATTGATAGAC CATTCTTGCT GCCAATCGAA GACGTATTCT      350
CTATCTCAGG TCGTGGTACA GTCGTCACTG GTCGTGTAGA GCGTGGGATC      400
GTTAAAGTTG GCGAAGAAGT TGAAATCGTT GGTATTATCG ATTCCATTAG      450
AACAACATGT ACTGGCGTTG AAATGTTCCG CAAATTGCTG GACGAAGGCC      500
GCGCGGGTGA GAACGTTGGT GTTCTACTGC GTGGGACTAA ACGTGATGAC      550
GTACAGCGTG GTCAGGTATT AGCTAAGCCA GGTTCTATCA AGCCACATAC      600
TAAATTCGAA TCCGAAGTTT ATATTCTGAG CAAAGATGAA GGCGGGCGTC      650
ACACGCCGTT CTTCAAAGGC TACCGTCCTC AGTTCTACTT CCGTACAACG      700
GATGTAACCG GTACTATTGA ATTGCCAGAC GGCGTTGAGA TGGTGATGCC      750
AGGTGATAAC ATTCAAATGA TTGTTAACCT GATTGCACCT ATTGCGATGG      800
ATGATGGTCT GCG                                             813
```

2) INFORMATION FOR SEQ ID NO: 238

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia pestis*
(B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

```
GGAGCGATCT TGGTTGTTGC TGCAACCGAT GGCCCTATGC CGCAGACTCG      50
TGAGCATATC CTGCTGGGCC GCCAGGTTGG TGTCCCATAC ATTATTGTCT     100
TCCTGAACAA ATGTGACATG GTTGACGATG AAGAGTTGCT AGAGTTGGTT     150
GAAATGGAGG TTCGTGAGCT TCTGTCTCAA TACGATTTCC CAGGCGACGA     200
CACTCCAGTC ATCCGTGGTT CAGCGTTGAA AGCCCTGGAA GGTGACGCTG     250
AGTGGGAAGC TAAAATTATC GAGTTGGCAG AAGCTCTGGA TAGCTATATT     300
CCGCAACCAG AACGCGCTAT TGATAGACCA TTCCTATTGC CAATTGAAGA     350
CGTATTCTCT ATTTCTGGTC GTGGTACTGT AGTTACTGGT CGTGTAGAAC     400
GTGGTATTGT TAAGGTCGGC GAAGAAGTTG AAATCGTTGG TATTATCGAT     450
ACGATTAAAA CAACTTGTAC TGGCGTTGAA ATGTTCCGCA AGCTGCTGGA     500
TGAAGGCCGT GCTGGTGAAA ATGTTGGTGT TCTGCTGCGT GGTACTAAGC     550
GTGACGATGT TCAGCGTGGT CAAGTACTGG CGAAACCAGG TTCTATCAAG     600
CCACACACGA AGTTTGAGTC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG     650
CGGCCGTCAT ACACCGTTCT TCAAGGGCTA CCGTCCTCAG TTCTACTTCC     700
GTACAACTGA CGTGACCGGT ACCATTGAGC TGCCAGAAGG CGTTGAAATG     750
GTCATGCCTG GTGACAACGT AAACATGGTT GTTAACCTAA TTGCTCCTAT     800
CGCAATGGAT GATGGTCTGC GCTTCGCAA                            829
```

2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia pseudotuberculosis*
(B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

```
TGGAGCGATC TTGGTTGTTG CTGCAACCGA TGGCCCTATG CCGCAGACTC      50
GTGAGCATAT CCTGCTGGGC CGCCAGGTTG GTGTCCCATA CATTATTGTC     100
TTCCTGAACA AATGTGACAT GGTTGACGAT GAAGAGTTGC TAGAGTTGGT     150
TGAAATGGAG GTTCGTGAGC TTCTGTCTCA ATACGATTTC CCAGGCGACG     200
ACACTCCAGT CATCCGTGGT TCAGCGTTGA AAGCCCTGGA AGGTGACGCT     250
```

GAGTGGGAAG CTAAAATTAT CGAGTTGGCA GAAGCTCTGG ĀTAGCTATAT 300
TCCGCAACCA GAACGCGCTA TTGATAGACC ATTCCTATTG CCAATTGAAG 350
ACGTATTCTC TATTTCTGGT CGTGGTACTG TAGTTACTGG TCGTGTAGAA 400
CGCGGTATTG TTAAGGTCGG CGAAGAAGTT GAAATCGTTG GTATTATCGA 450
TACGATTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGC AAGCTGCTGG 500
ATGAAGGCCG TGCTGGTGAA AATGTTGGTG TTCTGCTGCG TGGTACTAAG 550
CGTGACGATG TTCAGCGTGG TCAAGTACTG GCGAAACCAG GTTCTATCAA 600
GCCACACACG AAGTTTGAGT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
GCGGCCGTCA TACACCGTTC TTCAAGGGCT ACCGTCCTCA GTTCTACTTC 700
CGTACAACTG ACGTGACCGG TACCATTGAG CTGCCAGAAG GCGTTGAAAT 750
GGTCATGCCT GGTGACAACG TAAACATGGT TGTTAACCTA ATTGCTCCTA 800
TCGCAATGGA TGATGGT 817

2) INFORMATION FOR SEQ ID NO: 240

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia rohdei*
(B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCAATG CCACAGACTC 50
GCGAGCACAT CCTGTTGGGT CGTCAAGTGG GTGTTCCTTA CATCTTAGTC 100
TTCCTGAACA AGTGTGACAT GGTTGACGAC GAAGAGTTGC TGGAACTGGT 150
TGAAATGGAA GTTCGTGAGC TTCTGTCTCA ATACGATTTC CCTGGCGATG 200
ACACTCCGGT TATTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAGGCC 250
GAGTGGGAAG CCAAAATTAT TGAACTTGCT GAAGCACTGG ATAGCTACAT 300
TCCACAGCCA GAGCGCGCGA TTGATAAACC ATTCTTGCTG CCAATCGAAG 350
ACGTATTCTC TATCTCAGGC CGTGGAACAG TTGTTACCGG GCGTGTTGAG 400
CGCGGTATCG TCAGAGTGGG CGAAGAAGTT GAAATCGTGG GTATCATCGA 450
CACCATTAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAACTGCTGG 500
ACGAAGGCCG TGCCGGTGAG AACGTTGGTG TTCTGCTGCG CGGTACTAAA 550
CGCGATGACG TGCAACGTGG TCAAGTGTTG GCTAAACCAG GTTCTATTAA 600
GCCGCATACC AAATTTGAGT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
GTGGTCGTCA TACTCCGTTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGACG GTGTTGAGAT 750
GGTGATGCCA GGTGATAACA TTCAAATGAT TGTTAACCTG ATTGCGCCTA 800
TTGCAATGGA TGACGGTCTA CGATTTGCA 829

2) INFORMATION FOR SEQ ID NO: 241

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yokenella regensburgei*
(B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

```
TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG     100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT     150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG     200
ACACTCCGAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAAGCA     250
GAGTGGGAAG CTAAAATCGT TGAGCTGGCT GGCTTCCTGG ATTCTTACAT     300
CCCAGAACCA GTTCGTGCTA TCGACCTGCC GTTCCTGCTG CCGATCGAAG     350
ACGTATTCTC CATCTCCGGT CGTGGCACCG TTGTTACCGG TCGTGTAGAG     400
CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA     450
GACTGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAACTGCTGG     500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA     550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GTTCCATCAA     600
GCCGCACACC AAATTCGAAT CTGAAGTTTA TATCCTGTCC AAAGACGAAG     650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC     700
CGTACAACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT     750
GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA     800
TCGC                                                      804
```

2) INFORMATION FOR SEQ ID NO: 242

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*
(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

```
TCAGTTCCCC CGCGATCACA TGCCCAAGAT CTACGAAGCG CTTACTCTGG      50
CCGACGAGGG TTCCTCGTTC GCCGAAAAGG GTCTGACGCT GGAAGTGCAG     100
CAACAGCTGG GCGACGGCGT GGTGCGTACC ATCGCGCTGG GCTCCAGCGA     150
CGGCCTGCGC CGCGGTATGA AGGTCACCGG TACGGGCGCG CCGATCTCGG     200
TGCCGGTCGG CACCGGCACG CTGGGCCGCA TCATGGACGT GCTGGGTCGT     250
CCCATCGACG AAGCCGGCCC GATCCAGCAC GAAGAAAAGC GTGGCATTCA     300
CCAGCCGGCT CCCCGTTTCG ACGAACTGTC GCCGTCGGTG GAACTGCTGG     350
AAACCGGCAT CAAGGTTATT GACCTGGTCT GCCCGTTCGC CAAGGGCGGC     400
AAGGTCGGCC TGTTCGGCGG CGCCGGCGTG GGCAAGACCG TCAACATGAT     450
GGAACTGATC AACAACATCG CCAAGCAGCA CAGCGGCTTG TCGGTGTTCG     500
CCGGCGTGGG CGAGCGTACC CGCGAAGGCA ACGACTTCTA CCACGAAATG     550
GAAGAGTCGA ACGTTCTGGA CAAGGTTGCG ATGGTGTTCG GTCAGATGAA     600
CGAACCCCCG GGCAACCGTC TGCGCGTGGC GCTGACCGGC CTGACCATGG     650
CCGAGAAGTT CCGCGACGAA GGCCGCGACA TCCTGTTCTT CGTGGACAAC     700
ATCTACCGCT ACACCCTGGC CGGTACGGAA GTGTCCGCGC TGCTGGGCCG     750
TATGCCGTCG GCAGTGGGCT ACCAGCCCAC GCTGGCCGAA GAAATGGGCA     800
```

AGCTGCAAGA GCGCATCACC TCGACCAAGA CCGGCTCGAT CACCTCGAT 849

2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

TGAAACTACT TTAGAAGTTC AGCAACAACT TGGTGATGGT GTTGTTCGTA 50
CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAACT 100
AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGGCCG 150
TATCATGGAC GTTTTAGGTC GTCCTATCGA TGAAGCAGGT CCTGTTGCGA 200
CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250
GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300
TTGCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTCGGT GGTGCTGGTG 350
TTGGTAAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400
CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450
TAATGACTTC TATCACGAAA TGAAAGATTC TAACGTTCTT GACAAAGTAG 500
CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550
GCGTTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAGACGA 600
AAACGGTAAA GGTCGTGACG TATTATTATT CGTCGACAAC ATCTACCGTT 650
ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700
GCGGTAGGTT ACCAACCTAC ACTTGCAGAA GAAATGGGTG TTCTTCAAGA 750
GCGTATTACA TCTACTAAAT CTGGTTCGAT CACTTCG 787

2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Acinetobacter lwoffii*
(B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AAACTACATT 50
AGAAGTTCAG CAACAACTTG GTGATGGCGT AGTTCGTACT ATTGCAATGG 100
GTTCTACTGA AGGCCTTAAG CGTGGTTTGA ACGTAACTAA CACTAACGCG 150
CCGATTTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200
TCTTGGTCGC CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

TGCCGATTCA CCGTCAAGCA CCTTCTTATG CTGAACAAGC AGCTTCTACT 300
GACCTTTTAG AAACTGGTAT TAAAGTCATC GACTTACTTT GCCCGTTCGC 350
TAAAGGTGGT AAAGTTGGTC TGTTCGGTGG TGCCGGTGTT GGTAAAACTG 400
TAAACATGAT GGAGTTGATC AACAACATCG CTAAAGCGCA CTCAGGTTTA 450
TCTGTATTCG CTGGTGTTGG TGAGCGTACT CGTGAAGGTA ATGACTTCTA 500
TCACGAGATG AAAGACTCAA ACGTTCTAGA CAAAGTAGCA ATGGTCTACG 550
GTCAGATGAA CGAGCCACCG GGTAACCGTT TACGCGTAGC GTTGACTGGT 600
TTGACCATGG CTGAGTACTT CCGTGACGAG AAAGACGAAA ACGGCAAAGG 650
CCGTGACGTA CTATTGTTCG TAGATAACAT CTACCGTTAT ACACTAGCAG 700
GTACTGAAGT ATCAGCACTT CTAGGTCGTA TGCCGTCTGC AGTAGGTTAC 750
CAACCGACAC TTGCAGAAGA GATGGGTGTT CTTCAAGAAC GTATTACATC 800
GACTAAGTCT GGTTCGATTA CGTCA 825

2) INFORMATION FOR SEQ ID NO: 245

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 837 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: CSG-197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

CAATGAAGTT CCAGAAATTA ACAATGCCTT AGTCGTAGAC GTTGAAAGAG 50
ATGAAGGTAC AGTATCTCTT ACATTAGAAG TGGCATTACA ACTTGGCGAT 100
GATGTCGTAC GTACAATTGC AATGGATTCT ACTGATGGTG TTAAACGTGG 150
TACAGAAGTT CGAGATAGCG GAGATAGCAT CAGTGTTCCA GTTGGTGATG 200
CTACGTTAGG ACGTGTGTTT AATGTTCTTG GTGATACAAT TGACTTAGAC 250
GAGAAGCTTG ATACTTCTGT CAAACGTGAT CCAATTCATA GAGAAGCACC 300
TGCATTCGAT CAATTATCAA CAAAAGTTGA AATCTTAGAA ACAGGTATTA 350
AAGTAATTGA TTTACTTGCA CCATATATTA AAGGTGGTAA AATCGGTTTA 400
TTCGGTGGCG CTGGTGTAGG TAAAACAGTA TTAATTCAAG AATTAATTAA 450
TAATATAGCT CAAGAACATG GTGGTATTTC AGTATTTGCC GGCGTAGGTG 500
AACGTACGCG TGAAGGTAAT GACTTATACT ACGAAATGAG TGATAGTGGT 550
GTTATTAAGA AAACAGCTAT GGTCTTCGGA CAAATGAATG AGCCACCTGG 600
TGCGCGTATG CGTGTTGCTT TATCAGGCTT AACAATGGCT GAACACTTCC 650
GTGATGTACA AGGACAAGAT GTTTTACTAT TTATTGATAA CATATTCAGA 700
TTTACGCAAG CTGGTTCAGA AGTATCAGCA CTATTAGGTC GTATGCCATC 750
AGCCGTTGGT TATCAACCTA CCCTTGCTAC TGAAATGGGT CAATTACAAG 800
AACGTATTAC ATCAACAACT AAAGGATCTG TAACGTC 837

2) INFORMATION FOR SEQ ID NO: 246

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 851 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Alcaligenes faecalis*
(B) STRAIN: ATCC 15554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

```
TTCCCCCGCG ACAGCATCCC TAAAGTCTAC GAAGCATTGA CGCTCGTTGA      50
CGAAAGTTCG GCTTTCGCAG AAAAAGGCCT GACTTTTGAA GTACAGCAAC     100
AATTGGGTGA CGGTGTAGTT CGCACCATCG CCATGGGTTC CAGCGACGGC     150
CTGCGCCGCG GTATGGAAGT GGCCGGTTCG GGCGCTCCCA TCTCCGTTCC     200
CGTGGGTGTC GGCACCCTGG GTCGCATTAT GGACGTTCTG GGTCGCCCTA     250
TTGACGAAGT CGGTCCTATT CAGTCCGACG AGCGTCGCGC CATTCACCAG     300
CCTGCGCCTA CTTTCGACGA ACTGTCGCCT TCCGTAGAGC TGCTGGAAAC     350
CGGTATTAAA GTGATTGACC TGGTTTGCCC GTTCGCCAAG GGTGGTAAGG     400
TTGGTCTGTT CGGTGGTGCC GGTGTGGGCA AGACCGTGAA CATGCTGGAG     450
CTGATCAACA ACATCGCCAA GGCACACAGC GGTCTGTCCG TGTTTGCCGG     500
TGTGGGTGAG CGTACCCGTG AAGGTAACGA CTTCTACCAC GAAATGGCCG     550
ATGCTGGCGT TATCCAGATG GACAACCTGA GCGAGTCCAA AGTGGCCATG     600
GTGTTCGGTC AGATGAACGA ACCTCCAGGC AACCGTCTGC GTGTGGCACT     650
GTCCGGCCTG ACCATGGCCG AGAAGTTCCG TGACGAAGGC CGTGACATCC     700
TGTTCTTTGT GGACAACATC TACCGCTACA CGCTGGCCGG TACAGAAGTG     750
TCCGCTCTGC TGGGTCGTAT GCCTTCCGCA GTGGGTTACC AGCCTACGCT     800
GGCCGAGGAA ATGGGTAAGC TGCAAGAGCG CATTACCTCC ACCAAGACCG     850
G                                                         851
```

2) INFORMATION FOR SEQ ID NO: 247

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

```
GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAGAG      50
CAACGAAAAC GGAACAAGCA TTAACTTAAC ATTTGAAGTT GCACTTCATT     100
TAGGTGATGA CACAGTTCGT ACAGTTGCAA TGTCTTCCAC AGATGGACTT     150
GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT     200
TGGTGATGCA ACACTTGGTC GTGTATTTAA CGTATTAGGT GATGCAATTG     250
ACTTAGATGG TGAGGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT     300
CAAGCACCTG CATTCGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC     350
TGGTATTAAA GTAGTAGACT TACTTGCTCC TTACATTAAG GGTGGTAAGA     400
TCGGTCTATT CGGTGGTGCC GGTGTAGGTA AAACGGTATT AATTCAGGAA     450
TTAATCAATA ACATCGCACA AGAACACGGT GGTATCTCTG TATTCGCTGG     500
TGTAGGTGAG CGTACTCGTG AGGGTAATGA CTTATACCAC GAAATGAGCG     550
ATTCTGGCGT AATTAAGAAA ACTGCGATGG TATTCGGACA AATGAACGAG     600
CCACCTGGAG CACGTCAACG TGTTGCGTTA ACAGGTTTAA CAATGGCTGA     650
GCATTTCCGT GATGAGCAAG GACAAGATGT ACTTCTGTTC ATCGATAATA     700
TCTTCCGTTT CACGCAAGCA GGTTCTGAAG TATCTGCCCT TCTTGGCCGT     750
ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA     800
```

ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTCT 846

2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
CATGAACTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCGTGG CACAGAAGTA 150
GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200
ACGTGTATTC AACGTATTAG GTGATGCAAT TGACTTAGAT GGTGAACTTC 250
CTGCGGATGT ACACCGTGAT CCAATTCACC GTCAAGCACC TGCATTCGAA 300
GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350
CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
CCGGCGTAGG TAAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450
CAAGAGCACG GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG 500
TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
AAACTGCGAT GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
CGTGTTGCAT TAACAGGTTT AACAATGGCT GAGCATTTCC GTGATGAGCA 650
AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT 750
TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
ATCTACAAAT 810

2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 944 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacteroides distasonis*
(B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50
CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100
CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150
CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

```
TGCCGACCGG CGACCAAGTC AAAGGACGTT TAATGAATGT CACCGGCGAC      250
CCTATCGATG GCATGGCCCA GCTTACTAAA GACGGGGCTC TTCCCATCCA      300
TCGTGAGCCT CCTAAATTCG AGGATCTGAC AACGACCCAA GAGGTCTTGT      350
ACACGGGTAT TAAAGTAATC GATTTATTGG AACCTTACGC CAAAGGAGGC      400
AAGATCGGAC TTTTCGGAGG AGCCGGAGTC GGCAAAACGG TATTGATCAT      450
GGAATTGATC AACAACATCG CAAAGAAAAA CAACGGATTC TCCGTCTTCG      500
CCGGTGTGGG TGAACGTACA CGTGAAGGAA ATGACCTATT GCGTGAAATG      550
ATCCAATCCG GTGTCATCCG ATACGGCGAG GAGTTTAAGA AGAGTATGGA      600
GGCAGGCAAC TGGGACTTGT CGAAGATCGA TTACGATGAA TTGGCTAAGT      650
CGCAGGCTAC CTTGGTATTC GGGCAGATGA ACGAACCGCC GGGCGCCCGC      700
TCGTCCGTGG CCTTATCCGG TTTGACGATC GCCGAATCCT TCCGTGACAA      750
AGCCTCTGAG GGAGAAAGAA AAGATATATT ATTCTTCATC GATAATATCT      800
TCCGTTTCAC CCAAGCCGGT TCCGAGGTTT CCGCCTTGCT GGGGCGTATG      850
CCTTCCGCCG TAGGTTACCA ACCGACATTG GCCACGGAAA TGGGAGCTAT      900
GCAAGAGCGT ATCACTTCAA CCAAGAAGGG CTCCATCACC TCCG            944
```

2) INFORMATION FOR SEQ ID NO: 250

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacteroides ovatus*
- (B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

```
TTGAGGGTAC GGATGCAGAA TTGGTGCTGC CAAGCATCCA CGACGCACTG       50
GAGATAAAGA GGCCAAACGG CAAAATACTG GTTGTAGAAG TTCAGCAACA      100
TATCGGCGAA AATACGGTGC GTACCGTAGC GATGGACAGT ACTGACGGAC      150
TTCAGAGAGG CATGAAAGTG TATCCCACCG GAGGCCCGAT CACGATGCCG      200
ATTGGCGAAC AGATTAAAGG ACGACTGATG AACGTAGTCG GTGATTCGAT      250
CGACGGTATG AAAGGACTCG ACCGCAAAGG TGCATATTCC ATTCATCGCG      300
ACCCCCCTAA GTTTGAGGAT TTGACTACTG TGCAAGAGGT GCTCTTCACA      350
GGTATCAAAG TGATCGACCT GCTCGAACCG TATGCCAAAG GTGGTAAAAT      400
CGGTTTGTTC GGCGGTGCCG GTGTAGGAAA GACTGTATTG ATTCAGGAAC      450
TTATCAATAA TATCGCCAAG AAACATAATG GATTCTCTGT ATTTGCCGGA      500
GTAGGTGAAC GTACCCGTGA AGGTAACGAC TTGCTGCGCG AAATGATTGA      550
ATCCGGTGTA ATCCGTTACG GCGAAGCATT CAAAGAAGGA ATGGAGAAAG      600
GTCACTGGGA TCTTTCGAAA GTGGATTATA ACGAACTGGA GAAATCGCAA      650
GTGTCTCTGA TTTTCGGTCA GATGAACGAG CCTCCGGGCG CACGTGCCTC      700
TGTGGCATTG TCCGGACTGA CGGTGGCGGA ATCTTTCCGC GACGCAGGAA      750
AAGAAGGTGA GAAACGCGAT ATTCTGTTCT TTATTGATAA TATCTTCCGT      800
TTCACGCAAG CAGGTTCAGA AGTGTCCGCC CTTTTGGGAC GTATGCCCTC      850
CGCTGTTGGT TACCAGCCCA CGTTGGCTAC GGAAATGGGT GCGATGCAGG      900
AACGTATCAC GTCTACCCGC AAAGGTTCTA TCACCTCCG                  939
```

2) INFORMATION FOR SEQ ID NO: 251

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 833 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leclercia adecarboxylata*
(B) STRAIN: ATCC 23216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

```
CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTTC      50
AGAATGGTAA TGAGAGCCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC     100
GGTATTGTGC GTACCATCGC CATGGGTTCT TCCGACGGTC TGCGTCGTGG     150
TCTGGAAGTT AAAGACCTCG AGCACCCAAT CGAAGTACCA GTAGGTAAAG     200
CAACCCTGGG CCGTATCATG AACGTCCTGG GTCAGCCGAT CGACATGAAA     250
GGCGACATCG GCGAAGAAGA GCGTTGGGCT ATCCACCGTT CAGCACCTTC     300
CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG     350
TTATCGACCT GATGTGTCCG TTCGCGAAGG GCGGTAAAGT TGGTCTGTTC     400
GGCGGTGCGG GTGTAGGTAA AACCGTAAAC ATGATGGAGC TGATCCGTAA     450
CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC     500
GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA CTCCAACGTT     550
CTGGACAAAG TATCCCTGGT TTACGGCCAG ATGAACGAGC CACCAGGAAA     600
CCGTCTGCGC GTTGCGCTGA CCGGCCTGAC CATGGCTGAG AAGTTCCGTG     650
ACGAAGGTCG TGACGTACTG CTGTTCGTTG ACAACATCTA CCGTTACACC     700
CTGGCCGGTA CGGAAGTATC CGCACTGCTG GGTCGTATGC CATCAGCAGT     750
AGGCTACCAG CCGACCCTGG CGGAAGAGAT GGGTGTTCTG CAGGAACGTA     800
TCACCTCTAC CAAAACCGGT TCTATCACCT CCG                       833
```

2) INFORMATION FOR SEQ ID NO: 252

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stenotrophomonas maltophilia*
(B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

```
GTGTACGACG CACTGAAGGT GGAAAACACC GAGATCACCC TCGAAGTCCA      50
GCAGCAGCTG GGCGACGGCG TGGTGCGTAC CATCGCCCTC GGTTCCACCG     100
ACGGCCTGAA GCGCAACCTG GTTGCCGTCA ACACCGGCCG TGGCATCTCG     150
GTGCCGGTCG GCGCCGGCAC CCTGGGCCGC ATCATGGACG TGCTGGGCCG     200
TCCGATCGAC GAAGCCGGCC CGGTCGCTGC CAGCGACAAC TGGGAAATCC     250
ACCGCGCTGC GCCGTCGTAT GAAGACCAGT CCCCGGCCAC CGAGCTGCTG     300
GAAACCGGCA TCAAGGTCAT CGACCTGATG TGCCCGTTCG CCAAGGGCGG     350
CAAGGTCGGC CTGTTCGGCG GCGCCGGCGT CGGCAAGACC GTCAACATGA     400
TGGAACTGAT CAACAACATC GCCAAGGCGC ACAGCGGCCT GTCCGTGTTC     450
GCCGGCGTGG GTGAGCGTAC CCGTGAGGGC AACGACTTCT ACCACGAGAT     500
GAAGGACTCC AACGTCCTGG ACAAGGTGGC GATGGTGTAC GGCCAGATGA     550
ACGAGCCGCC GGGCAACCGT CTGCGCGTCG CCCTGACCGG CCTGACCATG     600
```

GCCGAGTACT TCCGCGATGA GAAGGACGAA AACGGCAAGG GCAAGGACGT 650
CCTGCTGTTC GTCGACAACA TCTACCGCTA CACCCTGGCC GGTACCGAAG 700
TGTCGGCACT GCTGGGCCGC ATGCCGTCCG CGGTGGGTTA CCAGCCGACC 750
CTGGCCGAGG AAATGGGCGT CCTGCAGGAG CGCATCACCT CGACCAAGAA 800
TGGTTCGATC ACCTCGATC 819

2) INFORMATION FOR SEQ ID NO: 253

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

AGTTTGAAGG CCCTTTGCCA AATATTCTCA ATGCATTAGA AACAGATAAT 50
TTGGGCAATC GGCTAGTTTT AGAAGTTGCT CAGCATTTGG GTGAAAATAC 100
CGTGCGTACC ATTGCCATGG ATACTACCGA TGGTCTTGTC CGTGGTCAAA 150
AAGTTTTTGA TACAGGAACA CAGATCAGTG TTCCCGTGGG AGAAGCAACA 200
CTTGGTCGTA TTATGAATGT GATTGGAGAG CCGGTTGATA ATGTTGGCCC 250
AATTGCTACA AGCAAAACCC GTTCCATTCA CCAAGAGGCT CCTGAATATG 300
TGGAGCAATC AACCGCATCA GAAATCCTTG TGACTGGTAT TAAAGTCGTT 350
GATCTGTTAG CTCCTTATTC TAAAGGGGGG AAGGTTGGTT TGTTTGGAGG 400
TGCCGGTGTT GGTAAAACCG TTCTCATTAT GGAGCTTATC AACAATATTG 450
CAAAGGCGCA TGGTGGCTAT TCAGTGTTTG CCGGTGTTGG TGAACGTACA 500
CGTGAGGGAA ATGATCTTTA TTATGAAATG ATCGAAAGCC GTGTGAATGT 550
GAATCCAAAA GACAACAATG GTTCAACAGA AGGATCAAAA TGTGCACTCG 600
TTTATGGGCA AATGAATGAA CCACCAGGGG CGCGTGCACG TGTGGCTCTT 650
TCAGGATTGA CCATTGCAGA AAGTTTCCGT GATGAGGGAC AAGATGTTTT 700
GTTCTTCGTA GATAATATTT TCCGTTTTAC GCAAGCAGGC GCTGAAGTGT 750
CAGCTCTTTT AGGGCGTATT CCTTCTGCTG TAGGGTATCA GCCAACTTTG 800
GCAACTGATA TGGGGGCTTT GCAAGAGCGT ATTACCAGTA CAAGAACAGG 850
CTCTATTACC TCTG 864

2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 866 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bifidobacterium adolescentis*
(B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

```
TTCCCGGTGG GCCACCTGCC CGACATTTAC AATGCACTTA CCGTTGAACT      50
GKCCAACACC GGYGTCCACG AASAGGGCGA GACCACCAAG AAGATCACCC     100
TTGMGGTTGA ACAGCATCTT GGCGATTCCA CCGTGCGTAC CGTCGCTCTG     150
AAGCCGACTG ACGGCCTTGT GCGTGGCGCC ACCGTGTATG ACACCGGCGG     200
CCCGATCTCT GTGCCGGTTG GCGATGTCAC CAAGGGCCAC GTATTCGACG     250
TGTCCGGCAA CATCCTCAAC AAGAAGGCCG ACGAGACCGT TAAGGTTACC     300
GAACGTTGGT CTATCCACCG TAACCCGCCG GCATTCGACC AGCTGGAGTC     350
CAAGACCCAG ATGTTCGAAA CCGGTATCAA GGTCATCGAT TTGCTGACCC     400
CGTATGTGCA GGGCGGCAAG ATCGGTCTGT TCGGCGGCGC AGGCGTCGGC     450
AAGACCGTGC TGATCCAGGA AATGATTCAG CGTGTGGCTC AGAACCACGG     500
CGGTGTGTCC GTGTTCGCAG GCGTCGGCGA GCGTACCCGT GAGGGTAACG     550
ATCTGATCGG CGAAATGGAC GAAGCCGGCG TGCTCGAGAA GACCGCACTG     600
GTCTTCGGCC AGATGGATGA GCAGCCGGGT ACCCGTCTGC GCGTGCCGCT     650
GACCGCACTG ACCATGGCAG AGTACTTCCG TGACGTACAG AATCAGGACG     700
TGCTGCTGTT CATCGATAAC ATCTTCCGTT TCACCCAGGC TGGTTCCGAG     750
GTGTCCACCC TGCTCGGCCG TATGCCGTCC GCAGTGGGCT ACCAGCCGAA     800
CCTGGCCGAT GAGATGGGCG CGCTGCAGGA GCGAATCACT TCGACCCGTG     850
GACACTCCAT CACCTC                                         866
```

2) INFORMATION FOR SEQ ID NO: 255

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
- (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

```
AAGGCCAGCT GCCGCTGATC CTGAACGCGC TTGAAGTGGA CAATCAGGGC      50
CATCGTCTGG TTCTCGAAGT TGCCCAGCAC CTCGGCGAAG ACACCGTGCG     100
CACCATCGCC ATGGACGCGA CCGAAGGTCT CGTTCGCGGT CAGGAAGCAC     150
GCGACACTGG CGAACCGATC ATGGTGCCGG TCGGCGTCGA AACGCTTGGC     200
CGCATCATGA ACGTCATCGG CGAGCCGGTT GACGAAGCAG GCCCCATCAA     250
GACCAAGGCA ACCCGCGCCA TCCACCAGAA CGCGCCGGAA TATATCGAAC     300
AGTCGACCGA AGCCGAAATT CTGGTCACGG GCATCAAGGT CGTCGACCTT     350
CTGGCGCCTT ACGCCAAGGG CGGCAAGATC GGCCTCTTCG GCGGTGCAGG     400
CGTCGGCAAG ACCGTTCTCA TCATGGAACT CATCAACAAC GTCGCCAAGG     450
CGCACGGCGG TTATTCCGTG TTCGCAGGCG TCGGTGAGCG TACCCGTGAG     500
GGCAACGACC TTTACCACGA AATGATCGAG TCGGGCGTGA ACAAGCTCGG     550
CGGCGGCGAA GGCTCCAAGG CAGCCCTCGT TTACGGCCAG ATGAACGAAC     600
CCCCGGGTGC CCGCGCCCGC GTTGCCCTTT CCGGTCTGAC GGTTGCTGAA     650
AACTTCCGTG ACCAGGGCCA GGACGTTCTG TTCTTCGTGG ACAACATCTT     700
CCGCTTCACG CAGGCAGGTT CGGAAGTGTC GGCTCTTCTC GGCCGTATTC     750
CTTCCGCTGT GGGTTATCAG CCGACGCTGG CAACCGACAT GGGCGCCATG     800
CAGGAACGCA TCACCACGAC GACCAAGGGT TCGATCACCT CG            842
```

2) INFORMATION FOR SEQ ID NO: 256

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cedecea davisae*
(B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

```
CGAGTTCCCT CAGGACGGCG TACCGCGCGT TKATGATGCG CTTGAAGTAC      50
AAAATAACAG CGAGCAGCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC     100
GGTATCGTGC GTACCATCGC TATGGGTTCT TCCGACGGTC TGCGTCGTGG     150
TCTGGAAGTT AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG     200
CGACCCTTGG CCGTATCATG AACGTGCTGG GTCAGCCGAT CGACATGAAA     250
GGCGATATCG GCGAAGAAGA CCGTTGGGCT ATTCACCGCG CTGCACCTTC     300
CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG     350
TAATCGACCT TATCTGTCCG TTCGCTAAGG GCGGTAAAGT AGGTCTGTTC     400
GGTGGTGCGG GCGTGGGTAA AACCGTAAAC ATGATGGAGC TTATCCGTAA     450
CATCGCGATC GAGCACTCCG GCTACTCCGT GTTTGCGGGC GTGGGTGAGC     500
GTACTCGTGA GGGTAACGAC TTCTATCACG AAATGACCGA CTCCAACGTT     550
CTGGACAAAG TTGCCCTGGT TTACGGCCAG ATGAACGAGC CACCGGGTAA     600
CCGTCTGCGC GTAGCGCTGA CCGGTCTGAC CATCGCGGAG AAATTCCGTG     650
ACGAAGGTCG TGACGTTCTG CTGTTCGTTG ATAACATCTA CCGTTACACC     700
CTGGCCGGTA CTGAAGTATC CGCGCTGCTG GGTCGTATGC CTTCTGCGGT     750
AGGTTACCAG CCAACTCTGG CGGAAGAGAT GGGTGTTCTT CAGGAGCGTA     800
TTACCTCCAC CAAGACCGGT TCCATCACCT CCG                       833
```

2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cedecea lapagei*
(B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

```
TTCCCTCAGG ACGGCGTACC GCGCGTATAT GACGCGCTTG AGGTACAGAA      50
TAACAGCGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA     100
TCGTACGTAC CATCGCAATG GGTTCTTCCG ACGGTCTGCG TCGTGGTCTG     150
GAAGTGAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC     200
TCTGGGTCGT ATCATGAACG TGCTGGGTCA GCCAATTGAT ATGAAAGGCG     250
ACATCGGCGA AGAAGATCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAT     300
GAAGAGCTGT CCAGCTCTCA GGAACTGCTG GAAACCGGCA TCAAAGTTAT     350
CGACCTGATT TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG     400
GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC     450
GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCAGGCGTGG GTGAGCGTAC     500
```

TCGTGAGGGT AACGACTTCT ACCACGAGAT GACCGACTCC AACGTTCTGG 550
ACAAAGTTGC ACTGGTTTAC GGCCAGATGA ACGAGCCGCC AGGTAACCGT 600
CTGCGCGTAG CGCTGACCGG TCTGACCATC GCGGAGAAAT TCCGTGACGA 650
AGGCCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG 700
CCGGTACAGA AGTTTCTGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGT 750
TATCAGCCTA CTCTGGCAGA AGAGATGGGT GTTCTTCAGG AGCGTATTAC 800
CTCCACCAAG ACCGGTTCCA TCACTTCCG 829

2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cedecea neteri*
(B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

TCCCTCAGGA CGGCGTACCG CGCGTTTATG ACGCGCTTGA GGTACAGAAC 50
AACAATGAGA AGCTGGTGCT GGAAGTTCAG CAGCAGCTCG GCGGCGGTAT 100
CGTGCGTACC ATCGCAATGG GTTCTTCCGA CGGTCTGCGT CGTGGTCTGG 150
TAGTAACAGA CCTCGAGCAC CCGATCGAAG TCCCGGTAGG TAAAGCGACC 200
CTTGGCCGTA TCATGAACGT GCTGGGTCAG CCGATCGACA TGAAAGGCGA 250
CATCGGCGAA GAAGACCGTT GGGCGATTCA CCGCGCAGCA CCTTCCTACG 300
AAGAGCTGTC CAGCTCTCAG GAATTGCTGG AAACCGGCAT CAAAGTTATC 350
GACCTGATTT GTCCGTTCGC TAAGGGCGGT AAAGTAGGTC TGTTCGGTGG 400
TGCGGGCGTA GGTAAAACCG TAAACATGAT GGAGCTGATC CGTAACATTG 450
CGATCGAGCA CTCCGGTTAT TCCGTGTTTG CGGGCGTGGG TGAGCGTACT 500
CGTGAGGGTA ACGACTTCTA CCACGAAATG ACCGACTCCA ACGTTCTGGA 550
TAAAGTAGCA CTGGTTTACG GCCAGATGAA CGAGCCACCA GGTAACCGTC 600
TGCGCGTAGC GCTGACCGGT CTGACCATCG CGGAAAAATT CCGTGACGAA 650
GGCCGCGACG TTTTGCTGTT CGTTGATAAC ATCTACCGTT ATACCCTGGC 700
CGGTACCGAA GTATCTGCAC TGCTGGGTCG TATGCCTTCT GCGGTAGGTT 750
ATCAGCCAAC TCTGGCAGAA GAGATGGGTG TTCTTCAGGA GCGTATTACC 800
TCCACCAAGA CCGGTTCTAT CACCTCCGTA 830

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 931 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chryseobacterium meningosepticum*
(B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

```
TTTCAGGAAG TAGAGGAACT ACCAAACATT TATGACGCAC TTGAAGTTGT      50
CAGAGAAGGC CAGAAAGGTC TGATCTTAGA AGTTGAACAA CACATCGGTG     100
AGGATACAGT GAGATGTATC GCTATGGATG CAACAGACGG ACTTCAAAGA     150
GGACAATCTG TAATAGGACA TGGAAGACAA ATTACTATGC CTATTGGTGA     200
AGAAGTAAAT GGTAGATTGT TCAACGTGGT AGGAGATGCT ATCGACGGAC     250
TTCAGGAATT ATCTAAAGAC AATGGTTTGC CAATCCACAG AGAAGCACCT     300
AAATTCGATC AGTTATCAAC TTCTGCTGAA GTACTATATA CAGGTATCAA     350
AGTAATCGAC CTTATCGAGC CTTATGCAAA AGGTGGTAAA ATTGGTTTGT     400
TCGGTGGTGC TGGTGTAGGT AAAACAGTAT TGATCCAGGA ATTGATTAAT     450
AACATTGCTA AAGGACACGG TGGTCTTTCT GTATTCGCAG GAGTAGGTGA     500
GAGAACAAGA GAAGGAAATG ACCTTCTTCG TGAGATGTTA GAGTCTGGTA     550
TTATTAAATA TGGTGACGAA TTCATGCATT CTATGGAGAA CGGTGGATGG     600
GATCTTTCTA AAGTTGACAG TGAGTTGATG AAAGAGTCTA AAGCTGCTTT     650
CGTTTTCGGA CAGATGAACG AGCCACCAGG TGCAAGAGCA CGTGTAGCCC     700
TTTCTGGTCT TACTTTAGCT GAATACTACC GTGATGGTGG CGAAAGCGGA     750
CAAGGTAGAG ACGTTCTTTT CTTCGTAGAC AACATCTTCC GTTTTACACA     800
GGCTGGTTCT GAGGTGTCTG CACTTCTAGG TCGTATGCCT TCAGCGGTAG     850
GTTACCAACC AACTCTAGCT TCTGAGATGG GTGCAATGCA GGAGAGAATT     900
ACTTCAACTA AAAACGGATC TATTACATCT G                         931
```

2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 726 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter amalonaticus*
(B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

```
GTATCGTACG TACCATCGCA ATGGGTTCTT CCGACGGTCT GCGTCGTGGT      50
CTGGAAGTCA AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC     100
AACCCTGGGT CGTATCATGA ACGTCCTGGG TCACCCGATC GACATGAAAG     150
GCGATATCGG TGAAGAAGAG CGTTGGGCTA TCCACCGCGC AGCACCGTCC     200
TATGAAGAGC TGTCCAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT     250
TATCGACCTG ATGTGTCCGT TCGCGAASGG CGGTAAAGTG GGTCTGTTCG     300
GTGGTGCGGG TGTAGGTAAA ACCGTAAACA TGATGGAGCT TATCCGTAAC     350
ATCGCGATCG AGCACTCCGG TTACTCCGTG TTTGCGGGCG TAGGTGAACG     400
TACTCGTGAG GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTC     450
TGGATAAAGT ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCGGGAAAC     500
CGTCTGCGCG TTGCACTGAC CGGTCTGACC ATGGCAGAGA AATTCCGTGA     550
CGAAGGTCGT GACGTACTGC TGTTCGTCGA TAACATCTAT CGTTACACCC     600
TGGCCGGTAC GGAAGTTTCC GCACTGCTGG GTCGTATGCC ATCAGCGGTA     650
GGTTACCAGC CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT     700
CACTTCTACC AAAACCGGTT CTATCA                               726
```

2) INFORMATION FOR SEQ ID NO: 261

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter braakii*
(B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG 50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA 100
TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAT 150
CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACTC TGGGTCGTAT 200
CATGAACGTC CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCCTATGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC 450
TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC 550
TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT 600
CTGACCGGTC TGACCATGGC AGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
TCTGCTGTTC GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACAGAAG 700
TATCCGCTCT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCGACC 750
CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAAC 800
CGGTTCTATC AC 812

2) INFORMATION FOR SEQ ID NO: 262

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 811 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter koseri*
(B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

GCGCGTGTAC GACGCCCTTG AGGTGCAGAA TGGTAATGAA CATCTGGTGC 50
TGGAAGTTCA GCAGCAGCTC GGTGGCGGTA TCGTACGTAC CATCGCCATG 100
GGTTCTTCCG ACGGCCTGCG TCGTGGTCTG GATGTGAAAG ACCTTGAGCA 150
CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT ATCATGAACG 200
TACTGGGCGA ACCAGTAGAC ATGAAAGGCG AGATCGGTGA AGAAGAGCGT 250
TGGGCTATCC ACCGTGCGGC ACCGTCCTAC GAAGAGTTGT CAAACTCTCA 300
GGAACTGCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG TGCCCGTTCG 350
CGAAGGGCGG TAAAGTGGGT CTGTTCGGTG GTGCGGGTGT AGGTAAAACC 400
GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAAC ACTCCGGTTA 450
CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT AACGACTTCT 500

ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC CCTGGTTTAC 550
GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG CGCTGACCGG 600
CCTGACCATG GCGGAGAAAT TCCGTGACGA AGGTCGTGAC GTTCTGCTGT 650
TCGTCGACAA CATCTACCGT TACACCCTGG CCGGTACGGA AGTATCCGCA 700
CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TACCAGCCGA CCCTGGCGGA 750
AGAGATGGGT GTTTTGCAGG AACGTATCAC CTCCACCAAA ACCGGTTCTA 800
TCACCTCCGT A 811

2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter farmeri*
(B) STRAIN: ATCC 51112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTTATGA ATGGTAAAGA 50
GAGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT ATCGTACGTA 100
CCATCGCGAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA 150
GACCTCGAAC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CTCTGGGTCG 200
TATCATGAAC GTCCTGGGTC ACCCGATCGA CATGAAAGGC GATATCGGTG 250
AAGAAGAGCG TTGGGCTATC CACCGCGCAG CGCCATCCTA TGAAGAGCTG 300
TCCAGCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400
TAGGTAAAAC CGTAAACATG ATGGAACTCA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGATTC CAACGTTCTG GATAAAGTAT 550
CCCTGGTATA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
GCGCTGACCG GTCTGACCAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA 650
CGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
AAGTATCCGC ACTGCTGGGC CGTATGCCAT CAGCGGTAGG CTACCAGCCA 750
ACCCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CTTCTACCAA 800
AACCGGTTCT ATTACC 816

2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter freundii*
(B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

```
AGGATGCCGT ACCGCGCGTG TACGATGCTC TTGAGGTTAT GAATGGTAAA      50
GAGAGCCTGG TGCTGGAAGT TCAGCAGCAG CTCGGCGGCG GTATCGTACG     100
TACCATCGCC ATGGGTTCTT CTGACGGTCT GCGTCGTGGT CTGGAAGTTA     150
AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC AACGCTGGGT     200
CGTATCATGA ACGTTCTGGG TCACCCGATC GACATGAAAG GCGATATCGG     250
TGAAGAAGAG CGTTGGGCTA TCCACCGTGC AGCACCTTCC TACGAAGAGC     300
TGTCAAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT TATCGACCTG     350
ATGTGTCCGT TCGCTAAGGG CGGTAAAGTT GGTCTGTTCG GTGGTGCGGG     400
TGTAGGTAAA ACCGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG     450
AACACTCCGG TTACTCCGTG TTTGCGGGCG TAGGTGAACG TACTCGTGAG     500
GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTC TGGACAAAGT     550
ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCTGGAAAC CGTCTGCGTG     600
TTGCGCTGAC CGGTCTGACC ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT     650
GACGTTCTGC TGTTCGTTGA TAACATCTAT CGTTACACCC TGGCCGGTAC     700
AGAAGTATCT GCACTGCTGG GTCGTATGCC ATCAGCGGTA GGCTACCAGC     750
CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT CACCTCCACC     800
AAAACCGGTT CTATCACCT                                      819
```

2) INFORMATION FOR SEQ ID NO: 265

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Citrobacter koseri*
- (B) STRAIN: ATCC 27028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

```
GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTGCAGA ATGGTAATGA      50
ACATCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATCGTACGTA     100
CCATCGCCAT GGGTTCTTCC GACGGCCTGC GTCGTGGTCT GGATGTGAAA     150
GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CGCTGGGTCG     200
TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GAGATCGGTG     250
AAGAAGAGCG TTGGGCTATC CACCGTGCGG CACCGTCCTA CGAAGAGTTG     300
TCAAACTCTC AGGAACTGTT GGAAACCGGT ATCAAAGTTA TCGACCTGAT     350
GTGTCCGTTC GCGAAGGGCG GTAAAGTGGG TCTGTTCGGT GGTGCGGGTG     400
TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAA     450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG     500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT     550
CCTTGGTTTA CGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT     600
GCGCTGACCG GCCTGACCAT GGCGGAGAAA TTCCGTGACG AAGGTCGTGA     650
CGTTCTGCTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACGG     700
AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTACCAGCCG     750
ACCCTGGCGG AAGAGATGGG TGTTTTGCAG GAACGTATCA CCTCCACCAA     800
AACCGGTTCT ATCACCTCCG TA                                   822
```

2) INFORMATION FOR SEQ ID NO:266

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 820 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter sedlakii*
(B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTACAGA ATGGTAATGA 50
GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATTGTACGTA 100
CCATCGCCAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA 150
GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CGCTGGGTCG 200
TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GACATCGGTG 250
AAGAAGAGCG TTGGGCTATC CACCGTGCCG CGCCGTCCTA TGAAGAGTTG 300
TCTAACTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT 350
GTGTCCGTTC GCGAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGCG 400
TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT 550
CCCTGGTGTA CGGCCAGATG AACGAGCCGC CTGGAAACCG TCTGCGCGTC 600
GCACTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
CGTTCTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG 750
ACTCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CCTCAACCAA 800
AACCGGTTCT ATCACCTCCG 820

2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter werkmanii*
(B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG 50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA 100
TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACCC TGGGTCGTAT 200
CATGAACGTC CTGGGTCATC CGATCGACAT GAAAGGCGAT ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTACCTATGA AGAACTGTCC 300
AGTTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC 450
TCCGGTTACT CAGTGTTTGC GGGCGTTGGT GAACGTACTC GTGAGGGTAA 500

CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
CTGACCGGTC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
TCTGCTGTTC GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACTGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCAACC 750
CTGGCGGAAG AGATGGGTGT TCTGCAGGAA CGTATCACCT CTACCAAAAC 800
CGGTTC 806

2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Citrobacter youngae*
(B) STRAIN: ATCC 29935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG 50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA 100
TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC 150
CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200
CATGAACGTT CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGAGAAG 250
AAGAGCGTTG GGCTATTCAC CGCGCAGCAC CTTCCTATGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CTGTGTTTGC GGGTGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGATTCCAA CGTTCTGGAT AAAGTATCCC 550
TGGTTTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
CTGACCGGTC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT 650
ACTGCTGTTC GTCGATAACA TCTATCGTTA TACCCTGGCC GGTACGGAAG 700
TATCCGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGTTA CCAGCCGACC 750
CTGGCGGAAG AGATGGGTGT TCTGCAGGAA CGTATCACTT CTACCAAAAC 800
CGGTTCTATC 810

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium innocuum*
(B) STRAIN: ATCC 14501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```
TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
AAAGACAGTG AATCTCTGAT TGTCGAAGTT GCTCAGCATA TCGGTGATGA     100
ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA     150
TGGAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA     200
ATTCTGGGAA GAATGTTCAA TGTCCTCGGA CGTGAAATTG ATGGTCTGGG     250
ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT     300
TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC     350
ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG     400
TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA     450
TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA     500
ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT     550
TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA     600
GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT     650
CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTAC     700
CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG     750
TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC     800
ATTACATCCA CGAAGGATGG TTCCATT                              827
```

2) INFORMATION FOR SEQ ID NO: 270

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium perfringens*
(B) STRAIN: ATCC 13124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```
GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA     100
TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA     150
GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT     200
ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG     250
AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATTT     300
GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT     350
CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG     400
GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA     450
GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC     500
AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA     550
AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA     600
ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA     650
AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG     700
CTGGATCAGA GGTTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT     750
TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC     800
ATCAACTACC CATGGATCAA TTACATCAG                            829
```

2) INFORMATION FOR SEQ ID NO: 271

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

TTGTCCACGT TGGATRTCTT CA 22

2) INFORMATION FOR SEQ ID NO: 272

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

CCCGCGTGGC GAGCTGCCGG CACTGTACAA CGCGTTGACT GTCGAGGTCA 50
CCCTCGAGGC AGTCGCTAAG ACCATTACCC TTGAGGTTGC CCAGCACTTG 100
GGCGACAACC TCGTTCGCGC CGTGTCCATG GCCCCTACCG ACGGCCTCGT 150
CCGTGGTGCT GTTGTGACCG ACTCGGGCAA GCCAATCTCC GTGCCAGTTG 200
GCGACGTTGT TAAAGGCCAC GTTTTCAACG CACTGGGCGA TTGCTTGGAT 250
GAGCCAGGTC TCGGCCGCGA TGGTGAGCAG TGGGGAATTC ACCGCGATCC 300
ACCACCATTC GATCAGCTCG AAGGTAAGAC CGAAATCCTC GAGACCGGTA 350
TTAAGGTCAT CGACTTGCTC ACCCCTTACG TTAAGGGCGG CAAGATTGGT 400
CTGTTCGGTG GTGCAGGTGT GGGTAAGACC GTGCTCATCC AGGAGATGAT 450
CACTCGTATT GCTCGCGAGT TCTCCGGTAC CTCCGTCTTC GCTGGCGTTG 500
GTGAGCGTAC CCGTGAGGGC ACCGACCTCT TCCTCGAAAT GGAAGAAATG 550
GGCGTTCTTC AGGACACCGC TCTCGTGTTC GGCCAGATGG ACGAGCCACC 600
AGGAGTCCGT ATGCGCGTTG CTCTGTCCGG TCTGACCATG GCGGAGTACT 650
TCCGCGATGT TCAGCACCAG GACGTGCTTC TGTTCATCGA TAACATTTTC 700
CGTTTCACCC AGGCCGGTTC CGAGGTTTCG ACCCTTCTTG GTCGTATGCC 750
TTCCGCCGTG GGTTACCAGC CAACCTTGGC TGACGAGATG GGTGTTCTCC 800
AGGAGCGTAT TACCTCTA 818

2) INFORMATION FOR SEQ ID NO: 273

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
(B) STRAIN: ATCC 10700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

```
CGATGCCTGC TCTGTACAAC GCGCTGACTG TCGAGGTCAC CCTCGAGGCA       50
GTCGCCAAGA CCATCACGCT TGAGGTTGCA CAGCACCTCG GCGATAACCT      100
GATCCGGACC ATTGCGTTGG CACCTACGGA CGGTCTCGTC CGTGGCGCTG      150
AGGTTATCGA CACTGGTAAG CCAATTACTG TTCCCGTCGG CGATGCCGTC      200
AAAGGACACG TCTTCAATGC GCTCGGTGAG TGTTTGGACG AACCAGGATT      250
GGGCCGCGAC GGCGAACAGT GGGGAATCCA CCGCGATCCG CCACCATTCG      300
ATGCGCTGGA GGGCAAAACC GAGATTCTGG AGACTGGAAT CAAGGTTATC      350
GACCTCCTTA CCCCTTACGT TAAGGGTGGC AAAATTGGTC TGTTCGGTGG      400
CGCCGGCGTC GGCAAGACCG TTCTTATCCA GGAAATGATC ACTCGTATCG      450
CTCGTAACTT CTCCGGTACT TCCGTGTTCG CCGGCGTCGG TGAGCGTACC      500
CGTGAGGGTA CTGACCTGTT CCTGGAAATG GAAGAGATGG GCGTGTTGCA      550
AGACACCGCC CTTGTCTTCG GTCAAATGGA CGAACCACCA GGGGTTCGTA      600
TGCGCGTGGC CTTGTCTGGT CTAACCATGG CTGAATATTT CCGCGACGTT      650
CAAAACCAGG ACGTTTTGTT GTTCATTGAC AACATCTTCC GTTTTACTCA      700
GGCAGGTTCC GAGGTTTCCA CGCTGTTGGG CCGTATGCCT TCCGCCGTGG      750
GTTATCAGCC AACATTGGCT GATGAGATGG GTGTTTTGCA GGAACGGATT      800
ACCTCTACAC GTGGTAAGTC AATTACTTCC CTG                        833
```

2) INFORMATION FOR SEQ ID NO: 274

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium ulcerans*
(B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

```
CCGTGCTCAT CCAGGAGATG ATCACCCGTG TGGCCCGCAA CTTCGGCGGC       50
ACCTCTGTGT TCGCCGGCGT CGGCGAGCGC ACCCGTGAGG GCAACGACCT      100
CTGGGTCGAG ATGGACGAGG CCGACGTGCT CAAGGACACC GCCCTGGTGT      150
TCGGCCAGAT GGACGAGCCG CCGGGAACCC GTCTGCGCGT GGCCCTGTCC      200
GCGCTGACCA TGGCGGAGTA CTTCCGCGAT GTGCAGAACC AGGACGTGCT      250
GCTGTTCATC GACAACATCT TCCGCTTCTC CCAGGCCGGC TCCGAGGTCT      300
CCACCCTGCT GGGCCGCATG CCCTCCGCGG TGGGCTACCA GCCGAACCTG      350
GCGGACGAGA TGGGTGTGCT GCAGGAGCGC ATCACCTCGA CTCGCGGCCA      400
CTCCATCACC TCGATGC                                         417
```

2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium urealyticum*
(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

GGGCAGCAGC CAGCACTATT CAACGCGCTG CACGTCGAGG TTGACCTCGA 50
GGCAGTTGCG AAGACCATTA CCCTGGAGGT CGCACAGCAC CTGGGTGACA 100
ACCTGGTGCG CACCGTCTCC ATGGCCCCGA CCGACGGCCT GGTCCGCGGT 150
GCAGAGGTCA AGGACACCGG TAAGCCGATC TCTGTGCCAG TCGGCGATGT 200
TGTCAAGGGG CACGTCTTCA ACGCCCTGGG CGACTGCCTG GATGAGCCAG 250
GTCTCGGCCG CGACGGCGAG CAGTGGGGCA TCCACCGCGA GCCACCGGCA 300
TTCGACGAGC TCGAGGGTAA GACCGAGATC CTGGAGACCG GCGTTAAGGT 350
CATCGACCTG CTGACCCCTT ACGTCAAGGG CGGCAAGATT GGCCTCTTCG 400
GTGGTGCAGG TGTGGGTAAG ACCGTCCTGA TTCAGGAGAT GATTACCCGT 450
ATCGCCCGCG AGTTCTCCGG TACCTCCGTG TTCGCCGGCG TCGGCGAGCG 500
TACCCGTGAG GGTACGGACC TCTTCCTCGA GATGGAGGAG ATGGGCGTGC 550
TCCAGGACAC CGCGCTGGTG TTCGGTCAGA TGGATGAGCC GCCGGGAGTC 600
CGTATGCGCG TGGCTCTGTC CGGTCTGACC ATGGCGGAGT ACTTCCGCGA 650
TGTTCAGGGC CAGGACGTGC TGCTGTTCAT CGACAACATC TTCCGTTTCA 700
CCCAGGCAGG TTCTGAGGTC TCCACGCTGC TCGGCCGCAT GCCGTCCGCA 750
GTGGGTTACC AGCCGACCCT GGCTGACGAG ATGGGTGTTC TGCAGGAGCG 800
CATTACCTCC ACGAAGGGTA AGTCCATTAC CTCCC 835

2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Coxiella burnetii*
(B) STRAIN: Nine Mile phase II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

CCCGTCACGC TGTCCCGAAA GTGTACGATG CTTTGCAGGT GGATGAAAAT 50
AATTTAACGC TCGAAGTCCA ACAGCAACTC GGGGACGGTG TCGTGCGCAC 100
AATTGCCATG GGCAGCACTG AGGGCTTAAA ACGCGATATC GCCGTAAAAA 150
ATACGGAAAA ACCGATTGAA GTTCCCGTAG GAAAAGAAAC TTTAGGTCGT 200
ATCATGAACG TGCTGGGTGA GCCGATCGAT GAGTTAGGTC CCATTAATTC 250
AAAAGAAAAA CTCCCTATTC ATCGTCCTGC GCCGAGCTTT ATTGAGCAAT 300
CTGGCGCTAC CGAATTATTA GAAACCGGTA TTAAAGTGGT CGATTTGCTT 350
TGCCCCTTTG CTAAGGGAGG CAAAGTGGGT CTTTTTGGAG GCGCGGGCGT 400
TGGAAAAACG GTTAATATGA TGGAATTAAT CCGTAATATC GCCATTGAAC 450
ACAGCGGTTA TTCTGTTTTT GCGGGTGTGG GAGAAAGAAC GCGAGAAGGC 500
AATGATTTTT ATCATGAAAT GAAAGAATCC AATGTCTTGG ATAAAGTGGC 550
GTTGGTGTAC GGACAAATGA ACGAGCCGCC AGGGAACCGC TTGCGGGTGG 600
GTTTGACGGG GCTTACGCTG GCGGAAGCCT TCCGTGACGA AGGACGCGAC 650
GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTTGG CAGGGGTTGA 700

AGTCTCTGCC CTCCTCGGTC GGATGCCATC GGCTGTGGGT TATCAGCCGA 750
CGTTGGCCGA AGAGATGGGG GCCCTGCAAG AACGCATTAC TTCCACTAAA 800
AAAGGGTCCA TTACGTCG 818

2) INFORMATION FOR SEQ ID NO: 277

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Edwardsiella hoshinae*
(B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG ACGCCGTGCC GAAGGTGTAT AACGCACTGG AAGTAAAAGG 50
CGGTGCCACG AAACTGGTAC TGGAAGTGCA GCAGCAGCTG GGTGGCGGCG 100
TAGTTCGCTG CATCGCGATG GGCTCTTCCG ACGGTCTGCG CCGTGGGCTA 150
GAGGTTGAAG ACCAAGACCA TCCGATCGAG GTTCCTGTTG GCAAGGCGAC 200
TCTGGGCCGT ATCATGAACG TACTGGGTGA TCCGGTCGAC ATGAAGGGCG 250
AGATCGGTGA AGAAGAGCGT TGGGCTATCC ATCGTGCTGC ACCGAGCTAT 300
GAAGATCTGT CTAACTCTCA GGAACTGCTG GAGACCGGCA TTAAGGTTAT 350
CGACCTGATT TGCCCGTTCG CTAAAGGCGG TAAAGTGGGC CTGTTCGGTG 400
GGGCCGGTGT GGGTAAGACC GTTAACATGA TGGAGCTTAT CCGTAACATC 450
GCTATCGAGC ACTCCGGTTA CTCAGTCTTC GCCGGTGTGG GTGAGCGTAC 500
CCGTGAGGGT AACGACTTCT ACCACGAGAT GACCGATTCC AACGTATTGG 550
ATAAAGTTTC TCTGGTGTAT GGTCAGATGA ACGAGCCACC GGGAAACCGT 600
CTGCGCGTGG CGCTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGATGA 650
AGGTCGTGAT GTACTGTTGT TCATCGATAA CATCTACCGT TATACCTTGG 700
CCGGTACTGA AGTCTCCGCT CTGCTGGGCC GTATGCCGTC GGCGGTAGGT 750
TATCAGCCGA CTCTGGCGGA GGAAATGGGG GTGCTGCAAG AGCGTATTAC 800
CTCCACTAAG ACCGGGTCCA TCACCTCTG 829

2) INFORMATION FOR SEQ ID NO: 278

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Edwardsiella tarda*
(B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

GCCGTGCCGA AGGTGTATAA CGCACTGGAA GTAAAAGGCG GTGCCACGAA 50
ACTGGTACTG GAAGTGCAGC AGCAGCTGGG TGGCGGCGTC GTTCGCTGCA 100

```
TCGCGATGGG CTCCTCCGAC GGTCTGCGCC GTGGGCTGGT GGTTGAAGAC      150
CAAGACCATC CGATCGAGGT TCCGGTCGGT AAGGCGACCC TGGGCCGTAT      200
CATGAACGTA CTGGGTGATC CGGTCGACAT GAAGGGCGAG ATCGGCGAAG      250
AAGAGCGTTG GGCTATCCAC CGCGCGGCGC CGAGCTATGA AGATCTGTCC      300
AACTCTCAGG AGCTGCTGGA GACCGGCATC AAGGTTATCG ACCTGATTTG      350
CCCGTTCGCC AAAGGCGGTA AAGTTGGCCT GTTCGGTGGT GCCGGTGTGG      400
GTAAGACCGT TAACATGATG GAGCTTATCC GTAACATCGC TATCGAGCAC      450
TCCGGTTACT CCGTATTTGC CGGTGTAGGC GAGCGTACCC GTGAGGGTAA      500
CGACTTCTAC CACGAGATGA CCGACTCCAA CGTATTGGAT AAAGTTTCTC      550
TGGTATACGG CCAGATGAAT GAGCCGCCGG GAAACCGTCT GCGTGTGGCG      600
TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGCGATGT      650
GTTGTTGTTC ATCGATAACA TTTATCGTTA TACCTTGGCT GGTACCGAAG      700
TTTCTGCTCT GCTGGGTCGT ATGCCGTCGG CGGTAGGTTA TCAGCCGACC      750
CTGGCGGAAG AGATGGGTGT GTTGCAAGAG CGTATCACCT CAACGAAGAC      800
GGGCTCTAT                                                  809
```

2) INFORMATION FOR SEQ ID NO: 279

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 840 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Eikenella corrodens*
(B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

```
TTTCCGCGTA CCGCCATTCC GCGTGTTTAC GATGCACTCA AACTGGTTGA       50
TACTGATTTG ACGCTGGAAG TACAGCAGCA GCTTGGTGAC GGCGTTGTCC      100
GTACCATTGC GATGGGTAGT ACAGACGGTT TGAAACGTGG CTTGGCTGTG      150
CAAAATACTG GTGCACCGAT TACTGTGCCG GTGGGGAAAG CCACCCTAGG      200
CCGCATCATG GACGTTCTGG GCAACCCCGT GGACGAACAA GGTCCGATCG      250
GTTCTGACCA AACCCGTGCT ATTCATCAAT TTGCACCTAA GTTCGACGAA      300
CTCTCCAGCA CTACCGAATT GTTGGAAACA GGCATTAAAG TGATCGATTT      350
GCTTTGTCCG TTTGCTAAAG GTGGTAAAGT GGGTCTGTTT GGCGGTGCCG      400
GTGTGGGCAA AACCGTGAAC ATGATGGAGC TGATTAACAA CATTGCCAAA      450
GCGCACAGTG GTCTTTCCGT ATTCGCCGGT GTGGGTGAGC GTACTCGTGA      500
AGGTAACGAC TTCTACCACG AAATGAAAGA CTCCAACGTG TTGGATAAAG      550
TGGCAATGGT GTATGGCCAG ATGAACGAGC CGCCTGGTAA CCGCTTGCGT      600
GTTGCTCTAA CTGGTTTGTC GATGGCTGAA TACTTCCGTG ACGAAAAAGA      650
CGAAAACGGC AAAGGCCGTG ACGTATTATT CTTTGTGGAT AATATCTACC      700
GCTATACTCT GGCGGGTACC GAAGTGTCGG CTCTGCTTGG CCGTATGCCT      750
TCTGCTGTGG GTTATCAGCC AACTTTGGCT GAAGAAATGG GTCGTTTGCA      800
GGAGCGTATT ACCTCCACCC AAACTGGTTC CATTACCTCT                 840
```

2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter agglomerans*
(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

GCCGTACCAC GAGTGTACGA TGCACTTGAG GTAAAGAATG GTGAAGAGCG 50
TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CGGTGGCGTT GTACGTACCA 100
TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC 150
CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
CATGAACGTA CTGGGCGAAC CAGTAGACAT GAAAGGCGAC ATCGGTGAAG 250
AAGAGCGTTG GGCGATCCAC CGTGCAGCAC CGTCCTACGA AGAGTTGTCA 300
AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
TGGTGTATGG TCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
CTGACCGGTC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
ACTGTTGTTC GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
TATCCGCACT GCTGGGCCGT ATGCCTTCTG CGGTAGGTTA TCAGCCGACG 750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC 800
CGG 803

2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter amnigenus*
(B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC 50
AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT 100
GGTATCGTAC GTACTATCGC CATGGGTTCT TCCGACGGTC TGCGTCGTGG 150
TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCCG GTAGGTAAAG 200
CAACACTGGG TCGTATCATG AACGTTTTGG GTCAACCAAT CGACATGAAA 250
GGCGACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC 300
CTATGAAGAG CTGTCTAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG 350
TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC 400
GGCGGTGCGG GCGTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 450
CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC 500
GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT 550
CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA 600
CCGTCTGCGC GTTGCGCTGA CCGGTCTGAC TATGGCTGAG AAGTTCCGTG 650
ACGAAGGTCG TGACGTACTG CTGTTCGTAG ATAACATCTA CCGTTACACC 700

```
CTGGCCGGTA CTGAAGTATC TGCGCTGCTG GGCCGTATGC CTTCAGCGGT      750
AGGTTACCAG CCGACCCTGG CGGAAGAGAT GGGCGTTCTG CAGGAACGTA      800
TCACTTCTAC CAAAACCGGT TCTATCACCT CCG                        833
```

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter asburiae*
(B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

```
GCCGTACCAC GCGTGTACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG       50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA      100
TCGCGATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTCAAAGAC      150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT      200
CATGAACGTA TTGGGTCAAC CAATCGACAT GAAAGGCGAC ATCGGTGAAG      250
AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCCTACGA AGAGCTGTCC      300
AGCTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG      350
TCCGTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTTG      400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
TCCGGTTACT CCGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC      550
TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG      600
CTGACCGGTC TGACGATGGC TGAGAAGTTC CGTGATGAAG GCCGTGACGT      650
TCTGCTGTTC GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA CCAGCCTACG      750
CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAAC      800
CGGTTCTATC                                                 810
```

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 811 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter cancerogenus*
(B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

```
GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTACAGAATG GTAACGAGAG       50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACTA      100
```

TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTAAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
CATGAACGTA TTGGGTCAAC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTTCCTACGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTATT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC 550
TGGTGTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
CTGACCGGCC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
ACTGCTGTTC GTTGATAACA TCTACCGTTA CACCCTGGCC GGTACCGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCTACG 750
CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CAACCAAAAC 800
CGGTTCTATC A 811

2) INFORMATION FOR SEQ ID NO: 284

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter cloacae*
(B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

GCCGTACCAC GCGTGTACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
TCGCGATGGG GTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCCTACGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CCGTATTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
CTGACTGGTC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650
TCTGCTGTTC GTTGATAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCTACG 750
CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAAC 800
CGGTTCTATC ACTTCCG 817

2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter gergoviae*
(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

AATGAGAGCC TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATCGT 50
GCGTACCATC GCAATGGGTT CTTCTGACGG TCTGCGTCGC GGTCTGGAAG 100
TTAAAGATCT CGAACATCCG ATCGAAGTCC CGGTAGGTAA AGCGACCCTC 150
GGCCGTATTA TGAACGTGCT GGGTCAGCCG GTTGATATGA AAGGCGATAT 200
CGGCGAAGAA GAGCGTTGGG CGATCCACCG CGCTGCGCCG TCCTATGAAG 250
AGCTCTCCAG CTCTCAGGAA CTGCTGGAAA CCGGTATCAA GGTAATGGAC 300
CTGATTTGCC CGTTCGCGAA GGGCGGTAAA GTCGGTCTGT TCGGCGGTGC 350
GGGCGTTGGT AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA 400
TCGAGCACTC CGGCTACTCC GTGTTTGCGG GCGTGGGTGA ACGTACTCGT 450
GAGGGTAACG ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGACAA 500
AGTATCCCTG GTGTACGGCC AGATGAACGA GCCGCCGGGA AACCGTCTGC 550
GCGTGGCGCT GACCGGTCTG ACCATGGCTG AGAAATTCCG TGACGAAGGT 600
CGTGACGTTC TGCTGTTCGT CGATAACATC TACCGCTATA CCCTCGCCGG 650
TACTGAAGTA TCCGCACTGC TGGGCCGTAT GCCTTCTGCA GTAGGTTACC 700
AGCCGACGCT GGCGGAAGAG ATGGGTGTTC TGCAGGAACG TATCACCTCC 750
ACCAAAACCG GTTCTA 766

2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter hormaechei*
(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

GCCGTACCAC GCGTGTACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTGAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200
CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCCTACGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
CTGACTGGCC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650
TCTGCTGTTC GTCGATAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCAACG 750

CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAAC 800
CGGTT 805

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterobacter sakasakii*
(B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

TACGACGCCC TTGAGGTAAC GAATGGTAAT GAGCGTCTGG TGCTGGAAGT 50
CCAGCAGCAG CTCGGCGGCG GTATCGTACG TACCATCGCG ATGGGCTCTT 100
CCGACGGTCT GCGTCGCGGT CTGCCTGTTG CAGACCTTGA GCACCCGATC 150
GAAGTGCCGG TAGGTAAAGC GACGCTGGGT CGTATCATGA ACGTCCTGGG 200
TCAGCCTATC GACATGAAAG GCGACATCGG CGAAGAAGAG CGTTGGGCGA 250
TTCATCGCGC GGCGCCGTCC TATGAAGAGC TGTCCAGCTC TCAGGAACTG 300
CTGGAAACCG GCATCAAAGT TATCGACCTG ATGTGTCCGT TCGCGAAGGG 350
CGGTAAAGTC GGTCTGTTCG GTGGTGCAGG TGTAGGTAAA ACCGTAAACA 400
TGATGGAGCT TATTCGTAAC ATCGCGATTG AGCACTCCGG TTACTCCGTG 450
TTTGCGGGCG TGGGCGAACG TACCCGTGAA GGTAACGACT TCTACCACGA 500
AATGACCGAC TCCAACGTAC TGGATAAAGT ATCCCTGGTG TACGGCCAGA 550
TGAACGAGCC GCCGGGAAAC CGTCTGCGCG TTGCGCTGAC CGGCCTGACC 600
ATGGCTGAGA AATTCCGTGA CGAAGGTCGT GACGTTCTGC TGTTCGTCGA 650
CAACATCTAC CGTTACACCC TGGCCGGTAC TGAAGTATCC GCACTGCTGG 700
GCCGTATGCC TTCAGCGGTA GGTTATCAGC CGACCCTGGC GGAAGAGATG 750
GGTGTTCTGC AGGAGCGTAT CACCTCCACC AAAACCGGTT C 791

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

TTTCTTTAGA TCAATCCTTA CCAGACATCA ACAATGCGTT GATTGTTTAC 50
AAAAAAGATA AAACAAAAGT TGTTCTTGAA GTTGCTTTGG AACTTGGTGA 100
TGGTGTTATC CGCACAATCG CTATGGAGGC TACTGATGGA TTGCAACGTG 150
GAATGGAAGT TGTCGATACT GGCAAATCAA TCTCCGTTCC TGTAGGTAAA 200

GATACTCTAG GTCGTGTGTT TAACGTATTA GGTGAAACGA TTGATAAAGA 250
AGCACCTTTT CCAGAAGATG CAGAAAGAAG CGGCATTCAT AAAAAGGCGC 300
CTGCTTTTGA AGACCTTAGT ACAAGTAACG AGATTTTGGA AACAGGGATC 350
AAGGTTATCG ACTTATTAGC CCCTTATTTA AAAGGTGGGA AAGTCGGACT 400
ATTCGGTGGT GCCGGTGTTG GTAAAACCGT TTTGATCCAA GAATTAATTC 450
ATAATATCGC CCAAGAACAC GGTGGTATTT CAGTGTTTAC CGGTGTTGGG 500
GAACGTACTC GTGAAGGGAA CGACCTTTAT TATGAAATGA AAGACTCTGG 550
CGTTATTGAG AAAACAGCCA TGGTGTTCGG ACAAATGAAC GAGCCGCCTG 600
GTGCACGTAT GCGTGTTGCC TTGACTGGTT TGACATTAGC TGAATATTTC 650
CGTGATGAAG AAGGACAAGA TGTGTTGCTA TTTATTGACA ACATCTTCCG 700
CTTTACTCAA GCCGGATCAG AAGTTTCTGC CTTATTAGGA CGTATGCCAT 750
CAGCCGTTGG GTATCAACCA ACTTTGGCAA CTGAAATGGG GCAATTACAA 800
GAACGAATCA CTTCAACCAA AAAAGGTTCG ATCACTTCA 839

2) INFORMATION FOR SEQ ID NO: 289

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 847 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

TTCTCTCTAG ACCAATCATT ACCAGATATC AACAATGCGT TGATTGTTTA 50
CAAAAAAGAT GAGCAGAAAA CAAAAGTTGT GTTAGAAGCT GCCTTAGAAC 100
TTGGCGACGG CGTTATCCGT ACGATTGCCA TGGAATCAAC AGATGGCTTA 150
CAACGAGGAA TGGAAGTAAT CGATACAGGC GCCTCCATTT CTGTTCCAGT 200
TGGGACAGAA ACCTTAGGAC GGGTGTTTAA TGTCTTAGGG GACACCATCG 250
ATTTAGAAGC GCCGTTCCCT GAAGAAGCAC CCCGCAGTGG GATTCACAAA 300
AAAGCACCTG ACTTTGATGA ATTGTCAACA AGTACGGAGA TCCTTGAAAC 350
TGGGATCAAA GTTATCGATT TGTTAGCCCC TTATTTAAAA GGGGGGAAAG 400
TTGGACTTTT CGGTGGTGCC GGTGTTGGTA AAACCGTCTT GATCCAAGAA 450
TTGATCCACA ACATCGCCCA AGAGCATGGT GGGATCTCTG TCTTCACAGG 500
TGTTGGTGAA CGGACACGTG AAGGAAATGA CCTTTATAAT GAAATGAAAG 550
AATCTGGCGT TATCGAAAAA ACAGCCATGG TGTTTGGACA AATGAACGAA 600
CCACCAGGTG CTCGGATGCG GGTAGCCTTG ACTGGTTTGA CATTAGCCGA 650
GTACTTCCGT GATGTGGAAG GACAAGACGT GCTCTTGTTT ATCGATAATA 700
TCTTCCGCTT CACTCAAGCA GGTTCTGAAG TATCTGCCTT ACTAGGTCGG 750
ATGCCGTCTG CCGTTGGGTA TCAGCCAACA TTAGCAACTG AGATGGGGCA 800
ATTACAAGAA CGGATCACAT CGACGAAGAA AGGTTCCGTT ACGTCTA 847

2) INFORMATION FOR SEQ ID NO: 290

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus durans*
(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

```
TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCTTT AGTTGTTTAT      50
AAAAATGATG AGAAGAAATC GAAAGTTGTT CTTGAAACAG CGCTAGAATT     100
AGGTGACGGT GTCATCCGTA CAATCGCGAT GGAATCAACA GATGGTTTAC     150
AACGCGGAAT GGAAGTCATT GATACAGAAA AAGCAATTTC TGTACCAGTG     200
GGTAAAGAAA CGTTAGGTCG TGTATTCAAT GTATTAGGAG ATACGATCGA     250
TTTATCTGCA CCTTTCCCAG AAGATGCAAA ACGTAGCGAA ATCCATAAAA     300
AAGCACCAAA CTTTGATGAG TTAAGTACAA GTACTGAGAT CCTTGAAACT     350
GGGATCAAAG TTATTGACTT GCTTGCTCCT TACTTAAAAG GTGGGAAAGT     400
TGGATTATTC GGTGGTGCCG GTGTAGGTAA AACTGTATTG ATCCAAGAAT     450
TGATCCATAA TATCGCTCAA GAACACGGTG GTATTTCTGT ATTTACTGGT     500
GTTGGTGAAC GTACACGTGA AGGTAATGAC CTTTATTATG AAATGAAAGA     550
TTCAGGAGTT ATTGAAAAAA CAGCCATGGT GTTTGGTCAA ATGAACGAAC     600
CACCAGGTGC ACGTATGCGT GTTGCCTTGA CTGGTTTGAC GATTGCTGAA     650
TACTTCCGTG ATGTTGAAGG GCAAGACGTG CTATTGTTTA TTGATAATAT     700
TTTCCGTTTC ACTCAAGCCG GTTCAGAAGT TTCTGCCCTA TTAGGTCGTA     750
TGCCTTCTGC CGTTGGGTAC CAACCAACGC TAGCAACAGA AATGGGTCAA     800
TTACAAGAAC GGATCACTTC AACGAAAAAA GGTTCAATCA CTTCA          845
```

2) INFORMATION FOR SEQ ID NO: 291

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 840 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

```
TTAGATCAAT CCTTACCCGA TATTAACAAC GCTTTAGTCG TTTATAAAAA      50
TGGCGAAGCA AAACAAAAAG TAGTACTTGA AGTCGCTTTA GAACTAGGTG     100
ATGGAGTGAT TCGTTCTATC GCCATGGAAT CGACAGATGG TTTACAACGT     150
GGAATGGAAG TTATCGATAC AGGAAAATCA ATTTCAGTTC CTGTTGGTAA     200
AGATACATTA GGTCGTGTGT TTAACGTTTT AGGAGACACA ATTGACTTAG     250
AAGCGCCATT CCCTGCAGAT GCTGAACGTA GTGGGATTCA TAAAAAAGCG     300
CCAGCATTTG ATGAATTAAG TACCAGTAAT GAAATTTTAG AAACAGGGAT     350
TAAAGTTATT GACTTATTAG CACCTTATCT AAAAGGTGGT AAAGTCGGAC     400
TTTTCGGTGG TGCCGGTGTT GGTAAAACCG TCTTAATTCA AGAATTAATT     450
CATAATATTG CCCAAGAACA TGGAGGGATT TCCGTCTTTA CTGGTGTTGG     500
TGAACGGACA CGTGAAGGGA ACGATCTGTA CTATGAAATG AAAGATTCAG     550
GCGTTATTGA AAAAACAGCC ATGGTTTTTG GTCAAATGAA CGAACCGCCA     600
GGTGCACGGA TGCGTGTGGC CTTAACTGGG TTAACGATTG CTGAATATTT     650
CCGTGATGTG GAAGGACAAG ACGTGCTATT ATTTATTGAT AACATTTTCC     700
GTTTCACCCA AGCCGGTTCA GAAGTTTCTG CCCTTTTAGG TCGGATGCCG     750
TCAGCCGTTG GTTACCAACC AACCTTAGCG ACTGAAATGG GACAATTACA     800
```

AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT 840

2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCCTGTA 200
GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
TTTAGAAACA CCTTTCCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
TGCCTTCTGC GGTTGGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
TTGCAAGAAC GTATCACATC TACGAAAAAA G 831

2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150
TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

```
GGCCGAGTAT TTAATGTACT AGGCGATACT ATCGACTTGG AAGCACCATT      250
CCCAGAAGAT GCCAAACGTA GTGGCATCCA CAAAAAAGCC CCAGATTTCG      300
ATGAATTGTC AACAAGTACA GAAATCCTTG AAACTGGGAT CAAAGTTATC      350
GATTTATTAG CTCCTTACTT AAAAGGTGGT AAAGTCGGCT TGTTCGGTGG      400
TGCCGGTGTT GGTAAAACCG TATTGATTCA AGAATTGATT CACAATATCG      450
CTCAAGAGCA TGGGGGAATT TCAGTATTTA CCGGTGTTGG CGAACGGACG      500
CGTGAAGGTA ATGACTTGTA TTATGAAATG AAAGAATCAG GCGTTATCGA      550
AAAGACAGCC ATGGTTTTCG GTCAAATGAA TGAACCACCA GGTGCCCGGA      600
TGCGGGTTGC TTTGACTGGT TTGACCATTG CTGAGTATTT CCGTGACGTT      650
GAAGGACAAG ATGTGCTCTT GTTTATCGAT AATATTTTCC GTTTCACACA      700
AGCGGGTTCT GAAGTATCTG CCTTGTTAGG CCGGATGCCA TCAGCCGTTG      750
GTTATCAACC AACTCTAGCA ACTGAAATGG GTCAATTACA AGAACGAATC      800
ACTTCTACGA AAAAAGGATC TGTAAC                                826
```

2) INFORMATION FOR SEQ ID NO: 294

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus saccharolyticus*
- (B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

```
TTTCTTTGGA CCAATCCTTA CCAGACATCA ACAATGCGTT GGTGGTCTAT       50
AAAAAGAATG ATGAAAAAAC AAAAGTGGTA CTTGAAACAG CTTTAGAACT      100
TGGTGATGGT GTCGTACGTA CGATTGCTAT GTCGTCAACA GACGGTTTGC      150
AACGTGGGAT GGAAGTCATC GATACAGGAG CATCAATTTC TGTTCCTGTT      200
GGGAAAGAGA CATTAGGACG TGTATTTAAC GTTTTAGGGG AGACTATCGA      250
CTTAGATGGT CCATTCCCAG AAGAAGTAGC ACGAGATGGT ATTCATAAAA      300
AGGCACCTGA TTTTGATGAA TTAAGTACAA GTACGGAGAT TCTTGAAACA      350
GGGATTAAAG TAATCGATTT ATTAGCGCCT TACTTAAAAG GTGGGAAAGT      400
TGGTTTATTC GGTGGTGCCG GTGTAGGTAA AACGGTATTA ATTCAAGAAT      450
TGATTAACAA TATTGCGCAA GAACATGGTG GTATTTCAGT ATTTGCGGGT      500
GTTGGTGAGC GTACTCGTGA AGGAAATGAC CTTTATTATG AAATGAAAGA      550
GTCGGGCGTT ATTGAGAAAA CAGCGATGGT TTTTGGACAA ATGAACGAAC      600
CACCAGGTGC ACGTATGCGA GTTGCTTTAA CTGGTTTAAC CATTGCAGAA      650
TACTTCCGTG ATGTTGAAGG ACAAGATGTA TTACTATTTA TTGATAACAT      700
TTTCCGTTTT ACTCAAGCTG GTTCAGAAGT TTCAGCTTTA TTAGGACGTA      750
TGCCTTCAGC GGTAGGGTAT CAACCGACAT TAGCAACAGA AATGGGACAA      800
TTACAAGAAC GTATTACGTC AACGAAAAAA GGCTCAATTA CATCAA          846
```

2) INFORMATION FOR SEQ ID NO: 295

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia fergusonii*
(B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295

```
GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTGCAAAATG GTAATGAGCG      50
TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGTGGTATC GTGCGTACCA     100
TCGCAATGGG GTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAAAGAC     150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT     200
CATGAACGTA CTGGGTGAAC CGGTCGACAT GAAAGGCGAG ATCGGTGAAG     250
AAGAGCGTTG GGCGATTCAC CGCGCAGCAC CTTCCTACGA AGAGCTGTCA     300
AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG     350
TCCGTTCGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG     400
GTAAAACTGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC     450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA     500
CGACTTCTAC CACGAAATGA CTGACTCCAA CGTTATCGAC AAAGTATCCC     550
TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA     600
CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT     650
TCTGCTGTTC GTTGACAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG     700
TATCCGCACT GCTGGGCCGT ATGCCTTCAG CGGTAGGTTA TCAGCCGACT     750
CTGGCGGAAG AGATGGGCGT TCTTCAGGAA CGTATCACCT CCACCAAAAC     800
TGG                                                       803
```

2) INFORMATION FOR SEQ ID NO: 296

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia hermannii*
(B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296

```
GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA ATGGTGATGA      50
GCGTCTGGTG CTGGAAGTGC AGCAGCAGCT CGGCGGCGGT ATCGTGCGTA     100
CCATCGCAAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GACTGTCGTC     150
GACCTCGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCGA CCCTGGGCCG     200
TATCATGAAC GTGCTGGGTC AGCCGATCGA CATGAAAGGC GATATCGGTG     250
AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCGTCCTA TGAAGAGCTG     300
TCCAGCTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT     350
GTGTCCGTTC GCGAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGCG     400
TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG     450
CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG     500
TAACGACTTC TACCATGAAA TGACCGACTC CAACGTTCTG GACAAAGTAT     550
CCCTGGTTTA CGGCCAGATG AACGAACCGC CGGGAAACCG TCTGCGCGTT     600
GCACTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA     650
CGTTCTGTTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACTG     700
AAGTATCCGC ACTGCTGGGC CGTATGCCTT CTGCGGTAGG TTACCAGCCG     750
ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAGCGTATCA CCTCCACCAA     800
```

AACCGGTTCT ATCACCTCCG TA

2) INFORMATION FOR SEQ ID NO: 297

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia vulneris*
(B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50
GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100
TGGGTTCTTC CGACGGTCTG CGTCGTGGTC TGGAAGTTCA GGACCTCGAG 150
CACCCGATCG AAGTGCCGGT AGGTAAAGCG ACCCTGGGTC GTATCATGAA 200
CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250
GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300
CAGGAACTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350
CGCCAAGGGC GGTAAAGTCG GCCTGTTCGG CGGCGCGGGC GTGGGTAAAA 400
CCGTAAACAT GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT 450
TACTCCGTGT TTGCAGGCGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 500
CTACCACGAG ATGACCGACT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550
ACGGCCAGAT GAACGAGCCG CCGGGAAACC GTCTGCGCGT GGCACTGACC 600
GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650
GTTCGTTGAC AACATCTATC GTTACACCCT GGCCGGTACG GAAGTATCTG 700
CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750
GAAGAGATGG GCGTTCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTC 800
TATCACCT 808

2) INFORMATION FOR SEQ ID NO: 298

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Eubacterium lentum*
(B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GGCGATTTAC AACGCGCTGA CGGTTGATGC 50
CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100
TGCCGGGCAA CCTTGTCCGC TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150
GTCCGCGGCC TCGAGGTCGT CGACACGGGC AACCCGATCA TGATGCCCGT 200

GGGTCCCGAG ACCCTGGGTC GCATCTGGAA CGTCATGGGC GAGCCCGTCG 250
ACGAGAAGCC GATGCCCGAG GTGAAGGGCT ACATGCCCAT CCACCGTCCG 300
GCTCCGGACT ACGACGAGCT GTCCACCACC ACCGAGATCT TCGAGACCGG 350
CATCAAGGCC ATCGACCTCG TCGAGCCCTT CGTCAAGGGC GGCAAGACGG 400
GTCTGTTCGG CGGCGCCGGC GTGGGCAAGA CGGTTATCAT CCAGGAGCTC 450
ATCAACAACC TGGCCCAGGA GCACGGCGGC ACGTCGGTGT TCACGGGCGT 500
GGGCGAGCGT ACCCGCGAGG GTACCGACCT CTACCTGGAG ATGAGCGACT 550
CGGGCGTCAT CAACAAGACC TGCCTCGTGT ACGGTCAGAT GAACGAGCCT 600
CCGGGAGCGC GTCTGCGCGT GGGTCTCGCG GGCCTCACCG AGGCGGAGTA 650
CTTCCGCGAT CAGGGCCAGG ACGTGCTTCT GTTCGTGGAC AACATCTTCC 700
GCTTCACGCA GGCCGGCTCC GAGGTGTCCG CTCTGCTGGG CCGCATGCCC 750
TCTGCCGTGG GTTACCAGCC GACGCTGGCA ACCGAGATGG GCGACCTGCA 800
GGAGCGCATC ACGTCGACGT CCACCGGCTC CATCACGTCC GTG 843

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Ewingella americana*
(B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

TCCCTCAGGA TGCAGTACCG AACGTGTACA ATGCTCTTGA GGTAGAAAAC 50
GGTGCCTCCA AACTGGTTCT GGAAGTTCAG CAACAGTTAG GCGGCGGCGT 100
TGTTCGTTGT ATCGCAATGG GTACCTCAGA CGGCCTTCGT CGCGGTCTGA 150
AAGTGAACAA CCTGGAACAC CCAATTGAAG TTCCGGTTGG TAAAGCGACT 200
CTGGGTCGTA TCATGAACGT ATTGGGTGAA CCAATCGACA TGAAAGGTGA 250
AATCGGCGAA GAAGAACGTC GTGCAATTCA CCGTCCAGCG CCTTCTTATG 300
AAGAGCTGGC TAACTCCCAA GAATTGCTGG AAACCGGTAT CAAAGTTATG 350
GACCTGATGT GTCCGTTCGC TAAGGGCGGT AAAGTCGGTC TGTTCGGTGG 400
TGCGGGTGTT GGTAAAACTG TAAACATGAT GGAGCTGATC CGTAACATCG 450
CGATCGAGCA CTCCGGTTAC TCAGTGTTTG CAGGCGTGGG TGAGCGTACT 500
CGTGAGGGTA ACGACTTCTA CCACGAAATG ACTGACTCCA ACGTTATCGA 550
CAAAGTTTCC CTGGTCTATG GTCAGATGAA TGAGCCACCA GGTAACCGTC 600
TGCGCGTTGC ACTGACCGGC CTGACCATGG CGGAGAAATT CCGTGATGAA 650
GGTCGTGACG TACTGCTGTT CGTTGACAAC ATTTACCGTT ACACCCTGGC 700
AGGTACCGAA GTGTCCGCAC TTCTGGGCCG TATGCCATCG GCGGTAGGTT 750
ATCAGCCAAC GCTGGCGGAA GAGATGGGTG CTCTGCAAGA GCGTATCACC 800
TCTACCAAAA GTGGTTCTAT CACCTCCGT 829

2) INFORMATION FOR SEQ ID NO: 300

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Francisella tularensis*
(B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300

```
AACACGCCTA AAGTATATGA TGCTTTAAAT GTAGTAGAAG CTGGTTTAGT      50
ATTAGAAGTT CAGCAACAAA TTGGTGATGG CGTAGTTCGT ACAATTGCTA     100
TGGGATCTAG TGATGGTCTT AGACGTGGTA TGGAAGTTAA GAACACAAAT     150
GCGCCTATTT CTGTTCCAGT TGGACATGGC ACACTTGGAC GTATCATGAA     200
TGTTTTAGGT GAACCAATTG ATGAAGCTGG TCCAATTGAA TATACTGAGA     250
AAAGATCTAT CCATCAAGCT CCTCCTGCAT ATGATGAGTT AGCATTAAGT     300
ACAGAAATAT TAGAAACAGG TATCAAAGTA GTTGACCTTA TTTGTCCATT     350
TGCTAAGGGC GGTAAAGTTG GTTTATTTGG CGGTGCAGGT GTTGGTAAAA     400
CTGTAACGAT GATGGAACTT ATCAACAATA TTGCAAAAGA ACATAGTGGC     450
TACTCTGTAT TTTCCGGTGT TGGTGAAAGA ACTCGTGAAG GTAATGACTT     500
CTACTATGAG ATGAAATATT CTAATGTATT GGATAAAGTA TCATTAGTAT     550
ATGGTCAGAT GAATGAGCCG CCTGGAAACA GATTAAGAGT AGCTCTTAGT     600
GGCTTAACAA TAGCAGAAGG ATTCCGTGAT GAAAAGCGTG ATGTTTTGAT     650
GTTTATCGAT AACATCTATC GTTATACATT AGCAGGTACA GAGGTATCGG     700
CGCTACTTGG TCGTATGCCA TCTGCTGTGG GTTATCAGCC AACGCTTGCA     750
GCTGAGATGG GTGCTTTACA GGAGCGTATT ACATCTACTA AGACAGGATC     800
TATTA                                                     805
```

2) INFORMATION FOR SEQ ID NO: 301

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium gonidiaformans*
(B) STRAIN: ATCC 25563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301

```
GACGAATTGC CAAAAATATA CAATGCATTA AAGGTGCAAG TTGGAGAAAA      50
AGAACTTGTA TTGGAAGTGC AACAACATTT GGGAAATAAT GTTGTGAGAA     100
CAGTAGCGAT GGACTCAACA GATGGATTGC TTCGAGGAAT GGAAGTAATG     150
GATACCGGAG CACCGATTAC TGTTCCAGTA GGGAAGGCGG TTTTAGGAAG     200
AATATTGAAT GTTTTGGGAG AGCCTGTGGA TCAAAAAGGG CCTGTGGAAA     250
CAGAAGAATA TTTACCTATC CATAGAGAAG CACCAAAATT TGAAGAACAA     300
GAAACAGTAA CAGAAATTTT TGAAACAGGA ATTAAAGTCA TAGATTTGTT     350
AGCCCCTTAT ATCAAAGGAG GAAAGACAGG TCTATTCGGT GGAGCCGGAG     400
TAGGGAAAAC AGTTTTAATT ATGGAATTAA TTAATAACAT TGCAAAGGGC     450
CACGGAGGAA TTTCTGTGTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG     500
AAGAGATTTA TACAACGAAA TGACAGAGTC CGGAGTTTTG AATAAGACCT     550
CGTTGGTGTA TGGTCAAATG AATGAGCCGC CCGGAGCAAG ACTTCGTGTG     600
GCGTTGACAG GATTAACGGT TGCTGAAAAC TTTAGAGATA AAGAAGGGCA     650
AGATGTATTG TTGTTTATCG ACAATATCTT CCGTTTCACA CAAGCAGGAT     700
CAGAAGTATC GGCTCTATTG GGAAGAATTC CATCGGCAGT AGGATATCAA     750
CCGAACTTAG CGACAGAAAT GGGAACTTTA CAAGAAAGAA TTACTTCTAC     800
```

AAAATCAGGA TCTATCACTT CGGTA

2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium necrophorum* subsp. *necrophorum*
(B) STRAIN: ATCC 25286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

ACAATGCATT AAAGGTACAG GTGGGAGAAA GGGAACTTGT GTTGGAAGTG 50
CAGCAACATT TAGGAAATAA TGTTGTCAGA ACAGTAGCAA TGGATTCAAC 100
AGACGGATTA CTTCGGGGAA TGGAAGTGAG AGATACAGGA GTTCCCATTA 150
CTGTTCCGGT AGGAAAGGCG GTTTTGGGAA GAATATTAAA TGTCTTAGGG 200
GAGCCTGTGG ACGAAAAAGG TCCGATAGAG ACAGAAGAAT ATTTACCAAT 250
ACATAGAGAA GCACCGAAAT TTGAAGAACA GGAAACGGTG ACAGAAATTT 300
TTGAAACAGG AATTAAAGTC ATTGATTTGT TAGCTCCTTA TATTAAAGGA 350
GGAAAAACAG GCCTATTCGG AGGAGCCGGA GTAGGAAAAA CCGTTTTGAT 400
TATGGAACTG ATCAATAATA TTGCAAAAGG TCATGGAGGA ATTTCTGTTT 450
TTGCAGGAGT TGGAGAAAGA ACGAGAGAGG GAAGAGATCT ATACAACGAA 500
ATGACAGAGT CCGGAGTTTT GAATAAAACT TCTTTGGTAT ATGGGCAAAT 550
GAATGAGCCG CCCGGAGCAA GACTTCGAGT GGCTTTAACC GGACTTACTG 600
TTGCCGAAAA TTTCAGAGAT AAAGAGGGAC AGGATGTCTT ATTGTTCATT 650
GACAATATTT TCCGTTTCAC ACAAGCAGGT TCGGAAGTAT CGGCACTTTT 700
GGGGAGAATT CCTTCTGCAG TGGGATATCA ACCGAACTTG GCGACAGAAA 750
TGGGAAGCTT ACAAGAAAGA ATTACTTCTA CAAAATCCGG TTCTATCACT 800
TCCGTG 806

2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC CTGCAATATA TAATGCTTTA AAAGTAAAAT TAGAAGATAA 50
GGAACTTGTT CTAGAAGTTG AACAACATCT TGGTAACAAT GTTGTAAGAA 100
CTGTTGCTAT GGATTCAACT GATGGATTAA AAAGAGGAAT GGAAGTTATA 150

GATACAGGTA AACCAATTAC AGTACCAGTT GGTAAAGCTG TTCTTGGTAG 200
AATATTAAAT GTTTTAGGAG AACCTGTTGA TAATCAAGGT CCTATAAATG 250
CTGAAACATT TTTACCTATT CATAGAGAAG CACCAGAATT TGATGACTTA 300
GAAACTGAAA CTGAAATATT TGAAACAGGA ATAAAAGTTA TAGACTTATT 350
AGCACCATAT ATTAAAGGTG GAAAAATAGG ATTATTTGGT GGAGCTGGAG 400
TAGGAAAAAC AGTTTTAATA ATGGAACTTA TCAACAACAT TGCAAAAGGA 450
CATGGAGGAA TTTCAGTTTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG 500
TAGAGACTTA TATGGTGAAA TGACTGAATC AGGAGTTATC ACAAAAACAG 550
CTCTTGTTTA TGGACAAATG AATGAGCCAC CTGGAGCAAG ACTTAGAGTT 600
GCATTAACAG GGCTTACTGT TGCAGAAAAC TTTAGAGATA AAGATGGGCA 650
AGATGTTCTT CTATTTATAG ATAATATATT TAGATTTACA CAAGCAGGTT 700
CAGAAGTTTC AGCTTTACTT GGAAGAATAC CATCAGCTGT TGGATATCAA 750
CCAAACCTAG CAACTGAAAT GGGTGCTTTA CAAGAAAGAA TAACATCTAC 800
AAAATCTGGT TCAATTACAT C 821

2) INFORMATION FOR SEQ ID NO: 304

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 864 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Gardnerella vaginalis*
(B) STRAIN: ATCC 49145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

TTCCCAGTTG GCTATCTTCC AGATATTTAT AATGCTCTCA AGGTTGATAT 50
CAACACCGTT GGAAACACGG AGGGAGATAC CGTCCACGAG ATTACATTGG 100
AAGTTGAGCA GCACCTTGGT GATTCAACTG TGCGAGCAGT GGCACTTAAG 150
CCTACGGACG GCTTGGTCCG TGGTGCTTTA GTGCGAGATA CTGGTGGCCC 200
AATTTCTGTG CCTGTTGGAG ATGTTACAAA AGGTCACGTT TTTGACGTAA 250
CTGGTAACAT TTTAAACGCT AAACCAGGCG AAAACATTGA GGTGACCGAG 300
CGCTGGCCAA TCCACCGCAA CCCACCTGCT TTCGATCAGC TTGAGTCTAA 350
GACTCAAATG TTTGAAACAG GCATTAAGGT TATCGATTTG CTTACGCCTT 400
ACGTTCAGGG CGGAAAGATT GGTCTGTTCG GTGGTGCAGG CGTTGGTAAA 450
ACTGTGTTGA TTCAGGAGAT GATTCAGCGC GTTGCACAGA ACCACGGCGG 500
TGTGTCTGTG TTTGCTGGCG TTGGCGAACG TACTCGTGAG GGTAACGATT 550
TGATTGGCGA AATGGCTGAG GCTGGCGTTT TGGAGAAAAC AGCGCTTGTC 600
TTTGGTCAGA TGGATGAGCC TCCTGGGACT CGTCTTCGTG TGCCTCTTAC 650
TGCTTTGACT ATGGCTGAGT ATTTCCGTGA TGTTCAGAAT CAGGATGTGT 700
TGCTGTTTAT CGACAACATC TTCCGCTTTA CTCAGGCAGG TTCTGAGGTT 750
TCCACGTTGC TTGGTCGTAT GCCTTCTGCA GTTGGTTATC AGCCAAACTT 800
GGCGGATGAA ATGGGTGCGT TGCAGGAGCG CATTACTTCT ACGCGCGGTC 850
ATTCTATTAC GTCG 864

2) INFORMATION FOR SEQ ID NO: 305

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 848 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Gemella haemolysans*
(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

```
TCGAATCAGG GCATATGCCA AATCTATTAA ACGCTTTAGA AGTTTACATA      50
GAAAAAGGCG ATGGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA     100
AATTGGTGAT AACGTAGTAA GAACAATCGC TATGTCATCT ACTGATGGAT     150
TAAATAGGGG AGCAGAAGTA GTAGATACAG GAGCACCAAT TACAGTTCCT     200
GTAGGTAACT ACACATTAGG TCGTGTGTTC AACGTATTAG GTGAAGCAGT     250
TGACCACGGT GAAGAAGCAG GAGCAGAAGT TCGTAAAGAT TCAATTCACA     300
AAGAAGCTCC AACATTCGAT GAATTATCAA CTCACGTTGA GGTTCTTGAA     350
ACAGGTATTA AAGTTATCGA CTTACTTGCA CCATATATTA AAGGTGGTAA     400
AATCGGTCTT TTCGGTGGTG CGGGAGTTGG TAAAACGGTT CTTATCCAAG     450
AACTTATCAA CAACGTTGCG CAACAACACG GTGGATTATC AGTATTCACA     500
GGTGTAGGTG AGCGTACTCG TGAAGGAAAT GACTTATACT ATGAAATGAA     550
AGATTCTGGT GTTATTAACA AAACAGCCAT GGTATTCGGA CAAATGAACG     600
AACCACCAGG TGCTCGTATG CGTGTAGCAT TAACAGGATT AACAATGGCG     650
GAATACTTCC GTGATGAAGA AGGACAAGAC GTGCTTCTAT TCATCGATAA     700
CATTTTCCGT TTCACACAAG CAGGTTCTGA GGTTTCTGCG TTATTAGGAC     750
GTATGCCATC AGCCGTTGGT TACCAACCAA CACTTGCTAC AGAGATGGGA     800
CGTTTACAAG AACGTATAAC ATCAACTAAA AAAGGTTCTG TTACATCT       848
```

2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 848 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Gemella morbillorum*
(B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

```
TCGAATCAGG GCATATGCCT AATCTACTAA ACGCTTTAGA AGTTTATATA      50
GAAAAAGGCG ATGGAAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA     100
AATCGGGGAT AATGTCGTAA GAACTATTGC GATGTCATCT ACTGATGGAT     150
TAAACAGAGG GGCAGAAGTA GTTGATACTG GAGCGCCAAT TACAGTGCCA     200
GTAGGTAACT ATACATTAGG ACGTGTGTTC AACGTATTAG GTGAAGCAGT     250
TGACCACGGA GAAGAAGCTG GAGCAGAAGT TCAAAAAGAA TCTATTCATA     300
AAGAAGCTCC AACTTTCGAA GAATTATCAA CACATGTTGA GGTATTAGAA     350
ACAGGTATTA AAGTTATCGA CCTTCTTGCA CCATATATTA AAGGTGGTAA     400
GATTGGACTA TTCGGTGGTG CTGGAGTTGG GAAAACAGTT CTTATCCAAG     450
AACTTATTAA CAACGTAGCA CAACAACACG GAGGACTTTC AGTATTTACT     500
GGGGTAGGTG AACGTACTCG TGAGGGTAAC GACTTGTACT ATGAAATGAA     550
AGACTCTGGA GTTATTAATA AAACTGCCAT GGTATTTGGT CAAATGAATG     600
AGCCACCAGG TGCACGTATG CGTGTTGCCT TAACAGGATT AACAATGGCA     650
GAGTACTTCC GTGATGAAGA AGGACAAGAC GTACTATTAT TTATCGATAA     700
```

TATCTTCCGT TTCACACAAG CAGGGTCTGA GGTATCTGCA TTATTAGGGC 750
GTATGCCTTC AGCCGTTGGA TATCAACCAA CTCTTGCAAC AGAAATGGGA 800
CGTCTTCAAG AACGTATTAC ATCAACTAAA AAAGGATCTG TTACATCT 848

2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus ducreyi*
(B) STRAIN: DSM 8925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC CAAAAGTATA TGATGCTTTA AAAGTTGAAT CAGGTTTAAC 50
CTTAGAAGTT CAACAACAAT TAGGTGGTGG TTTAGTACGT TGTATCGCAT 100
TAGGTACCTC AGATGGTTTA AAGCGTAGCT TAAAGGTTGT AAATACAGGT 150
AACCCTATTC AAGTTCCTGT AGGCACTAAA ACATTAGGCC GTATTATGAA 200
TGTATTAGGC GAACCAATTG ATGAAAAAGG ACCTATTAGC GAAGAAGCTC 250
GTTGGGATAT TCATCGTGCG GCTCCAAATT ATGAAGAACA GTCAAATAGT 300
ACTGAATTAC TTGAAACCGG TATCAAAGTT ATTGACTTAA TTTGTCCATT 350
TGCAAAAGGT GGTAAAGTCG GCTTATTTGG TGGAGCTGGT GTAGGTAAAA 400
CCGTTAATAT GATGGAATTG ATCCGTAATA TTGCTATTGA GCACTCAGGT 450
TATTCGGTTT TTGCTGGTGT AGGTGAGCGT ACTCGTGAAG GTAATGATTT 500
TTATCATGAA ATGACGGATT CTAATGTATT AGATAAAGTA TCACTAGTAT 550
ATGGTCAAAT GAATGAACCA CCAGGTAACC GCCTACGTGT TGCGTTAACA 600
GGTTTAACTA TGGCTGAAAA ATTCCGTGAT GAAGGTCGTG ATGTATTATT 650
TTTCGTAGAT AATATTTATC GTTATACTTT AGCCGGTACA GAAGTTTCTG 700
CTTTATTAGG CCGTATGCCA TCAGCGGTAG GTTATCAACC AACCCTTGCA 750
GAAGAAATGG GTGTATTACA AGAACGTATT ACCTCAACTA AAACTGGTTC 800
AATCACGGCA GTA 813

2) INFORMATION FOR SEQ ID NO: 308

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus haemolyticus*
(B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA CAAGATGCAG TGCCAAAAGT TTACGATGCA TTAAAAGTTG 50
AATCAGGTTT AACACTTGAG GTGCAACAAC AATTAGGTGG CGGTGTGGTA 100

CGTTGTATCG CATTAGGTGC TTCTGACGGT TTAAAACGTG GTTTAAAAGT 150
AGAAAACACG AATGATCCGA TTCAAGTACC GGTAGGCACA AAAACCCTTG 200
GTCGTATCAT GAATGTATTG GGTGAACCAA TTGACGAACA AGGTCCAATC 250
GGTGAAGAAG AGCGTTGGGC TATCCATCGT TCTGCACCAA GCTATGAAGA 300
ACAATCAAAC AGTACGGAAT TATTAGAGAC TGGTATCAAA GTTATCGACT 350
TAATTTGTCC ATTCGCAAAA GGTGGTAAAG TTGGTCTATT CGGTGGTGCG 400
GGTGTAGGTA AAACCGTTAA CATGATGGAA TTAATCCGTA ACATCGCGAT 450
CGAGCACTCA GGTTACTCCG TATTTGCGGG TGTAGGTGAA CGTACTCGTG 500
AAGGTAACGA CTTCTATCAT GAAATGAAAG ATTCTAACGT ATTAGATAAA 550
GTATCTTTGG TTTATGGTCA GATGAATGAG CCACCAGGTA ACCGTTTACG 600
TGTTGCGTTA ACTGGTTTAA CCATGGCAGA AAAATTCCGC GATGAAGGTC 650
GTGATGTATT ATTCTTCGTG GATAATATCT ATCGTTATAC CCTTGCTGGT 700
ACGGAAGTAT CTGCGTTATT AGGTCGTATG CCATCTGCGG TAGGTTACCA 750
ACCAACTCTT GCTGAAGAAA TGGGTGTGTT ACAAGAACGT ATCACTTCAA 800
CCAAAACAGG TTCTATTACA TCTGTA 826

2) INFORMATION FOR SEQ ID NO: 309

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus parahaemolyticus*
(B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

GATGCAGTAC CAAAAGTATA TGATGCGTTA AAAGTTGAAT CAGGTTTAAC 50
GCTTGAAGTT CAACAACAAT TAGGCGGTGG CTTAGTGCGC TGTATCGCAT 100
TAGGTACGTC TGATGGTTTA AAACGTGGCT TAAAAGTAGA AAATACAGGC 150
AACCCAATTG AAGTGCCAGT GGGCACTAAA ACCCTTGGTC GTATTATGAA 200
CGTATTGGGT GAGCCGATTG ACGAAAAAGG TCCTATCGGT GAAGAAGCAC 250
GCTGGGCAAT CCACCGTGCA GCACCAAGCT ACGAAGAGCA ATCAAATAGC 300
ACGGAATTAC TCGAAACAGG TATCAAAGTT ATCGACTTAA TCTGCCCATT 350
CGCAAAAGGG GGTAAAGTTG GTTTATTTGG TGGTGCAGGT GTAGGTAAAA 400
CCGTAAATAT GATGGAGTTA ATCCGTAACA TCGCGATCGA ACACTCTGGT 450
TACTCTGTAT TTGCAGGGGT AGGTGAGCGT ACTCGTGAAG GTAATGACTT 500
CTACCACGAA ATGACAGACT CTAACGTATT AGATAAAGTA TCGTTAGTGT 550
ATGGTCAAAT GAACGAACCA CCAGGTAACC GTTTACGCGT AGCTTTAACA 600
GGCTTAACCA TGGCGGAAAA ATTCCGCGAT GAAGGTCGTG ACGTATTATT 650
CTTCGTCGAT AACATCTACC GTTATACCCT AGCAGGTACG GAAGTGTCAG 700
CACTTCTCGG TCGTATGCCA TCTGCGGTAG GTTATCAGCC AACCTTAGCA 750
GAAGAAATGG GTGTATTACA AGAGCGTATC ACTTCAACCA AAACTGGTTC 800
TATCACCTC 809

2) INFORMATION FOR SEQ ID NO: 310

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus parainfluenzae*
(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

```
CGAATTTCCA CAAGATGCAG TACCAAAAGT TTATGATGCA TTAAAAGTTG      50
AATCGGGTTT AACCCTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA     100
CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT     150
TGAAAATACC AATAAACCAA TTTCAGTACC GGTTGGTGTA AAAACTCTCG     200
GTCGTATTAT GAACGTATTG GGCGAACCGA TTGATGAAAG AGGTCCTATC     250
GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA     300
ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT     350
TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGCG     400
GGTGTAGGTA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT     450
TGAGCACTCA GGTTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG     500
AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA     550
GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG     600
TGTTGCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC     650
GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG     700
ACTGAAGTAT CGGCACTTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA     750
GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA     800
CCAAAACAGG TTCTATTACT TCTG                                 824
```

2) INFORMATION FOR SEQ ID NO: 311

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 811 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Hafnia alvei*
(B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

```
GCCGTGCCTA AAGTGTATAA CGCACTTGAG GTGAAAGGCG GTGCCACTAA      50
ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA     100
TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC     150
CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT     200
TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCGAAG     250
AAGATCGCTG GGCTATTCAC CGTGAAGCTC CAAGCTACGA AGAACTGTCT     300
AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG     350
TCCGTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTTG     400
GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC     450
TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTACTC GTGAGGGTAA     500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC     550
TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG     600
CTGACCGGTC TGACTATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT     650
ACTGCTGTTC ATCGATAACA TCTACCGTTA TACCTTGGCC GGTACCGAAG     700
```

TATCTGCACT GTTGGGTCGT ATGCCTTCTG CGGTAGGTTA TCAGCCAACG 750
CTGGCGGAAG AGATGGGTGT TCTGCAAGAA CGTATCACCT CGACCAAAAC 800
GGGTTCAATC A 811

2) INFORMATION FOR SEQ ID NO: 312

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Kingella kingae*
(B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

GCGATGCTAT TCCACGCGTT TACGATGCGT TGAAACTGGT TGATGTGGAC 50
TTGACATTAG AAGTGCAACA ACAACTGGGC GATGGCGTAG TGCGTACCAT 100
TGCGATGGGT AGTACCGATG GTTTGAAACG CGGCTTAGCC GTGAACAACA 150
CAGGCGCACC TATTACAGTG CCTGTTGGTA AAGCAACATT GGGTCGTATT 200
ATGGACGTAT TGGGTAATCC TGTTGATGAA GCAGGTCCAA TTGGTTCTGA 250
CCAAACGCGT GCTATTCACC AACCAGCTCC TAAATTTGAT GAACTGTCTA 300
GCGCAACCGA ATTGCTGGAA ACAGGCATCA AAGTGATTGA CTTGCTTTGC 350
CCATTTGCAA AAGGTGGTAA AGTAGGTTTG TTTGGTGGTG CAGGTGTGGG 400
CAAAACTGTG AACATGATGG AGTTGATTAA CAACATTGCC AAAGCGCACA 450
GTGGTTTGTC TGTATTTGCA GGCGTGGGTG AACGTACTCG CGAAGGTAAT 500
GACTTCTATC ACGAGATGAA AGATTCTAAC GTGTTGGATA AAGTTGCCAT 550
GGTGTATGGT CAAATGAATG AACCTCCTGG CAACCGTTTG CGCGTTGCAT 600
TGACTGGTTT GTCTATGGCA GAACACTTCC GTGATGAAAA AGACGAAAAT 650
GGCAAAGGTC GCGATGTATT GTTCTTTGTG GACAACATCT ATCGCTACAC 700
ATTGGCAGGT ACAGAAGTAT CGGCATTGCT GGGTCGTATG CCCTCTGCGG 750
TAGGTTATCA ACCAACATTG GCAGAAGAAA TGGGTCGTTT GCAAGAGCGT 800
ATTACTTCAA CGCAAACAGG TTCGATTACT T 831

2) INFORMATION FOR SEQ ID NO: 313

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
(B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC ACGCGTGTAC GAAGCCCTTG AGGTACAGAA TGGTAATGAA 50
GTTCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGTA TCGTACGTAC 100

CATCGCCATG GGTTCTTCTG ATGGTCTGCG CCGCGGTCTG GATGTAAAAG 150
ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT 200
ATCATGAACG TACTGGGTCA ACCGGTTGAC ATGAAAGGCG ACATCGGCGA 250
AGAAGAGCGT TGGGCTATCC ACCGCGCGGC ACCGTCCTAT GAAGAGCTGT 300
CCAGCTCTCA GGAACTGCTG GAAACCGGCA TCAAAGTTAT CGACCTGATG 350
TGTCCGTTCG CCAAGGGCGG TAAAGTTGGT CTGTTCGGCG GTGCGGGTGT 400
AGGTAAAACT GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450
ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAGCGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ATAAAGTATC 550
CCTGGTGTAC GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
CGCTGACCGG CCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC 650
GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG CCGGTACTGA 700
AGTATCCGCG CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TATCAGCCGA 750
CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAAA 800
ACCGGTTCTA TC 812

2) INFORMATION FOR SEQ ID NO: 314

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella ornithinolytica*
(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAGAA TGGTAATGAG 50
AGCCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGTGGTA TCGTACGTGC 100
TATCGCCATG GGTTCTTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG 150
ACCTTGAGCA CCCGATCGAA GTCCCGGTTG GTAAAGCAAC GCTGGGTCGT 200
ATCATGAACG TGCTGGGTCA GCCAATCGAT ATGAAAGGCG ACATCGGCGA 250
AGAAGAGCGT TGGGCTATTC ACCGTGCAGC TCCGTCCTAT GAAGAGCTGT 300
CCAGCTCTCA GGAACTGCTG GAAACCGGCA TCAAAGTTAT CGACCTGATG 350
TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG GTGCGGGTGT 400
AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450
ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTCTGG ATAAAGTATC 550
CCTGGTTTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
CTCTGACCGG CCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC 650
GTTCTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG CCGGTACTGA 700
AGTATCCGCA CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TATCAGCCGA 750
CCCTGGCGGA AGAGATGGGT GTTCTGCAGG AACGTATCAC CTCCACCAAA 800
ACCGGTTCTA TC 812

2) INFORMATION FOR SEQ ID NO: 315

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT 50
GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATTGTT CGTACCATCG 100
CCATGGGTTC TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC 150
GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT 200
GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG 250
AGCGTTGGGC GATTCACCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC 300
TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC 350
GTTTGCGAAG GGCGGTAAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA 400
AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
GGTTACTCCG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG 550
TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG 600
ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT 650
GCTGTTCGTC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT 700
CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG 750
GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAAACGGG 800
TTCTATCACT TCC 813

2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella planticola*
(B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA 50
GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG 100
CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA 150
GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAAGCAA CGCTGGGTCG 200
TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG 250
AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG 300
TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT 350
GTGTCCGTTC GCTAAGGGCG GTAAAGTAGG TCTGTTCGGT GGTGCGGGCG 400
TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT 550
CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA 650
CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG 700

AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG 750
ACCCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CCTCCACCAA 800
AACCGGTTCT ATCACTTCCG TA 822

2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
(B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA TGAAGTTCTG GTGCTGGAAG TTCAGCAGCA GCTGGGCGGC 50
GGTATCGTAC GTACCATCGC CATGGGTTCT TCTGATGGTC TGCGCCGCGG 100
TCTGGATGTA AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG 150
CAACGCTGGG TCGTATCATG AACGTACTGG GTCAACCGGT TGACATGAAA 200
GGCGACATCG GCGAAGAAGA GCGTTGGGCT ATCCACCGCG CGGCACCGTC 250
CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG 300
TTATCGACCT GATGTGTCCG TTCGCCAAGG GCGGTAAAGT TGGTCTGTTC 350
GGCGGTGCGG GTGTAGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 400
CATCGCGATC GAGCACTCCG GTTACTCTGT GTTTGCGGGC GTAGGTGAGC 450
GTACTCGTGA GGGTAATGAC TTCTACCACG AAATGACCGA CTCCAACGTT 500
ATCGATAAAG TATCCCTGGT GTACGGCCAG ATGAACGAGC CGCCGGGAAA 550
CCGTCTGCGC GTTGCGCTGA CCGGCCTGAC CATGGCTGAG AAATTCCGTG 600
ACGAAGGTCG TGACGTACTG CTGTTCGTCG ATAACATCTA TCGTTACACC 650
CTGGCCGGTA CTGAAGTATC CGCACTGCTG GGTCGTATGC CTTCAGCGGT 700
AGGTTATCAG CCGACCCTGG CGGAAGAGAT GGGCGTTCTG CAGGAACGTA 750
TCACCTCCAC CAAAACCGGT TCTATCACCT CCGTA 785

2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Kluyvera ascorbata*
(B) STRAIN: ATCC 33433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG AAGTTCAGCA GCAGCTCGGC GGCGGTATCG TACGTWCCAT 50
CGCTATGGGT TCTTCCGACG GTCTGCGTCG CGGTCTGGAT GTTAAAGATC 100
TCGAGCACCC AATCGAAGTT CCGGTMGGTA AAGCAACMCT GGGTCGTATC 150

```
ATGAACGTAC TGGGTCAKCC AGTMGACATG AAAGGCGACA TCGGTGAAGA      200
AGAGCGTTGG GCTATCCACC GCGCTGCACC TTCCTACGAA GAGCTGTCTA      250
GCTCTCAGGA ATTGCTGGAA ACCGGTATCA AAGTTATCGA CCTGATGTGT      300
CCGTTCGCTA AGGGCGGTAA AGTCGGTCTG TTCGGTGGTG CSGGTGTTGG      350
TAAAACCGTA AACATGATGG AGCTGATCCG TAACATCGCG ATCGAGCACT      400
CCGGTTACTC CGTGTTTGCG GGCGTAGGTG AACGTACTCG TGAGGGTAAC      450
GACTTCTACC ACGAAATGAC CGACTCCAAC GTTATCGATA AAGTATCCCT      500
GGTATATGGC CAGATGAACG AGCCACCGGG AAACCGTCTG CGCGTTGCTC      550
TGACCGGTCT GACCATGGCT GAGAAATTCC GTGACGAAGG TCGTGACGTA      600
CTGCTGTTCG TCGATAACAT CTATCGTTAC ACCCTGGCCG GTACTGAAGT      650
ATCTGCWCTG CTGGGTCGTA TGCCTTCAGC GGTAGGTTAC CAGCCGACCC      700
TGGCGGAAGA GATGGGCGTT CTGCAGGAAC GTATCACCTC CACCAAGACC      750
GGTTCTATC                                                  759
```

2) INFORMATION FOR SEQ ID NO: 319

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Kluyvera cryocrescens*
- (B) STRAIN: ATCC 33435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

```
TTCCCTCAGG ATGCCGTACC GCGTGTGTAC GAAGCCCTTG AGGTTCAGAA       50
TGGTAATGAA GTGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA      100
TCGTACGTAC CATCGCTATG GGTTCTTCCG ACGGTCTGCG TCGTGGTCTG      150
GATGTAAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC      200
ACTGGGTCGT ATCATGAACG TACTGGGCCA ACCGGTAGAC ATGAAAGGCG      250
ACATCGGTGA AGAAGAACGT TGGGCTATCC ACCGTGCAGC ACCTTCCTAC      300
GAAGAGCTGT CAAGCTCTCA GGAACTGCTG GAAACCGGCA TCAAAGTTAT      350
CGACCTGATG TGTCCGTTTG CGAAGGGCGG TAAAGTTGGT CTGTTCGGTG      400
GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT TCGTAACATC      450
GCGATTGAGC ACTCCGGTTA TTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
ATAAAGTTTC CCTGGTTTAC GGCCAGATGA ACGAGCCACC AGGAAACCGT      600
CTGCGCGTTG CGCTGACTGG TCTGACTATG GCTGAGAAGT TCCGTGACGA      650
AGGTCGCGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
CCGGTACAGA AGTATCTGCA CTGCTGGGTC GTATGCCTTC AGCGGTAGGT      750
TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
CTCCACCAAA ACCGGTTCTA TCACCTCCGT A                          831
```

2) INFORMATION FOR SEQ ID NO: 320

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Kluyvera georgiana*
(B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

GCCGTACCGC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT 50
GCTGGTGCTG GAAGTTCAGC AGCAGCTCGG TGGCGGTATC GTGCGTACCA 100
TCGCCATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA AGTTAAAGAT 150
CTCGAGCACC CGATCGAAGT TCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
CATGAACGTA CTGGGTCACC CGGTAGACAT GAAAGGCGAC ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCTGCGC CTTCCTACGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGCGGT GCGGGTGTTG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC 550
TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT 650
ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACTGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA CCAGCCGACT 750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC 800
CGGTTCTATC 810

2) INFORMATION FOR SEQ ID NO: 321

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactobacillus acidophilus*
(B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

TCGATAAGAA TTTACCTGAT ATTAACAACG CCTTACGTGT AATCAAGTCC 50
GAAGATGAAA GCATCGTTCT TGAAGTTACA CTTGAACTCG GTGATGGTGT 100
TTTAAGAACA ATCGCCATGG AATCTACCGA TGGTCTTCGT CGTGGTATGA 150
AAGTCGAAGA TACTGGCGCT CCAATTTCAG TTCCAGTTGG AGAAGACACT 200
TTAGGTCGTG TGTTTAACGT TTTAGGACAG CCTATTGATG GTGGTCCAGC 250
CTTTCCAAAG GATCACCCAC GTGAGGGTAT CCACAAGGAA GCACCTAAAT 300
ATGAAGATTT AACTACTAGT CGTGAAATTC TTGAAACTGG TATCAAGGTT 350
ATCGACCTTC TTGAACCATA TGTTCGTGGT GGTAAAGTTG GTTTGTTTGG 400
TGGTGCCGGT GTTGGTAAAA CTACTATTAT TCAAGAATTA ATTCACAACA 450
TCGCTCAAGA ACACGGTGGT ATTTCCGTAT TTACTGGTGT TGGTGAAAGA 500
ACTCGTGAAG GTAATGACCT TTACTTTGAA ATGAAAGCTT CAGGCGTTTT 550
AAGTAAGACT GCCATGGTAT TTGGTCAGAT GAACGAGCCG CCTGGTGCCA 600
GAATGCGTGT TGCATTAACC GGTTTGACAC TTGCTGAATA CTTTAGAGAT 650
GTTGAAGGTC AAGACGTATT GCTCTTTATT GACAATATCT TTAGATTTAC 700
TCAGGCTGGT TCAGAGGTAT CTGCTTTGCT TGGTCGTATG CCAAGTGCCG 750
TAGGTTATCA GCCAACTTTG GCAACAGAAA TGGGTCAATT GCAGGAAAGA 800

ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
(B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

```
TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTTGAT      50
AGTGATCTGG TTTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG     100
TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG     150
AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA     200
CGCATTATGG ATGTTCTTGG GCGTCCTGTA GATGATGCTG GGCCTATCGA     250
TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC     300
AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTTG     350
CTTTGCCCTT TTGCCAAGGG AGGTAAAGTT GGTCTATTCG GTGGTGCCGG     400
TGTAGGCAAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG     450
AGCATAGCGG TTATTCAGTG TTTGCAGGGG TTGGTGAACG TACCCGTGAA     500
GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT     550
ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG     600
TTGCTCTAAC CGGTTTGACT ATGGCTGAAA AATTCCGGGA TGAAGGGCGA     650
GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT     700
TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC     750
CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA     800
AAAACAGGTT CTATTACTTC CATA                                 824
```

2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leminorella grimontii*
(B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

```
GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA      50
GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA     100
TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT     150
CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT     200
```

```
CATGAACGTG CTTGGTCACC CTATCGACAT GAAGGGCGAC ATCGGCGAAG      250
AAGAGCGTTG GGCTATTCAC CGCGCAGCGC CGAGCTACGA AGACCTGTCG      300
GGCGCAACCG AGCTGCTGGA GACCGGCATC AAGGTTATCG ACCTGATTTG      350
TCCGTTCGCC AAGGGCGGTA AAGTCGGCCT GTTCGGCGGC GCCGGCGTAG      400
GTAAAACCGT AAACATGATG GAGCTCATTC GCAACATTGC GACCGAGCAC      450
TCCGGTTACT CCGTGTTTGC AGGCGTAGGT GAACGTACCC GTGAGGGTAA      500
CGACTTCTAC CACGAAATGA CTGAATCCAA CGTATTGGAC AAGGTGTCGC      550
TGGTATACGG TCAGATGAAC GAGCCGCCTG GAAACCGTCT GCGCGTAGCG      600
TTAACGGGCT TGACCATGGC GGAGAAGTTC CGTGATGAAG GCCGTGACGT      650
TCTGCTGTTT ATCGACAACA TTTACCGCTA TACCCTGGCC GGTACGGAAG      700
TATCCGCACT GCTGGGCCGT ATGCCTTCAG CCGTAGGCTA CCAGCCGACT      750
CTGGCTGAGG AAATGGGCGT GCTTCAAGAG CGTATTACCT CTACCAAGAC      800
GGGGTCTATC ACCTCCGT                                        818
```

2) INFORMATION FOR SEQ ID NO: 324

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

```
GTGGAAACTT ACCTGAAATC TACAATGCCC TAGTTATTGA ATATAAATCT       50
GATGCAGAAG AAGCACCAAC TAGCCAACTT ACTTTAGAAG TAGCCATCCA      100
ATTAGGTGAT GATGTTGTAC GTACAATCGC AATGGCATCA ACAGATGGTG      150
TTCAAAGAGG TATGGAAGTT ATTGATACTG GGAGCCCAAT TACAGTTCCT      200
GTAGGTACAG TAACTCTTGG TCGTGTATTT AATGTATTAG GAAACACCAT      250
CGATTTGGAC GAACCACTTC CAAGCGATAT TAAACGTAAT AAAATTCACC      300
GCGAAGCTCC AACTTTCGAT CAATTAGCAA CGACAACAGA AATTCTTGAA      350
ACAGGAATTA AAGTAGTTGA CTTGCTAGCT CCTTACTTAA AAGGTGGTAA      400
AATCGGATTG TTCGGTGGTG CCGGTGTTGG TAAAACCGTT CTAATTCAAG      450
AGCTTATCCA TAATATCGCA CAAGAACATG GTGGTATTTC TGTGTTCGCT      500
GGCGTTGGAG AACGTACTCG TGAAGGTAAC GACCTTTACT TCGAAATGAA      550
AGATTCAGGC GTTATTGAAA AAACAGCGAT GGTATTCGGT CAAATGAACG      600
AGCCACCAGG TGCGCGTATG CGTGTTGCCT TAACTGGTCT AACAATTGCT      650
GAATATTTCC GTGATGAAGA ACATCAAGAT GTACTTTTAT TCATTGATAA      700
CATTTTCCGT TTCACACAAG CTGGTTCAGA GGTTTCGGCT TTACTAGGTC      750
GTATGCCATC TGCGGTAGGT TACCAACCAA CCCTAGCTAC TGAAATGGGT      800
CAACTACAAG AACGTATTAC ATCTACTAAC GTTGG                      835
```

2) INFORMATION FOR SEQ ID NO: 325

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Micrococcus lylae*
(B) STRAIN: ATCC 27566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

```
CCCGCGTGGC GAGTTGCCGG CACTGTTCAA CGCGCTGACT GTCGAGGTCA      50
CCCTCGAAGC AGTCGCTAAA ACCATTACCC TTGAGGTTGC TCAGCACCTC     100
GGCGACAACT TGGTTCGTGC CGTGTCCATG GCACCGACCG ACGGTCTCGT     150
CCGTGGCGCT GCTGTGATCG ACAGCGGTAA GCCGATCTCA GTTCCCGTTG     200
GTGACGTAGT CAAGGGACAC GTCTTCAACG CTCTGGGTGA TTGCCTCGAT     250
GAGCCAGGTC TTGGCCGTGA CGGTGAGCAG TGGGGCATCC ACCGCGATCC     300
GCCACCTTTT GACCAGCTTG AGGGTAAGAC CGAGATTCTG GAAACCGGTA     350
TTAAGGTCAT CGACCTGCTG ACCCCGTATG TTAAGGGCGG CAAGATCGGC     400
CTGTTCGGTG GTGCTGGTGT GGGTAAGACC GTTCTTATCC AGGAAATGAT     450
CACCCGTATC GCTCGCGAGT TCTCCGGTAC CTCGGTGTTC GCAGGCGTGG     500
GTGAGCGTAC CCGTGAGGGC ACCGACCTCT TCCTGGAAAT GGAAGAGATG     550
GGCGTTCTCC AGGACACCGC TCTTGTGTTC GGCCAGATGG ACGAGCCTCC     600
AGGAGTTCGT ATGCGCGTGG CGCTGTCCGG CCTGACCATG GCGGAGTACT     650
TCCGCGATGT GCAGCACCAG GACGTGCTTC TGTTCATCGA CAACATCTTC     700
CGTTTCACCC AGGCAGGTTC CGAGGTTTCC ACCCTCCTAG GCCGCATGCC     750
TTCTGCCGTG GGTTACCAGC CAACGCTGGC AGACGAGATG GGTGTTCTGC     800
AGGAGCGTAT TACCTCCACA AAGGGTAA                             828
```

2) INFORMATION FOR SEQ ID NO: 326

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moellerella wisconsensis*
(B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

```
GATGCCGTAC CAAAAGTGTA CGATGCTCTT GAGGTTCTTA ACGGTAAAGA      50
AAAATTGGTG CTGGAAGTTC AGCAACAATT AGGCGGTGGT GTTGTTCGTT     100
GTATCGCAAT GGGTACATCA GATGGTTTAA GCCGCGGTTT AGAAGTTAAA     150
AATACAGATC ATCCGATCGA AGTTCCTGTC GGTGTTAAAA CGCTTGGCCG     200
TATCATGAAC GTGCTGGGTG ACCCAATCGA CATGAAAGGT GATATCGGCG     250
AAGAAGAACG CTGGTCAATT CACCGCGCAG CACCAAGCTA TGAAGATCTG     300
GCTAACTCAA CAGAACTTCT AGAAACAGGT ATCAAAGTTA TGGACCTGAT     350
TTGCCCATTC GCTAAAGGGG GTAAAGTGGG TCTGTTCGGT GGTGCGGGTG     400
TCGGTAAAAC AGTTAACATG ATGGAGCTTA TTCGTAATAT CGCGATTGAG     450
CACTCAGGTT ATTCTGTATT CGCGGGTGTT GGTGAACGTA CTCGTGAAGG     500
TAACGATTTC TACCATGAAA TGACAGACTC AAACGTTCTG GATAAAGTTT     550
CATTGGTTTA TGGCCAGATG AATGAGCCAC CAGGAAACCG TCTGCGTGTT     600
GCTCTGACTG GTCTGACTAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA     650
CGTACTGTTA TTCGTAGATA ATATTTATCG TTATACCTTA GCAGGGACAG     700
AAGTATCTGC ACTGCTGGGT CGTATGCCTT CAGCGGTGGG TTATCAGCCA     750
ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCGACTAA     800
GACCGGCTCT ATCACTTCCG TA                                   822
```

2) INFORMATION FOR SEQ ID NO: 327

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 854 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Branhamella catarrhalis*
(B) STRAIN: ATCC 43628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

CCGTGGCGAT GTCCCCCAAA TCTTTGATGC ACTTCATGTT GATGGTACTG 50
AAACCACCCT TGAAGTCCAA CAACAGTTAG GTGATGGTGT GGTGCGTACC 100
ATTGCCATGG GTTCTACCGA AGGCTTAAAG CGTGGCTTGC CTGTCTCTAA 150
TTCAGGTGCA CCCATTTCGG TACCAGTCGG TCAAGCAACA CTGGGTCGCA 200
TTATGGATGT CCTAGGTCGC CCAATCGATG AAGCAGGTCC GGTAAATGCT 250
GAACAAAAAT GGTCCATTCA TCGTGAAGCA CCAAGTTATG ATGAACAGTC 300
AAATAGTACA GAACTTTTAG AAACAGGCAT CAAAGTGATT GATTTGCTTT 350
GTCCATTTGC CAAAGGTGGT AAAGTCGGTC TGTTCGGTGG TGCTGGTGTT 400
GGTAAGACCG TTAACATGAT GGAGCTTATC AATAATATCG CCCTAAAACA 450
CTCAGGTCTG TCGGTTTTTG CTGGTGTGGG TGAGCGTACT CGTGAGGGTA 500
ATGACTTCTA CCATGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAT 550
TTTACTCAGT CAAAAGTTGC CATGGTTTAT GGTCAGATGA ATGAGCCACC 600
AGGAAACCGT CTGCGTGTTG CCTTAACTGG TTTGACCATG GCAGAGTATT 650
TCCGTGATGA AAAAGACGAA GCAACGGGCA AAGGCCGTGA TGTTCTGCTG 700
TTCGTTGATA ATATTTATCG TTACACATTG GCAGGTACTG AGGTATCAGC 750
ACTTTTAGGT CGTATGCCAT CTGCGGTAGG TTATCAGCCG ACTTTGGCCG 800
AAGAGATGGG CTTGCTACAA GAGCGTATCA CCTCCACCCA ATCAGGCTCA 850
ATTA 854

2) INFORMATION FOR SEQ ID NO: 328

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Moraxella osloensis*
(B) STRAIN: ATCC 19976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

CCGTCAAAGC GTACCAAGAA TTTATGATGC CTTAAAAGTT GAAGGCACAG 50
AAACTACATT AGAAGTACAA CAACAATTGG GTGATGGTAT CGTACGTACT 100
ATTGCCATGG GTTCTACTGA AGGTCTAAAA CGTGGTCTAC CAGTTAGCAA 150
CACTGGCGCA CCAATCTCTG TACCTGTGGG TAAAGGTACA CTAGGTCGTA 200

```
TCATGGACGT TTTAGGACAC CCAATCGATG AGGCAGGTCC GGTAGAGCAT      250
AGTAACACTT GGGCGATTCA CCGTGAAGCG CCAAGCTATG ATGAACAATC      300
AAACTCTACT GAACTTTTAG AAACCGGTAT TAAAGTAATT GACTTACTAT      350
GCCCATTTGC TAAAGGTGGT AAAGTCGGTC TGTTCGGTGG CGCGGGTGTT      400
GGTAAAACCG TTAACATGAT GGAACTTATC AATAACATCG CAAAAGCACA      450
CTCAGGTTTA TCGGTATTTG CTGGTGTAGG TGAGCGTACT CGTGAAGGTA      500
ATGACTTCTA CCACGAGATG AAAGACTCAA ACGTACTTGA TAAAGTTGCG      550
ATGGTGTATG GTCAGATGAA TGAGCCACCA GGAAACCGTT TACGTGTTGC      600
CCTGACAGGT TTAACCATGG CAGAATACTT CCGTGACGAA AAAGATGAAA      650
ACGGTAAAGG TCGTGACGTA TTATTGTTCG TTGACAATAT TTATCGTTAC      700
ACGCTAGCGG GTACCGAAGT ATCAGCATTA TTAGGTCGTA TGCCATCTGC      750
AGTAGGGTAT CAGCCAACGC TTGCAGAAGA GATGGGTGTA CTACAAGAAC      800
GTATTACTTC AACCCAATCA GGCTCTATTA C                          831
```

2) INFORMATION FOR SEQ ID NO: 329

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Morganella morganii* subsp. *morganii*
(B) STRAIN: ATCC 25830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

```
CGAATTTCCT CAGGATGCAG TACCGAAAGT GTACGATGCG CTTGAGGTAA       50
CAAATGGTAA AGAAAAACTG GTGCTGGAAG TTCAGCAGCA GTTAGGCGGC      100
GGGGTTGTCC GTTGTATCGC TATGGGTACA TCTGATGGTC TGAGCCGTAA      150
TCTGGAAGTA ACCGATTTAG GCCACCCGAT CGAAGTCCCT GTCGGCGTGA      200
AAACCTTAGG ACGTATCATG AACGTTCTGG GTGATCCGAT CGATATGAAA      250
GGTGACATCG GCGCAGAAGA AAAATGGTCT ATTCACCGTG CTGCACCAAC      300
ATACGAAGAA CTGTCTAACT CCCAGGAACT GCTGGAAACA GGTATCAAAG      350
TAATGGACCT GATCTGCCCG TTCGCGAAGG GTGGTAAAGT CGGTCTGTTC      400
GGTGGTGCGG GTGTGGGTAA AACCGTAAAC ATGATGGAAC TGATCCGTAA      450
CATCGCGATC GAGCACTCCG GTTACTCTGT ATTCGCAGGG GTCGGTGAGC      500
GTACCCGTGA AGGTAACGAC TTCTATCATG AAATGACAGA CTCCAACGTT      550
CTGGACAAAG TATCACTCGT GTACGGCCAG ATGAACGAGC CACCGGGAAA      600
CCGTCTGCGC GTTGCTCTGA CCGGTCTGAC CATGGCGGAA AAATTCCGTG      650
ATGAAGGCCG CGATGTACTG CTGTTCGTTG ATAACATCTA CCGTTATACC      700
CTGGCCGGTA CTGAAGTATC CGCGCTGTTA GGCCGTATGC CTTCAGCGGT      750
AGGTTACCAG CCGACACTGG CGGAAGAAAT GGGTGTGCTT CAGGAACGTA      800
TCACATCGAC CAAAACAGGC TCTATCACGT CTGTA                      835
```

2) INFORMATION FOR SEQ ID NO: 330

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pantoea agglomerans*
(B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

GACGCGGTAC CGCAAGTGTA CAGCGCCCTC GAGGTTATGA ATGGTGATGC 50
GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGC GTAGTACGTA 100
CCATCGCAAT GGGTACGTCT GACGGCCTGA AGCGTGGTCT GAGCGTCAAC 150
GACCTGCAGA AACCGATTCA GGTACCCGTC GGTAAAGCGA CCCTGGGCCG 200
TATCATGAAC GTTCTCGGCG AGCCAATCGA TATGAAAGGC GAGCTGAAAG 250
AAGAAGATGG CAGCGCAGTA GAGATCGCCT CTATTCACCG CGCAGCCCCT 300
TCTTATGAAG ATCAGTCTAA CTCGCAGGAA CTGCTGGAAA CCGGCATCAA 350
GGTTATCGAC CTGATGTGTC CGTTTGCTAA AGGCGGTAAA GTCGGTCTGT 400
TCGGTGGTGC GGGTGTAGGT AAAACCGTCA ACATGATGGA ACTGATCCGT 450
AACATCGCGG CTGAACACTC AGGTTACTCA GTGTTTGCCG GTGTGGGTGA 500
GCGTACTCGT GAGGGTAACG ACTTCTACCA CGAAATGACT GACTCTAACG 550
TTATCGATAA AGTTGCACTG GTCTATGGCC AGATGAACGA GCCGCCGGGT 600
AACCGTCTGC GCGTAGCACT GACCGGTCTG ACCATGGCGG AAAAATTCCG 650
TGATGAAGGT CGCGACGTTC TGCTGTTCAT CGATAACATC TACCGTTATA 700
CCCTGGCCGG TACAGAAGTT TCTGCACTGC TGGGTCGTAT GCCATCTGCG 750
GTAGGTTACC AGCCAACGCT GGCAGAAGAG ATGGGTGTGT TGCAGGAGCG 800
TATTACCTCC ACCAAGACCG GTTC 824

2) INFORMATION FOR SEQ ID NO: 331

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pantoea dispersa*
(B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

TATACAGCGC TCTCGAGGTA AAAAATGGTG ATGCTCGTCT GGTGCTGGAA 50
GTACAGCAGC AGCTGGGCGG TGGCGTGGTG CGTACCATCG CCATGGGTTC 100
TTCTGACGGC CTGAAGCGCG GTCTGGAAGT CACCGACCTG AAAAAACCTA 150
TCCAGGTTCC GGTTGGTAAA GCAACACTCG GCCGTATCAT GAACGTGCTG 200
GGTGAGCCAA TCGACATGAA AGGCGACCTG AAAGAAGAAG ACGGCAGCGC 250
TGTAGAGGTT TCCTCTATTC ATCGCGCAGC GCCTTCTTAT GAAGATCAGT 300
CAAACTCGCA GGAACTGCTG GAAACCGGCA TCAAGGTTAT CGACCTGATG 350
TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG GTGCGGGTGT 400
AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGGCTGAGC 450
ACTCAGGTTA TTCGGTCTTT GCCGGCGTGG GTGAGCGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GACGGACTCC AACGTTATCG ATAAAGTAGC 550
GCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGTAACCGT CTGCGCGTAG 600
CACTGACCGG TCTGACCATG GCGGAAAAAT TCCGTGATGA AGGCCGTGAC 650
GTTCTGCTGT TCATCGACAA CATCTACCGT TACACCCTGG CCGGTACAGA 700
GGTTTCTGCA CTGCTGGGTC GTATGCCATC GGCGGTAGGT TATCAGCCAA 750
CGCTGGCTGA AGAGATGGGT GTGCTGCAGG AGCGTATTAC CTCCACCAAG 800

ACCGGTTC

2) INFORMATION FOR SEQ ID NO: 332

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pasteurella multocida*
(B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

GATGCAGTAC CAAAAGTATA TGATGCCTTA AATGTTGAAA CAGGTTTAGT 50
ACTTGAAGTT CAACAACAAT TAGGTGGTGG TGTAGTTCGC TGTATCGCAA 100
TGGGATCATC TGATGGATTA AAACGCGGTT TAAGCGTAAC AAATACGAAT 150
AACCCAATTT CTGTTCCAGT GGGAACGAAA ACATTGGGTC GTATCATGAA 200
CGTATTGGGT GAACCAATCG ATGAGCAAGG TGAAATCGGT GCAGAAGAGA 250
ATTGGTCTAT TCACCGTGCG CCACCAAGTT ATGAAGAACA ATCTAACAGT 300
ACTGAACTTT TAGAAACGGG AATTAAAGTT ATCGACTTAG TTTGTCCGTT 350
TGCGAAAGGG GGTAAAGTAG GTTTATTCGG TGGTGCGGGT GTCGGTAAAA 400
CCGTCAATAT GATGGAATTA ATCCGTAACA TCGCAATTGA GCACTCAGGT 450
TACTCTGTCT TTGCGGGGGT AGGTGAGCGT ACGCGTGAAG GTAACGACTT 500
CTATCATGAG ATGAAAGACT CTAACGTATT AGATAAAGTG TCTCTTGTTT 550
ATGGTCAAAT GAACGAGCCA CCAGGTAACC GTTTACGTGT GGCATTAACA 600
GGCTTAACTA TGGCGGAAAA ATTCCGTGAT GAAGGTCGTG ATGTCTTATT 650
CTTCGTTGAT AATATTTATC GTTATACTCT TGCTGGTACA GAAGTTTCTG 700
CATTATTAGG TCGTATGCCA TCTGCGGTAG GTTATCAACC AACCCTTGCA 750
GAAGAAATGG GTGTTCTGCA AGAGCGTATT ACCTCAACCA AAACAGGTTC 800
TATTA 805

2) INFORMATION FOR SEQ ID NO: 333

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pragia fontium*
(B) STRAIN: ATCC 49100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

TTTCCTCAAG ACGCCGTACC AAAAGTGTAC GACGCGCTTG AAGTTCAGAA 50
CGATGCCAAG CTGGTGCTGG AAGTTCAACA ACAGCTCGGT GGTGGTGTCG 100
TTCGTTGTAT CGCAATGGGT ACTTCCGATG GCTTAAGCCG CGGTTTAAAA 150
GTGCTTGATT TAGAACATCC TATCGAAGTA CCGGTTGGTA CTGCGACGCT 200

GGGCCGTATT ATGAACGTGC TCGGTCAGCC AATCGATATG AAAGGCGATA 250
TTGGTGAAGA AGAGCGTTGG GCTATTCACC GTGAAGCACC AAGTTATGAA 300
GATTTATCTG GCGCCAATGA ACTGCTGGAA ACGGGTATCA AGGTTATCGA 350
CCTGATTTGT CCGTTTGCTA AAGGTGGTAA AGTTGGTCTG TTTGGTGGTG 400
CGGGTGTAGG TAAAACCGTA AACATGATGG AGCTGATTCG TAACATTGCG 450
ACTGAGCACT CAGGTTACTC CGTATTCGCC GGTGTAGGGG AACGTACCCG 500
TGAAGGTAAT GACTTCTACC ACGAAATGAC CGAATCAAAC GTACTGGATA 550
AAGTATCTCT GGTTTATGGC CAGATGAACG AGCCACCAGG AAACCGTCTG 600
CGCGTGGCGT TAACGGGTTT GACCATGGCT GAAAAATTCC GTGATGAAGG 650
TCGTGACGTT CTGTTATTTA TCGATAACAT TTATCGCTAT ACCTTAGCCG 700
GTACCGAAGT ATCAGCACTG TTGGGGCGTA TGCCATCAGC GGTAGGTTAT 750
CAGCCAACGT TAGCAGAAGA GATGGGTGTG TTGCAGGAAC GTATTACTTC 800
AACCAAAACC GGTTCAATCA CTTCTGTA 828

2) INFORMATION FOR SEQ ID NO: 334

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*
(B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

GTCCCTAAAG TATACGACGC TCTTGAGGTT ATGAATGGTA AAGAAAAACT 50
GGTGCTGGAA GTTCAGCAAC AGTTAGGCGG TGGTATCGTT CGTTGTATCG 100
CAATGGGTAC ATCAGACGGT TTAAGCCGTG GCTTAAAGGT TGAAGATTTA 150
GGCCACCCAA TTGAAGTACC AGTAGGTAAA GCGACTTTAG GACGTATCAT 200
GAACGTTCTG GGTACACCTA TTGATATGAA AGGTGAGATT GAAACCGAAG 250
AGCGTTGGTC AATCCACCGT GAAGCACCAA CTTACGAAGA GTTATCAAAC 300
TCTCAAGAAC TGCTTGAAAC CGGTATCAAA GTTATGGACT TAATCTGTCC 350
ATTTGCTAAA GGTGGTAAAG TCGGTCTGTT CGGTGGTGCG GGTGTTGGTA 400
AAACAGTTAA CATGATGGAA TTGATCCGTA ATATCGCGAT CGAGCACTCA 450
GGTTACTCTG TATTTGCTGG TGTTGGTGAG CGTACTCGTG AGGGTAACGA 500
CTTCTATCAT GAAATGACAG ATTCTAACGT TCTTGACAAA GTATCGTTAG 550
TTTACGGTCA GATGAATGAG CCACCAGGAA ACCGTCTGCG TGTTGCACTG 600
ACTGGTCTGA CTATGGCTGA GAAATTCCGT GATGAAGGCC GTGACGTACT 650
GTTATTCGTC GATAACATCT ATCGTTACAC CTTAGCCGGT ACAGAAGTAT 700
CAGCACTGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA ACCAACATTG 750
GCTGAAGAGA TGGGTGTTCT GCAAGAGCGT ATCACTTCAA CCAAAACAGG 800
TTCTATC 807

2) INFORMATION FOR SEQ ID NO: 335

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 811 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus vulgaris*
(B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

```
CCCTAAAGTA TACGACGCTC TTGAGGTTAT GAATGGTAAA GAGAAACTGG      50
TGCTAGAAGT TCAGCAACAG TTAGGCGGTG GTATCGTTCG TTGTATCGCA     100
ATGGGTACAT CAGACGGTTT AAGCCGTGGC TTAAAAGTTG AAAACTTAGG     150
CCACCCAATT GAAGTACCAG TAGGTAAAGC AACACTGGGA CGTATCATGA     200
ACGTTCTGGG TACACCTATC GATATGAAAG GTGATATTGC AACTGAAGAA     250
CGTTGGTCTA TTCACCGCGA AGCGCCAACC TATGAAGAGT TATCAAGCTC     300
TCAAGAACTA CTAGAAACCG GTATCAAAGT AATGGACTTA ATCTGTCCGT     350
TTGCTAAAGG TGGTAAAGTA GGTCTCTTCG GTGGTGCGGG TGTTGGTAAA     400
ACAGTTAACA TGATGGAATT GATCCGTAAC ATCGCGATTG AGCACTCAGG     450
TTATTCTGTA TTTGCAGGTG TTGGTGAGCG TACTCGTGAG GGTAACGACT     500
TCTATCATGA AATGACAGAT TCTAACGTTC TTGACAAAGT ATCGTTAGTT     550
TATGGTCAGA TGAATGAGCC ACCAGGAAAC CGTCTACGTG TAGCACTGAC     600
GGGTTTAACC ATGGCGGAAA AATTCCGTGA TGAAGGCCGT GACGTACTGT     650
TATTCGTCGA TAACATCTAT CGTTACACCT TAGCCGGTAC CGAAGTATCA     700
GCACTGTTAG GCCGTATGCC ATCAGCAGTA GGTTACCAAC CAACATTGGC     750
TGAAGAGATG GGTGTTCTGC AAGAACGTAT CACTTCAACC AAAACAGGTT     800
CAATCACCTC T                                              811
```

2) INFORMATION FOR SEQ ID NO: 336

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia alcalifaciens*
(B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

```
TCAAGATAAC GTACCAAAAG TGTACGATGC TCTTGAGGTT ATTAACGGTA      50
AAGAAAAACT GGTGTTGGAA GTTCAACAAC AGTTAGGTGG TGGTGTTGTC     100
CGTTGTATCG CAATGGGTAC ATCAGATGGT CTGAGCCGTG GTTTAGAAGT     150
TGTAAACTTA GAGCACCCAA TCGAAGTACC AGTCGGTAAA GCAACTCTGG     200
GACGTATCAT GAACGTTCTG GGTGAACCAA TCGACATGAA AGGTGATATC     250
GGCGAAGAAG AGCGCTGGTC TATTCACCGT GCTGCACCAA GCTACGAAGA     300
ATTAGCTAAC TCAACTGAAC TGCTGGAAAC CGGTATCAAA GTAATGGACT     350
TAATCTGTCC ATTCGCGAAA GGTGGTAAAG TAGGTCTGTT CGGTGGTGCG     400
GGTGTTGGTA AAACCGTAAA CATGATGGAA CTGATCCGTA ACATCGCGAT     450
TGAGCACTCA GGTTACTCAG TGTTCGCTGG TGTTGGTGAG CGTACCCGTG     500
AAGGTAACGA CTTCTATCAT GAAATGACAG ACTCAAACGT TCTGGATAAA     550
GTATCACTGG TTTATGGCCA GATGAACGAG CCACCAGGAA ACCGTCTGCG     600
TGTTGCGCTG ACTGGTCTGA CTATGGCTGA AAAATTCCGT GACGAAGGTC     650
GTGACGTACT GCTGTTCGTT GACAACATTT ATCGTTATAC ACTGGCAGGT     700
ACTGAAGTAT CAGCACTGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA     750
ACCAACGCTG GCGGAAGAGA TGGGTGTTCT TCAAGAACGT ATTACCTCAA     800
```

CTCAAA

2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia rettgeri*
(B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA 50
CGGTAAAGAA ACACTGGTGC TGGAAGTTCA GCAACAGTTA GGCGGTGGTG 100
TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150
GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC 200
TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250
ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300
GAAGAGTTAG CTAACTCAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350
GGACTTAATC TGTCCATTCG CGAAAGGTGG TAAAGTTGGT CTGTTCGGTG 400
GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAACTGAT CCGTAACATC 450
GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTTG GTGAGCGTAC 500
TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550
ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600
CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650
AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACACTGG 700
CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750
TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800
CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia rustigianii*
(B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50
ACTGGTGTTG GAAGTTCAGC AGCAGTTAGG CGGTGGTGTT GTCCGTTGTA 100
TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150
TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

```
CATGAACGTT CTGGGTGACC CTATTGATAT GAAAGGTGAT ATCGGCGAAG      250
AAGAGCGCTG GTCTATTCAC CGTTCAGCGC CAAGCTATGA AGAATTAGCT      300
AACTCAACAG AACTGCTAGA AACCGGTATC AAAGTAATGG ACTTAATCTG      350
TCCATTCGCG AAAGGTGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTTG      400
GTAAAACAGT AAACATGATG GAACTGATCC GTAACATCGC GATTGAGCAC      450
TCAGGTTACT CAGTATTCGC TGGTGTTGGT GAGCGTACCC GTGAAGGTAA      500
CGACTTCTAT CATGAAATGA CTGATTCTAA CGTTCTGGAT AAAGTATCAC      550
TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGTGTTGCG      600
CTGACTGGTC TGACTATGGC TGAAAAATTC CGTGACGAAG GTCGTGACGT      650
ACTGCTGTTC GTTGACAACA TTTATCGTTA TACACTGGCA GGTACTGAAG      700
TATCAGCACT GTTAGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCAACA      750
TTGGCAGAAG AGATGGGTGT TCTACAAGAA CGTATCACTT CTACCAAAAC      800
CGGTTCTATC AC                                              812
```

2) INFORMATION FOR SEQ ID NO: 339

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Providencia stuartii*
(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

```
TCAAGATGCA GTACCAAAAG TGTACGATGC GCTTGAGGTT GTTAACGGTA       50
AAGAAAAACT GGTGCTGGAA GTTCAGCAAC AGTTAGGCGG TGGTGTTGTC      100
CGTTGTATCG CAATGGGTAC ATCAGATGGC CTAAGCCGTG GTTTAGAAGT      150
TAAAAATTTA GAACACCCAA TTGAAGTACC AGTAGGTAAA GCAACACTCG      200
GACGTATCAT GAACGTTCTG GGTGACCCTA TTGATATGAA AGGTGATATC      250
GGCGAAGAAG AGCGTTGGTC TATTCACCGC GCTGCACCAA GCTACGAAGA      300
GCTATCGAGC TCAACTGAAC TGCTAGAGAC AGGTATCAAA GTCATGGACT      350
TGATCTGTCC ATTCGCGAAA GGTGGTAAAG TTGGTCTGTT CGGTGGTGCG      400
GGTGTTGGTA AAACGGTAAA CATGATGGAA CTTATCCGTA ACATCGCGAT      450
TGAGCACTCA GGTTACTCAG TATTCGCAGG TGTTGGTGAG CGTACCCGTG      500
AAGGTAACGA CTTCTATCAT GAAATGACAG ATTCAAACGT TCTTGACAAA      550
GTATCACTGG TTTATGGTCA GATGAATGAG CCACCAGGAA ACCGTCTACG      600
CGTAGCATTG ACTGGTTTGA CTATGGCTGA GAAATTCCGT GACGAAGGCC      650
GTGATGTTCT GTTGTTCGTG GATAACATCT ATCGTTATAC ACTGGCAGGT      700
ACAGAAGTAT CGGCTCTGTT AGGTCGTATG CCATCAGCAG TAGGTTATCA      750
GCCAACATTG GCAGAAGAGA TGGGTGTTCT TCAAGAACGT ATCACTTCTA      800
CTAAGACAGG TTCTATCAC                                       819
```

2) INFORMATION FOR SEQ ID NO: 340

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 907 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Psychrobacter phenylpyruvicus*
(B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

```
AACCGCACTG ACGTGCCTCA AATTTATGAC GCGTTAGTTG TAGATGGTAC      50
CGAAACCACC CTAGAAGTTC AGCAGCAGCT GGGCGATGGT GTGGTACGTA     100
CTATTGCAAT GGGATCTACT GAAGGTCTTA AGCGTGGTTT ACCAGTAACA     150
AACACTGGTG CCCCAATTAC AGTTCCAGTA GGTGATGCGA CTTTAGGTCG     200
TATTATGGAC GTTTTAGGTC GTCCAATTGA CGAACAAGGT CCAGTTAATT     250
CTGAAGACCA TTGGTCAATC CACCGTCAAG CGCCATCATA TGATGAGCAA     300
GCTAACAGTA CTGACCTATT AGAGACAGGT ATTAAAGTAA TTGACTTACT     350
TTGTCCGTTC GCTAAAGGGG GTAAAGTTGG TCTGTTCGGT GGTGCCGGTG     400
TTGGTAAAAC CGTAAACATG ATGGAATTGA TTAATAACAT CGCTCTTAAG     450
CACTCAGGTT TATCAGTATT CGCTGGTGTG GGTGAGCGTA CTCGTGAAGG     500
TAACGACTTC TACCACGAGA TGCAAGAAGC GGGTGTTGTT GACGTTGAAA     550
ACTTCACCAA CTCAAAAGTT GCGATGGTTT ATGGTCAGAT GAATGAGCCA     600
CCAGGTAACC GTTTACGTGT TGCGTTAACC GGTCTGACTA TGGCTGAGTA     650
CTTCCGTGAT CAAAAAGATG AAAACGGTAA AGGTAAAGAC GTTCTATTAT     700
TCGTTGATAA CATCTACCGC TACACGCTAG CCGGTACTGA AGTATCAGCA     750
CTTCTAGGTC GTATGCCATC AGCAGTAGGT TATCAGCCAA CACTAGCGGA     800
AGAGATGGGT GTACTACAAG AGCGTATTAC TTCAACTCAG ACTGGTTCTA     850
TTACTTC                                                   907
```

2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Rahnella aquatilis*
(B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

```
GTTCCCTCAG GATGCAGTAC CGAACGTGTA CAATGCTCTT GAGGTAGAAA      50
ACGGTACCTC CAAACTGGTG CTGGAAGTTC AGCAACAGTT AGGCGGCGGC     100
GTTGTTCGTT GTATCGCAAT GGGTACCTCA GACGGCCTGC GTCGCGGTCT     150
GAAAGTGAAC AACCTGGAAC ACCCAATTGA AGTACCGGTA GGTAAAGCGA     200
CTCTGGGTCG TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAAGGT     250
GAAATCGGCG AAGAAGAACG TCGTGCTATT CACCGTGCTG CGCCTTCTTA     300
TGAAGAGCTG GCAAACTCCC AGGAATTGCT GGAAACCGGT ATCAAAGTTA     350
TGGACCTGAT GTGTCCGTTC GCTAAGGGCG GTAAAGTTGG TCTGTTCGGT     400
GGTGCGGGTG TAGGTAAAAC TGTGAACATG ATGGAGCTGA TCCGTAACAT     450
TGCGATCGAG CACTCCGGTT ATTCTGTGTT TGCAGGCGTG GGTGAACGTA     500
CTCGTGAGGG TAACGACTTC TACCACGAAA TGACTGATTC CAACGTTATC     550
GACAAAGTTT CCCTGGTGTA TGGCCAGATG AATGAGCCAC CAGGTAACCG     600
TCTGCGCGTT GCACTGACCG GCCTGACCAT GGCGGAAAAA TTCCGTGATG     650
AAGGTCGTGA CGTACTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG     700
GCCGGTACCG AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG     750
```

TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA 800
CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
(B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCCTAC 300
GAAGAGTTGT CAAACTCTCA GGAACTGCTG GAAACCGGTA TAAAAGTTAT 350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
TAYCASCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAAA ACCGGTTCTA TCAC 824

2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 820 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Choleraesuis
(B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100

CCATCGCGAT GGGGTCTTCT GACGGTCTGC GTCGCGGTCT GGATGTAAAA 150
GATCTCGAAC ACCCGATCGA AGTCCCGGTA GGTAAAGCCA CGCTGGGTCG 200
TATCATGAAC GTCCTGGGCG AACCGGTCGA CATGAAAGGC GAGATCGGCG 250
AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA CGAAGAGTTG 300
TCAAACTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
GTGTCCGTTC GCGAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400
TAGGTAAAAC CGTAAACATG ATGGAGCTTA TTCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCAGTGTT TGCGGGCGTA GGGGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GATAAAGTAT 550
CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
GCACTGACCG GCCTGACCAT GGCGGAGAAA TTCCGTGACG AAGGTCGTGA 650
TGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
AAGTATCCGC ACTGCTGGGC CGTATGCCTT CCGCAGTAGG TTACCAGCCG 750
ACTCTGGCGG AAGAGATGGG CGTTCTGCAG GAACGTATCA CCTCCACCAA 800
AACCGGTTCT ATCACCTCCG 820

2) INFORMATION FOR SEQ ID NO: 344

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
(B) STRAIN: ATCC 43973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC 200
GCTGGGTCGT ATCATGAACG TCCTGGGTGA ACCGGTCGAT ATGAAAGGCG 250
AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCGTCCTAC 300
GAAGAGTTGT CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT 350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
TATCAGCCGA CTCTGGCTGA AGAAATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAAA ACCGGTTCTA TCACCTCCGT A 831

2) INFORMATION FOR SEQ ID NO: 345

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

```
TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA      50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA     100
TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG     150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC     200
GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG     250
AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCTGC GCCGTCCTAC     300
GAAGAGTTGT CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT     350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG     400
GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC     450
GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC     500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG     550
ATAAAGTATC CCTGGTGTAT GGTCAGATGA ACGAGCCGCC GGGAAACCGT     600
CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA     650
AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG     700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT     750
TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC     800
CTCCACCAAG ACCGGTTCTA TCACCTCCGT A                         831
```

2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

```
TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA     100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG     150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC     200
GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG     250
AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCGTCCTAT     300
GAAGAGTTGT CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT     350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG     400
GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC     450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC     500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG     550
ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT     600
CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA     650
AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG     700
```

CCGGTACGGA AGTTTCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
TATCAGCCAA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAAA ACCGGTTCTA TCACCTCCG 829

2) INFORMATION FOR SEQ ID NO: 347

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Paratyphi A
(B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA 50
GCTGGTGCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATC GTGCGTACCA 100
TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAAAGAT 150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCTACGC TGGGTCGTAT 200
CATGAACGTC CTGGGCGAAC CGGTCGACAT GAAAGGCGAG ATCGGCGAAG 250
AAGAGCGTTG GGCGATTCAC CGCGCAGCGC CTTCCTACGA AGAGTTGTCA 300
AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTTATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CATGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC 550
TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA 600
CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT 650
ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
TATCCGCACT GCTGGGTCGT ATGCCTTCCG CGGTAGGTTA CCAGCCGACT 750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC 800
CGGTTCTATC ACCTCCG 817

2) INFORMATION FOR SEQ ID NO: 348

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Paratyphi B
(B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

```
GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA      50
GCTGGTGCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATT GTGCGTACCA     100
TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAAAGAT     150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCCACGC TGGGTCGTAT     200
CATGAACGTC CTGGGCGAAC CGGTCGACAT GAAAGGCGAG ATCGGCGAAG     250
AAGAGCGTTG GGCGATTCAC CGCGCAGCGC CTTCCTACGA AGAGTTGTCA     300
AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG     350
TCCGTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTGG     400
GTAAAACCGT AAACATGATG GAGCTTATCC GTAACATCGC GATCGAGCAC     450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA     500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC     550
TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA     600
TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT     650
ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG     700
TATCCGCACT GCTGGGCCGT ATGCCTTCCG CAGTAGGTTA CCAGCCGACT     750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC     800
CGGTTC                                                    806
```

2) INFORMATION FOR SEQ ID NO: 349

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

```
TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA     100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGKGGTCTG     150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC     200
GCTGGGCCGT ATCATGAACG TACTGGGCGA ACCGGTCGAC ATGAAAGGCG     250
AGATTGGTGA AGAAGAGCGT TGGGCTATTC ACCGTGCTGC GCCGTCCTAC     300
GAAGAGTTGT CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT     350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG     400
GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTCAT CCGTAACATC     450
GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC     500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG     550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT     600
CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA     650
AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG     700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT     750
TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC     800
CTCCACTAAA ACCGGTTCTA TCACCTCCGT A                         831
```

2) INFORMATION FOR SEQ ID NO: 350

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Typhi
(B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

```
TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA     100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG     150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC     200
GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAC ATGAAAGGCG     250
AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCAGC GCCTTCCTAC     300
GAAGAGTTAT CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT     350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG     400
GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC     450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC     500
TCGTGAGGGT AACGACTTCT ACCATGAAAT GACCGACTCC AACGTTATCG     550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT     600
CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAAT TCCGTGACGA     650
AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG     700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT     750
TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC     800
CTCCACCAAG ACCGGTTCTA TCA                                  823
```

2) INFORMATION FOR SEQ ID NO: 351

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Typhimurium
(B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

```
TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA     100
TTGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG     150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC     200
GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAC ATGAAAGGCG     250
AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCAGC GCCTTCCTAC     300
GAAGAGTTGT CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT     350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG     400
GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC     450
GCGATCGAGC ACTCCGGTTA CTCAGTGTTT GCGGGCGTAG GGGAACGTAC     500
```

```
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
CTGCGCGTTG CATTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGACGA      650
AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
CCGGTACGGA AGTATCCGCA CTGCTGGGCC GTATGCCTTC CGCAGTAGGT      750
TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
CTCCACCAAA ACCGGTTCTA TCACCTCCGT A                          831
```

2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Virchow
(B) STRAIN: ATCC 51955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

```
GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA       50
GCTGGTGCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATC GTGCGTACCA      100
TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAAAGAT      150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCCACGC TGGGTCGTAT      200
CATGAACGTC CTGGGCGAAC CGGTCGACAT GAAAGGCGAG ATCGGCGAAG      250
AAGAGCGTTG GGCGATTCAC CGCGCAGCAC CTTCCTACGA AGAGTTGTCA      300
AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG      350
TCCGTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC      450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGG GAACGTACTC GTGAGGGTAA      500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTCTCCC      550
TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA      600
TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT      650
ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
TATCCGCACT GCTGGGCCGT ATGCCTTCCG CAGTAGGTTA CCAGCCGACT      750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC      800
CGGTTCTATC                                                 810
```

2) INFORMATION FOR SEQ ID NO: 353

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 820 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia ficaria*
(B) STRAIN: ATCC 33105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

GATGCCGTAC CAAAAGTGTA CGATGCCCTT GAGGTAGAAA ACGGTACCGA 50
GAAACTGGTG CTGGAAGTTC AGCAGCAGCT GGGCGGTGGC GTCGTTCGCT 100
GTATCGCAAT GGGGACCTCT GACGGTCTGC GTCGCGGTCT GAAAGTGAAC 150
AACCTGGAAC ACCCGATTGA AGTGCCGGTG GGTAAAGCTA CCCTGGGCCG 200
TATCATGAAC GTATTGGGCG AACCAATCGA CATGAAAGGC GAGATCGGCG 250
AAGAAGAGCG TTGGGCGATT CACCGTCCTG CGCCAAGCTA CGAAGAGCTG 300
TCCAACTCCC AGGACCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
TTGTCCGTTC GCCAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGCG 400
TGGGCAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ATTCCGTGTT TGCGGGCGTG GGCGAGCGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGAACGACTC CAACGTTCTG GACAAAGTAT 550
CCCTGGTTTA CGGCCAGATG AACGAGCCGC CGGGTAACCG TCTGCGCGTT 600
GCATTGACCG GCCTGACCAT GGCGGAGAAA TTCCGTGACG AAGGCCGCGA 650
CGTTCTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG GCCGGTACCG 700
AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CCGCGGTAGG TTATCAGCCA 750
ACGCTGGCGG AAGAGATGGG CGTTCTGCAA GAACGTATCA CCTCGACCAA 800
GACCGGTTCC ATCACCTCCG 820

2) INFORMATION FOR SEQ ID NO: 354

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia fonticola*
(B) STRAIN: ATCC 29844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

GATGCCGTAC CGAAAGTGTA CAACGCTCTT GAGGTTGCAA ACGGCACCGA 50
GAAATTGGTG CTGGAAGTTC AGCAACAGCT GGGTGGCGGC GTGGTTCGCT 100
GTATCGCAAT GGGGACCTCA GACGGTCTGC GTCGTGGTCT GGCCGTAACC 150
GACCTGCAGC ACCCAATTGA AGTACCGGTA GGTAAAGCTA CCCTGGGCCG 200
TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GACATCGGCG 250
AAGAAGAACG TTGGGCTATT CACCGCCCTG CGCCAAGCTA CGAAGAGCTG 300
TCCAGCTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
CTGCCCGTTC GCCAAGGGTG GTAAAGTTGG TCTGTTCGGT GGTGCTGGTG 400
TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ATTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGATTC CAACGTACTG GACAAAGTTT 550
CCCTGGTTTA CGGCCAGATG AACGAGCCAC CAGGTAACCG TCTGCGCGTT 600
GCGCTGACCG GCCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
CGTACTGCTG TTCGTCGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700
AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCTACCAA 800
GACTGGTTCA ATCACC 816

2) INFORMATION FOR SEQ ID NO: 355

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia grimesii*
(B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA 50
TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT 100
GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA 150
GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAAGCTA CTCTGGGCCG 200
TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG 250
AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTTG 300
GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
CTGCCCGTTC GCCAAGGGTG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400
TTGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ATTCTGTGTT TGCGGGCGTG GGTGAGCGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGAACGACTC CAACGTACTG GACAAAGTAT 550
CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600
GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA 650
CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700
AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCTACCAA 800
GACTGGTTCA ATCACCTCCG TA 822

2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia liquefaciens*
(B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

ATGCCGTACC AAAAGTGTAC AATGCTCTTG AGGTAGAAAA CGGTACCGAG 50
AAGCTGGTGC TGGAAGTTCA GCAGCAGTTG GGCGGTGGCG TAGTTCGCTG 100
TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG 150
ATCTGGAACA CCCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT 200
ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA 250
AGAAGAACGT TGGGCGATTC ACCGTCCAGC GCCAAGCTAC GAAGATTTGT 300
CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT 350
TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG GTGCTGGTGT 400
TGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450

ACTCCGGTTA TTCCGTGTTT GCAGGCGTGG GTGAGCGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GAACGACTCC AACGTACTGG ACAAAGTATC 550
CCTGGTTTAC GGCCAGATGA ACGAGCCACC GGGTAACCGT CTGCGCGTTG 600
CTCTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGACGA AGGCCGCGAC 650
GTTCTGCTGT TCGTTGATAA CATTTACCGT TATACCCTGG CCGGTACCGA 700
AGTGTCCGCA CTTCTGGGCC GTATGCCATC TGCGGTAGGT TATCAGCCAA 750
CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC CTCTACCAAG 800
ACCGGTTCTA TCACTTCCG 819

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia marcescens*
(B) STRAIN: ATCC 13880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

TCAGGATGCC GTACCGAAAG TGTACGACGC CCTTGAGGTA GAAAACGGCA 50
CCGAAAAACT GGTGTTGGAA GTTCAGCAAC AGCTGGGCGG TGGCGTGGTT 100
CGCTGTATCG CAATGGGGAC CTCCGACGGT CTGCGTCGCG GTCTGAAAGT 150
GAACAACCTG GACCACCCGA TTGAAGTGCC GGTGGGTAAA GCTACCCTGG 200
GTCGTATCAT GAACGTATTG GGTCAACCGA TCGACATGAA AGGCGACATC 250
GGCGAAGAAG AGCGTTGGGC GATTCACCGC GCGGCGCCAA GCTACGAAGA 300
GCTGTCAAGC TCTCAGGAAC TGCTGGAAAC CGGTATCAAG GTAATGGACC 350
TGATTTGTCC GTTCGCCAAG GGCGGTAAAG TCGGTCTGTT CGGCGGTGCG 400
GGCGTAGGTA AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT 450
CGAGCACTCC GGTTATTCCG TGTTTGCGGG CGTGGGCGAG CGTACTCGTG 500
AGGGTAACGA CTTCTACCAC GAAATGACCG ACTCCAACGT TCTGGACAAA 550
GTATCCCTGG TTTACGGCCA GATGAACGAG CCACCAGGTA ACCGTCTGCG 600
CGTTGCGCTG ACCGGTCTGA CCATGGCGGA GAAATTCCGT GACGAAGGCC 650
GTGACGTTCT GCTGTTCGTT GACAACATCT ACCGTTACAC CCTGGCCGGT 700
ACCGAAGTGT CCGCACTTCT GGGCCGTATG CCATCCGCGG TAGGTTATCA 750
GCCAACGCTG GCGGAAGAGA TGGGCGTTCT GCAAGAACGT ATCACCTCGA 800
CCAAG 805

2) INFORMATION FOR SEQ ID NO: 358

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia odorifera*
(B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

```
GATGCCGTAC CAAAAGTGTA CGATGCCCTT GAGGTAGAAA ACGGTACCGA      50
AACTCTGGTG CTGGAAGTTC AGCAGCAGCT GGGCGGTGGC GTGGTTCGTT     100
GTATCGCTAT GGGCACCTCC GACGGTTTGC GTCGCGGCCT GAAAGTGAAC     150
GATCTGCAAC ACCCAATCGA AGTCCCGGTT GGCAAGGCAA CGCTGGGTCG     200
TATCATGAAC GTATTGGGTC AACCAATCGA CATGAAAGGC GACATCGGCG     250
AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCAAGCTA CGAAGAACTG     300
TCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTTA TGGACCTGAT     350
CTGCCCGTTT GCCAAGGGTG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG     400
TTGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG     450
CACTCCGGTT ATTCAGTGTT TGCGGGCGTG GGTGAGCGTA CTCGTGAGGG     500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTACTG GACAAGGTTT     550
CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT     600
GCGCTGACCG GTCTGACCAT GGCCGAGAAA TTCCGTGACG AAGGTCGTGA     650
CGTTCTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG GCCGGTACCG     700
AAGTGTCTGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA     750
ACGCTGGCGG AAGAGATGGG CGTTCTGCAA GAACGTATCA CCTCGACCAA     800
GACCGGTTCT ATCACCTCCG TA                                   822
```

2) INFORMATION FOR SEQ ID NO: 359

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 805 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Serratia plymuthica*
- (B) STRAIN: ATCC 183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

```
GTGTACAACG CTCTTGAGGT AGAAAACGGT GCCAATAAGC TGGTGCTGGA      50
AGTTCAGCAA CAGCTGGGCG GTGGCGTGGT TCGCTGTATC GCGATGGGGA     100
CCTCTGATGG TCTGCGTCGC GGTCTGAAAG TGATCGACCT GGATCACCCG     150
ATTGAAGTAC CGGTAGGTAA AGCTACCCTG GGCCGTATCA TGAACGTATT     200
GGGTGAACCA ATCGACATGA AAGGCGACAT CGGCGAAGAA GAACGTTGGG     250
CAATTCACCG TCCAGCGCCA AGCTACGAAG ATTTGGCCAA CTCCCAGGAT     300
CTGCTGGAAA CCGGTATCAA GGTTATGGAC CTGATCTGTC CGTTCGCTAA     350
GGGCGGTAAA GTGGGTCTGT TCGGCGGTGC GGGCGTGGGT AAAACCGTAA     400
ACATGATGGA GCTGATCCGT AACATCGCGA TCGAACACTC CGGTTATTCC     450
GTGTTTGCGG GCGTGGGTGA GCGTACTCGT GAGGGTAACG ACTTCTACCA     500
CGAAATGAAC GACTCCAACG TACTGGACAA AGTATCCCTG GTTTACGGCC     550
AGATGAACGA GCCACCGGGT AACCGTCTGC GCGTTGCTCT GACCGGTCTG     600
ACCATGGCGG AGAAATTCCG TGACGAAGGC CGCGACGTTC TGCTGTTCGT     650
TGATAACATC TACCGTTATA CCCTGGCCGG TACCGAAGTG TCCGCACTTC     700
TGGGCCGTAT GCCATCTGCG GTAGGTTATC AGCCAACGCT GGCGGAAGAG     750
ATGGGCGTTC TGCAAGAACG TATCACCTCT ACCAAGACCG GTTCTATCAC     800
CTCCG                                                     805
```

2) INFORMATION FOR SEQ ID NO: 360

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia rubidaea*
(B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA 50
CGGTAACGAA AAACTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGCG 100
TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG 150
AAAGTTAACG ACCTCGAGCA CCCAATCGAA GTGCCAGTTG GTAAAGCAAC 200
GCTGGGTCGT ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG 250
ACATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCAAGCTAC 300
GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT 350
GGACCTGATC TGCCCGTTCG CCAAGGGTGG TAAAGTTGGT CTGTTCGGTG 400
GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC 450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC 500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG 550
ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT 600
CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG 700
CCGGTACCGA AGTGTCCGCA CTGCTCGGCC GTATGCCATC TGCGGTAGGT 750
TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC 800
CTCGACCAAG ACCGGTTCAA TCACCTCCGT A 831

2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas putida*
(B) STRAIN: LCDC D7172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

CCGTAAACAT GATGGAACTG ATCCGTAACA TCGCCATCGA GCACAGCGGT 50
TATTCCGTGT TCGCCGGTGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 100
CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT 150
ACGGTCAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC 200
GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT 250
GTTCGTCGAC AACATCTATC GTTACACCCT GGCCGGTACC GAAGTATCCG 300
CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT 350
GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTC 400
GATCAC 406

2) INFORMATION FOR SEQ ID NO: 362

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella boydii*
(B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

TTCCCTCAGG ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA 50
TGGTAATGAG CGTCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA 100
TCGTGCGTAC CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG 150
GATGTAAAAG ACCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC 200
TCTGGGCCGT ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG 250
AGATCGGTGA AGAAGAGCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAC 300
GAAGAGCTGT CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT 350
CGACCTGATG TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG 400
GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC 450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT 600
CTGCGCGTTG CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA 650
AGGTCGTGAC GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG 700
CCGGTACGGA AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT 750
TATCAGCCGA CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAAA ACTGGTTCTA TCACCTCCGT A 831

2) INFORMATION FOR SEQ ID NO: 363

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 802 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella dysenteriae*
(B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

GCCGTACCGC GCGTGTACGA TGCTCTTGCG GTGCAAAATG GTAATGAGCG 50
TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
TCGCAATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAAAGAC 150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT 200
CATGAACGTA CTGGGTGAAC CGGTCGACAT GAAAGGCGAG ATCGGTGAAG 250

AAGAGCGTTG GGCTATTCAC CGCGCAGCAC CTTCCTACGA AGAGCTGTCA 300
AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
TCCGTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTCATTC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT 600
CTGACCGGTC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT 650
TCTGCTGTTC GTTGACAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
TATCCGCACT GCTGGGCCGT ATGCCTTCAG CGGTAGGTTA TCAGCCGACC 750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC 800
CG 802

2) INFORMATION FOR SEQ ID NO: 364

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella flexneri*
(B) STRAIN: ATCC 12022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA TGGTAATGAG 50
CGTCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA TCGTGCGTAC 100
CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG GATGTAAAAG 150
ACCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC TCTGGGCCGT 200
ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG AGATCGGTGA 250
AGAAGAGCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAC GAAGAGCTGT 300
CAAACTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG 350
TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG GTGCGGGTGT 400
AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC GCGATCGAGC 450
ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC 550
CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC 650
GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG CCGGTACGGA 700
AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT TATCAGCCGA 750
CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAAA 800
ACTGGTTCTA TCACCTCCG 819

2) INFORMATION FOR SEQ ID NO: 365

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 802 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella sonnei*
(B) STRAIN: ATCC 29930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

GTACCGCGCG TGTACGATGC TCTTGAGGTG CAAAATGGTA ATGAGCGTCT 50
GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATCGTG CGTACCATCG 100
CAATGGGTTC CTCCGACGGT CTGCGTCGCG GTCTGGATGT AAAAGACCTC 150
GAACACCCGA TCGAAGTCCC GGTAGGTAAA GCGACTCTGG GCCGTATCAT 200
GAACGTACTG GGTGAACCGG TCGACATGAA AGGCGAGATC GGTGAAGAAG 250
AGCGTTGGGC GATTCACCGC GCAGCACCTT CCTACGAAGA GCTGTCAAAC 300
TCTCAGGAAC TGCTGGAAAC CGGTATCAAA GTTATCGACC TGATGTGTCC 350
GTTCGCTAAG GGCGGTAAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA 400
AAACCGTAAA CATGATGGAG CTCATTCGTA ACATCGCGAT CGAGCACTCC 450
GGTTACTCTG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGACAAA GTATCCCTGG 550
TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCTCTG 600
ACCGGTCTGA CCATGGCTGA GAAATTCCGT GACGAAGGTC GTGACGTTCT 650
GCTGTTCGTT GACAACATCT ATCGTTACAC CTGGCCGGT ACGGAAGTAT 700
CCGCACTGCT GGGCCGTATG CCTTCAGCGG TAGGTTATCA GCCGACCCTG 750
GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAAACTGG 800
TT 802

2) INFORMATION FOR SEQ ID NO: 366

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

TAACGCCTTG GTTATTGATG TGCCTAAAGA AGAAGGTACA ATACAACTAA 50
CATTAGAAGT TGCGCTGCAA TTAGGTGACG ACGTTGTTCG TACAATTGCG 100
ATGGATTCAA CTGATGGTGT CCAAAGAGGC ATGGATGTAA AAGATACAGG 150
CAAAGAAATT AGTGTACCTG TTGGTGATGA AACATTAGGT CGTGTATTTA 200
ATGTACTAGG TGAAACAATT GACCTTAAAG AAGAAATTAG TGATTCTGTT 250
CGCCGCGATC CTATCCATCG TCAAGCACCA GCATTCGATG AACTTTCAAC 300
AGAAGTTCAA ATTTTAGAAA CAGGTATTAA AGTAGTAGAT TTACTAGCAC 350
CTTATATTAA AGGTGGTAAA ATCGGATTGT TCGGTGGTGC CGGTGTAGGT 400
AAAACAGTAT TAATCCAAGA ATTAATTAAC AACATCGCTC AAGAGCACGG 450
TGGTATTTCT GTATTCGCCG GTGTAGGTGA ACGTACTCGT GAAGGTAACG 500
ATTTATACTT CGAAATGAGT GATAGTGGTG TAATTAAGAA AACAGCCATG 550
GTATTCGGGC AAATGAATGA GCCACCTGGT GCACGTATGC GTGTTGCATT 600
ATCTGGTTTA ACAATGGCTG AATATTTCCG TGACGAACAA GGTCAAGACG 650
TATTATTATT CATCGATAAC ATTTTCAGAT TTACACAAGC TGGTTCTGAG 700
GTATCTGCAT TATTAGGTCG TATGCCTTCT GCAGTAGGTT ACCAACCAAC 750
ACTTGCTACT GAAATGGGAC AATTACAAGA ACGTA 785

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus auricularis*
(B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG AAGTGCCTAA TATTAATAAC GCCTTAGTAC TCGATGTTGA 50
AAGAGAAGAC GGAACAGTGT CTTTAACTTT AGAAGTAGCT TTACAATTAG 100
GCGATGACGT TGTTCGTACC ATTGCAATGG ATTCAACTGA TGGTGTTAAA 150
CGTGGTAACG AAGTCAAAGA TACTGGTAAT AGCATTAGCG TACCAGTCGG 200
AGACGAAACT TTAGGACGTG TCTTCAACGT TCTAGGTGAA ACAATTGATT 250
TAGAAGATAA ACTTGATGAT TCTGCGCGAC GTGACCCTAT ACATAGAGAA 300
GCGCCAGCGT TTGATCAATT ATCAACTCAA GTTGAAATTT TAGAAACAGG 350
AATTAAAGTT GTTGACTTAT TAGCACCTTA TATTAAAGGT GGTAAAGTTG 400
GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTTTAAT CCAAGAATTA 450
ATCAACAACA TCGCTCAAGA ACACGGTGGT ATTTCAGTCT TTGCCGGTGT 500
AGGTGAACGT ACACGTGAAG GTAACGACTT GTACTATGAA ATGAGCGACA 550
GTGGTGTAAT CAAGAAAACA GCCATGGTCT TCGGACAAAT GAACGAACCA 600
CCTGGCGCAC GTATGCGTGT TGCTTTATCT GGTTTAACAA TGGCTGAATA 650
TTTCCGTGAT GAACAAGGAC AAGACGTATT GTTATTCATC GACAATATTT 700
TCCGTTTCAC ACAAGCCGGT TCAGAAGTTT CTGCCTTACT AGGTCGTTTA 750
CCATCAGCCG TTGGTTATCA ACCTACATTA GCAACAGAAA TGGGACAATT 800
ACAAGAACGT ATTACTTCAA CAACAAAAGG ATCAGTTACT TCA 843

2) INFORMATION FOR SEQ ID NO: 368

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
(B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA TAATGAAGTT CCTGATATTA ACAATGCCTT ACACATCGAA 50
GTTCCTAAAG AAGATAGCAC ACTTCATTTA ACTTTAGAAG TTGCACTTCA 100
ATTAGGTGAC GATGTAGTAC GTACAATCGC AATGGACTCA ACTGACGGCG 150
TTCAAAGAGG TATGGAAGTT AAAGATACAG GTAAAGATAT TAGCGTACCT 200
GTTGGTGATG CAACTTTAGG AAGAGTATTT AACGTATTAG GAGAAACAAT 250
CGATTTAGAT GAAAAGATTG ATGATTCAGT ACGTCGTGAT CCTATTCATA 300
GACAGGCACC TGGCTTCGAT GAATTATCTA CTAAAGTAGA AATCTTAGAA 350

ACAGGTATCA AAGTAGTAGA CTTATTAGCA CCTTACATTA AAGGTGGTAA 400
AATTGGATTA TTCGGTGGTG CCGGTGTTGG TAAGACAGTT TTAATCCAAG 450
AACTTATCAA TAATATCGCT CAAGAGCATG GTGGTATTTC AGTATTCGCC 500
GGTGTTGGTG AACGTACACG TGAAGGTAAC GACCTTTACT ATGAAATGAG 550
CGATAGTGGT GTAATTAAGA AAACAGCGAT GGTATTCGGT CAGATGAACG 600
AGCCACCTGG TGCTCGTATG CGTGTTGCAT TATCAGGTTT AACAATGGCA 650
GAATATTTCC GTGATGAAGA AGGCCAAGAC GTATTATTAT TCATTGATAA 700
TATCTTCAGA TTCACACAAG CTGGTTCTGA AGTTTCAGCA TTACTTGGAC 750
GTATGCCTTC AGCCGTTGGT TATCAACCAA CACTTGCTAC TGAAATGGGT 800
CAATTACAAG AACGTATTAG TTCAACTAAT AAAGGTTCTG TTACTTCAA 849

2) INFORMATION FOR SEQ ID NO: 369

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus cohnii*
(B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

GAAGTTCCAG AAATTAATAA TGCCTTAGTT CTCGATATAG AAAGAGAAGA 50
AGGTACTGTT GAATTAACGT TAGAAGTTGC ATTACAACTT GGTGATGACG 100
TAGTACGAAC AATCGCAATG GATTCAACTG ATGGTGTTAA ACGTGGTACA 150
GAAGTTAGAG ATAGCGGAAA TAGTATCAGC GTACCAGTTG GTAATGAAAC 200
ATTAGGTAGA GTATTTAATG TATTAGGTGA TACGATAGAT TTAGATGAAG 250
ACATAGATGA CTCAGTGCGT CGTGACCCAA TTCATAGAGA AGCACCTGCA 300
TTTGATCAGT TATCTACTAA AGTTGAAATT TTAGAAACAG GTATCAAAGT 350
CATTGATTTA TTAGCACCAT ATATCAAAGG TGGTAAAGTT GGATTATTCG 400
GTGGTGCCGG TGTTGGTAAA ACTGTATTAA TTCAAGAATT AATCAATAAT 450
ATCGCTCAAG AGCATGGTGG TATATCCGTA TTTGCTGGTG TAGGTGAGCG 500
TACGCGTGAA GGTAATGACC TATACTTTGA AATGAGTGAT AGTGGTGTTA 550
TTAAAAAGAC AGCTATGGTA TTTGGACAAA TGAACGAACC ACCTGGTGCG 600
CGTATGCGAG TAGCACTTTC TGGTTTAACA ATGGCTGAAT ATTTCCGGGA 650
TGAACAAGGA CAAGATGTTC TATTATTCAT AGATAACATC TTTAGATTTA 700
CTCAAGCTGG TTCAGAAGTT TCTGCGTTAT TAGGTCGTAT GCCTTCAGCT 750
GTTGGTTACC AACCAACGTT AGCAACTGAA ATGGGACAAT TACAAGAACG 800
TATTACTTCT ACAACTAAAG GTTCAGTAAC 830

2) INFORMATION FOR SEQ ID NO: 370

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

```
AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT      50
AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG     100
CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA     150
GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACTCTAG GAAGAGTGTT     200
TAACGTACTA GGAGAAACTA TTGACTTAGA TGAAAAAATT GATGATTCAG     250
TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA     300
ACAAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC     350
ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG     400
GTAAAACCGT ACTAATCCAA GAACTTATTA ATAACATCGC TCAAGAACAC     450
GGTGGTATCT CAGTATTCGC TGGTGTTGGT GAACGTACAC GTGAAGGTAA     500
TGATCTTTAC TATGAAATGA GTGACAGTGG TGTTATCAAG AAAACTGCAA     550
TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA     600
TTATCCGGAT TAACAATGGC CGAATATTTC CGAGATGAAG AAGGCCAAGA     650
TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG     700
AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT     750
ACACTTGCTA CAGAAATGGG TCAATTACAA GAACGTA                   787
```

2) INFORMATION FOR SEQ ID NO: 371

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

```
GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA      50
TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAACTA GGTGATGACG     100
TTGTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTCA ACGTGGTATG     150
GAAGTTCAGA ACACTGGAAA AGACATTTCA GTACCAGTTG GCGAAGTAAC     200
TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA     250
AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC     300
TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT     350
TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAAATC GGTCTATTTG     400
GTGGTGCCGG TGTTGGTAAA ACCGTTTTAA TCCAAGAATT GATTAATAAT     450
ATCGCACAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG     500
TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTTA     550
TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA     600
CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA     650
TGAACAAGGA CAAGACGTTC TGTTATTCAT CGATAACATT TTCAGATTTA     700
CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT     750
GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG     800
TATTACATCA ACGAATAAAG GTTCAGTAAC                           830
```

2) INFORMATION FOR SEQ ID NO: 372

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
(B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50
CCCAAAAATG ATGGCACATT TAAATTAACA TTAGAAGTTG CATTGCAACT 100
AGGTGATGAT GTTGTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTC 150
AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCCTGTA 200
GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250
TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300
GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350
GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400
TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT 450
TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500
GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550
TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600
CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650
TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT 700
TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATTA TTAGGACGTA 750
TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800
TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA 846

2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus hominis*
(B) STRAIN: CSG 175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50
CCCAAAAATG ATGGCACATT CAAATTAACA TTAGAAGTTG CATTGCAACT 100
AGGTGATGAT GTTGTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTC 150
AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCCTGTA 200
GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250
TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300
GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350
GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400

TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT 450
TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500
GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550
TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600
CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650
TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT 700
TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATTA TTAGGACGTA 750
TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800
TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA 846

2) INFORMATION FOR SEQ ID NO: 374

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus lugdunensis*
(B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

ATAATGAAGT GCCTGAAATA AATAATGCGC TCATTGTTGA AATTCCTAAA 50
AGTGATACAA CAATCAGTTT AACACTTGAA GTTGCTTTGC AATTAGGTGA 100
CGATGTTGTA CGTACTATTG CAATGGATTC AACTGATGGC GTTCAACGTG 150
GTATGGAAGT TCAAAACACA GGTAAAGACA TCAGTGTACC TGTTGGAGAT 200
GAAACATTAG GAAGAGTATT TAACGTTTTA GGAGAATCTA TTGATTTAGA 250
AGAAAAGCTA GATGACTCTG TGCGTAGAGA TCCAATTCAT AGACTAGCAC 300
CTAAATTTGA TGAATTATCT ACAGAAGTAG AAATTCTTGA AACTGGTATT 350
AAAGTTGTTG ATTTATTAGC ACCATATATT AAAGGTGGTA AAGTTGGATT 400
GTTTGGTGGT GCCGGAGTAG GTAAAACGGT ATTAATTCAA GAATTAATCA 450
ACAATATTGC TCAAGAACAT GGTGGTATTT CTGTGTTTGC CGGAGTAGGT 500
GAACGTACAC GTGAAGGTAA TGACTTATAT TATGAAATGA GCGATAGTGG 550
CGTAATTAAG AAAACAGCGA TGGTATTTGG CCAAATGAAT GAACCACCTG 600
GTGCACGTAT GAGAGTTGCG TTATCTGCCT TAACAATGGC TGAATATTTC 650
CGTGACGAGC AAGGACAAGA CGTATTGCTG TTTATCGATA ATATATTCCG 700
TTTTACACAA GCAGGTTCAG AAGTATCTGC ATTACTTGGA CGTATGCCAT 750
CTGCCGTTGG TTATCAACCA ACATTGGCTA CAGAAATGGG ACAATTGCAA 800
GAAAGAATTA CATCTACAAA TAAAGGTTCT GTAAC 835

2) INFORMATION FOR SEQ ID NO: 375

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

```
GAGCACAATG AAGTTCCAGA AATTAACAAT GCCTTAGTCG TAGACGTTGA      50
AAGAGATGAA GGTACAGTAT CTCTTACATT AGAAGTGGCA TTACAACTTG     100
GCGATGATGT CGTACGTACA ATTGCAATGG ATTCTACTGA TGGTGTTAAA     150
CGTGGTACAG AAGTTCGAGA TAGCGGAGAT AGCATCAGTG TTCCAGTTGG     200
TGATGCTACG TTAGGACGTG TGTTTAATGT TCTTGGTGAT ACAATTGACT     250
TAGACGAGAA GCTTGATACT TCTGTCAAAC GTGATCCAAT TCATAGAGAA     300
GCACCTGCAT TCGATCAATT ATCAACAAAA GTTGAAATCT TAGAAACAGG     350
TATTAAAGTA ATTGATTTAC TTGCACCATA TATTAAAGGT GGTAAAATCG     400
GTTTATTCGG TGGCGCTGGT GTAGGTAAAA CAGTATTAAT TCAAGAATTA     450
ATTAATAATA TAGCTCAAGA ACATGGTGGT ATTTCAGTAT TTGCCGGCGT     500
AGGTGAACGT ACGCGTGAAG GTAATGACTT ATACTACGAA ATGAGTGATA     550
GTGGTGTTAT TAAGAAAACA GCTATGGTCT TCGGACAAAT GAATGAGCCA     600
CCTGGTGCGC GTATGCGTGT TGCTTTATCA GGCTTAACAA TGGCTGAACA     650
CTTCCGTGAT GTACAAGGAC AAGATGTTTT ACTATTTATT GATAACATAT     700
TCAGATTTAC GCAAGCTGGT TCAGAAGTAT CAGCACTATT AGGTCGTATG     750
CCATCAGCCG TTGGTTATCA ACCTACCCTT GCTACTGAAA TGGGTCAATT     800
ACAAGAACGT ATTACATCAA CAACTAAAGG ATCTGTAACG TC             842
```

2) INFORMATION FOR SEQ ID NO: 376

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus simulans*
(B) STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

```
TGATGAACTG CCTAAGATTA ATAACGCATT AGTGCTAGAT GTACCTAAGA      50
AAGATGGCAC GACTGAATCT CTTACATTAG AAGTAGCACT TGAATTAGGC     100
GACGACGTAG TTAGAACTAT CGCCATGGAC TCTACAGACG GAATTAAACG     150
TGGTGACGAC GTTAAAGACA CTGGTCGTCC AATCAGTGTA CCTGTCGGTG     200
AAGATACGTT AGGAAGAGTA TTTAACGTTT TAGGTGATCC AATCGATAAT     250
GATGGACCGA TTTCTGAATC AGTTCCACGT GAACCAATTC ATAGACAACC     300
ACCTAAATTT GATGAATTAT CAACAAAAGT TGAACTACTT GAAACTGGTA     350
TCAAAGTAGT AGACTTATTA GCACCATATA TCAAAGGTGG TAAAGTTGGT     400
TTATTCGGTG GTGCCGGAGT AGGTAAAACT GTATTAATCC AAGAATTAAT     450
TAATAACATC GCTCAAGAAC ACGGCGGTAT TTCAGTATTC GCAGGTGTTG     500
GTGAACGTAC ACGTGAAGGT AACGACTTGT ACTTCGAAAT GAGCGACAGT     550
GGTGTTATCA AGAAAACAGC GATGGTATTC GGACAAATGA ACGAACCACC     600
TGGTGCACGT ATGCGTGTAG CTTTATCAGG TTTAACAATG GCTGAATACT     650
TCCGTGATGT TAAAGGACAA GACGTTCTTT TATTCATCGA TAACATTTTC     700
CGCTTCACAC AAGCAGGTTC TGAGGTATCA GCATTGCTTG GCCGTATGCC     750
ATCAGCCGTT GGTTACCAAC CAACATTGGC AACAGAAATG GGTCAATTAC     800
AAGAACGTAT CACTTCTACA ATGAAAGGTT CTATCACATC TA             842
```

2) INFORMATION FOR SEQ ID NO: 377

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus warneri*
(B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

CATAACGAAG TCCCTGATAT TAATAATGCC CTTATTATTG AAGTTCCAAA 50
AGAAGATGGA ACGTTAAACT TAACATTAGA AGTTGCACTA CAATTAGGTG 100
ATGATGTTGT ACGTACAATT GCAATGGATT CAACTGATGG TGTTCAAAGA 150
GGCATGGATG TTAAAGACAC AGGTAAAGAT ATTAGTGTAC CTGTAGGCGA 200
TGAAACGCTT GGAAGAGTGT TTAATGTACT AGGTGAAACA ATTGACTTGG 250
AAGAGAAAAT TGATGATTCC GTACGTCGTG ATCCAATCCA TAGACAATCA 300
CCAGGTTTCG ATGAATTATC TACTGAAGTA GAAATCTTAG AAACAGGTAT 350
TAAAGTAGTA GACTTATTAG CACCTTACAT TAAAGGTGGT AAAGTTGGAC 400
TATTCGGTGG TGCCGGAGTA GGTAAAACCG TTTTAATCCA AGAATTAATT 450
AACAATATTG CACAAGAACA TGGTGGTATT TCAGTATTCG CGGGTGTAGG 500
TGAACGTACT CGTGAAGGTA ATGATTTATA CTATGAAATG AGTGATAGTG 550
GTGTAATTAA GAAAACAGCG ATGGTATTTG GACAAATGAA TGAACCACCT 600
GGCGCACGTA TGCGTGTAGC TTTATCTGGT TTAACTATGG CTGAATACTT 650
CCGTGATGAA CAAGGACAAG ACGTACTTTT ATTCATCGAT AATATTTTCA 700
GATTTACACA AGCTGGTTCT GAAGTTTCTG CATTACTTGG TCGTATGCCT 750
TCAGCCGTTG GTTACCAACC AACATTAGCA ACTGAAATGG GTCAATTACA 800
AGAACGAATT ACATCTACAA ATAAAGGTTC TGTAACATCT A 841

2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus acidominimus*
(B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

TTTAACACGA ATGAACCGCT TCCTGAGATA AATAATGCAC TTGTTGTTTA 50
CAAAGACAGT GAGAAAAAAC ATAAAATCGT TCTTGAAGTA GCTCTTGAAC 100
TTGGTGAAGG CCTCGTTCGT ACCATTGCTA TGGAATCAAC TGATGGTTTG 150
ACACGTGGTC TAGAAGTTCT TGATACAGGC CGTGCAATCA GTGTACCAGT 200
TGGTAAAGAA ACGCTTGGAC GTGTCTTCAA CGTTCTTGGT GATGCTATCG 250
ATCTTGAAGA ACCATTTGGA GAAGATGCAG AACGTCACCC CATTCATAAG 300
AGTGCCCCAA CTTTTGATGA ATTATCAACG TCAACAGAAA TCCTTGAAAC 350
AGGGATTAAA GTTATCGACC TACTTGCCCC TTACTTAAAA GGAGGGAAGG 400

TTGGACTTTT CGGTGGTGCC GGAGTTGGTA AGACCGTTCT TATCCAAGAG 450
TTGATTCATA ACATTGCTCA AGAGCATGGT GGTATTTCAG TATTTACCGG 500
AGTTGGTGAA CGTACACGTG AAGGTAATGA CCTCTATTGG GAAATGAAAG 550
AATCAGGCGT TATTGAAAAA ACAGCTATGG TATTTGGTCA GATGAATGAG 600
CCACCTGGTG CACGTATGCG TGTAGCCCTT ACTGGTTTGA CAATCGCTGA 650
ATATTTCCGT GATGTTGAAG GACAGGACGT GCTTCTCTTT ATTGATAACA 700
TTTTTCGTTT CACACAAGCA GGTTCTGAAG TTTCAGCTCT TCTTGGACGT 750
ATGCCATCAG CCGTTGGTTA TCAACCAACC TTGGCAACTG AAATGGGTCA 800
ATTGCAAGAA CGTATCACGT CAACTAAAAA AGGTTCTGTT ACATCA 846

2) INFORMATION FOR SEQ ID NO: 379

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTA CTCTTGAACT 100
TGGTGACGGC CTCGTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA 350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400
TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT 500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CCTCAA 846

2) INFORMATION FOR SEQ ID NO: 380

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*

(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

```
TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT     100
TGGTGACGGC CTCGTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA     150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT     200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA     250
TCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA     300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT     350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT     400
TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT     450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT     500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA     550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC     600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG     650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT     700
CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA     750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA     800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CCTCAA         846
```

2) INFORMATION FOR SEQ ID NO: 381

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

```
TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT     100
TGGTGACGGC CTCGTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA     150
CACGTGGTTT GGAAGTATTA GATACTGGTC GTGCAATTAG TGTGCCGGTT     200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA     250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA     300
AAGCACCATC ATTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA     350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT     400
TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT     450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT     500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA     550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC     600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG     650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT     700
CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA     750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA     800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CCTCA         845
```

2) INFORMATION FOR SEQ ID NO: 382

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: ATCC 27591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT 100
TGGTGACGGC CTCGTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT 350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400
TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT 500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CATCA 845

2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: CDC ss1073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT 100
TGGTGACGGC CTCGTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT 350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400

TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT 500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CATCA 845

2) INFORMATION FOR SEQ ID NO: 384

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus dysgalactiae*
(B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

TTGCTAGTGG GGACAAACTT CCAGAGATTA ATAATGCATT GATTGTTTAT 50
AAAGATAGTG ATAAAAAGCA AAAAATCGTC CTTGAAGTTG CTCTGGAACT 100
TGGTGACGGT ATGGTGCGAA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
CACGTGGGTT AGAAGTTCTT GACACTGGTC GTGCGATTAG TGTACCAGTA 200
GGTAAAGAAA CTTTGGGACG CGTCTTTAAT GTACTTGGAG AAACCATTGA 250
CTTGGAAGAA CCATTTGCAG AAGACGTTGA CCGTCAGCCA ATCCATAAAA 300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT TCTTGAAACT 350
GGTATCAAGG TAATTGACCT TCTTGCCCCT TACCTTAAAG GTGGTAAAGT 400
TGGACTTTTC GGGGGTGCCG GAGTTGGTAA GACTGTCCTT ATCCAAGAAT 450
TAATCCACAA TATCGCCCAA GAACACGGAG GTATTTCAGT ATTTACCGGT 500
GTTGGTGAGC GAACACGTGA AGGAAATGAC CTTTACTGGG AAATGAAAGA 550
ATCAGGCGTT ATTGAGAAAA CTGCCATGGT TTTTGGTCAG ATGAATGAGC 600
CGCCTGGGGC ACGTATGCGT GTAGCCCTTA CTGGTTTAAC CATTGCTGAG 650
TATTTCCGTG ATGTAGAAGG CCAAGATGTT TTGCTCTTTA TTGATAATAT 700
CTTCCGTTTC ACTCAGGCAG GTTCAGAAGT ATCAGCCCTC TTAGGCCGTA 750
TGCCTTCTGC TGTTGGTTAC CAACCGACCC TTGCTACTGA AATGGGACAA 800
TTGCAAGAAC GTATTACGTC AACTCAAAAA GGATCTGTTA CTTCT 845

2) INFORMATION FOR SEQ ID NO: 385

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus equi* subsp. *equi*

(B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

```
TTGCGAGTGG GGACAAACTA CCAGAGATTA ATAATGCGTT GATAGTTTAT      50
AAAGATGGCG ATAAAAAGCA AAAAATCGTT CTCGAGGTTG CCCTAGAGCT     100
TGGAGACGGT ATGGTACGTA CAATTGCTAT GGAATCAACC GATGGGCTTA     150
CACGTGGATT AGAGGTTCTT GATACTGGTC GTGCCATTAG TGTACCAGTT     200
GGTAAAGAGA CTCTAGGTCG TGTTTTCAAC GTTCTTGGTG AAACCATCGA     250
CCTAGAAGCA CCATTTGCAG ATGATGTTAA TCGTGAACCG ATCCATAAAA     300
AAGCACCAGC CTTTGATGAA TTGTCAACAT CATCAGAAAT TCTTGAAACA     350
GGTATCAAGG TTATTGACCT GCTTGCCCCT TACTTAAAGG GTGGTAAGGT     400
CGGTCTTTTC GGTGGTGCCG GAGTTGGTAA AACCGTTCTT ATCCAAGAAT     450
TAATCCACAA TATCGCTCAA GAGCATGGTG GGATCTCGGT ATTTACCGGT     500
GTTGGTGAGC GTACGCGTGA AGGAAATGAC CTTTACTGGG AAATGAAGGA     550
ATCAGGCGTT ATTGAAAAAA CAGCCATGGT TTTTGGTCAG ATGAATGAAC     600
CACCAGGAGC CCGTATGCGT GTTGCCTTGA CCGGCTTGAC AATTGCTGAA     650
TATTTCCGCG ATGTTGAAGG CCAAGACGTC CTGCTCTTCA TTGACAATAT     700
TTTCCGCTTT ACTCAAGCAG GCTCAGAGGT ATCAGCCCTT CTAGGTCGTA     750
TGCCTTCAGC CGTTGGTTAC CAGCCAACAC TTGCCACTGA AATGGGACAA     800
TTGCAAGAGC GTATCACCTC AACGAAAAAA GGCTCTGTTA CCTCTA         846
```

2) INFORMATION FOR SEQ ID NO: 386

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus anginosus*
(B) STRAIN: ATCC 27335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

```
TTGCAGCTGG TGATAAATTA CCTGAGATAA ATAATGCACT TGTAGTCTAT      50
AAAAATGACG AAAATAAATC AAAAATCGTC CTTGAAGTAG CTCTTGAGCT     100
TGGTGATGGA GTGGTTCGAA CTATTGCCAT GGAATCCACT GATGGGTTGA     150
CTCGTGGCAT GGAAGTTCTA GATACTGGTC GACCAATTTC TGTTCCAGTT     200
GGGAAAGAAA CACTTGGTCG CGTCTTTAAC GTTTTAGGCG ATACCATTGA     250
TTTGGATACT CCATTCGGCG AAGATGCAGA ACGTCAACCA ATCCATAAAA     300
AAGCTCCAAC TTTTGATGAG TTATCTACTT CATCAGAAAT CTTAGAAACA     350
GGAATAAAGG TTATTGACCT TTTAGCCCCC TACCTCAAAG GTGGGAAAGT     400
CGGCCTCTTC GGTGGTGCTG GCGTTGGGAA AACTGTCTTG ATTCAAGAGT     450
TGATTCATAA TATCGCCCAA GAACACGGCG GGATTTCAGT CTTTACTGGT     500
GTTGGGGAAC GAACTCGTGA AGGGAATGAC CTGTACTGGG AAATGAAAGA     550
ATCTGGTGTT ATCGAAAAGA CGGCTATGGT CTTTGGGCAA ATGAATGAAC     600
CGCCTGGAGC ACGTATGCGT GTAGCTTTGA CTGGGTTAAC GATTGCAGAG     650
TATTTCCGTG ATGTGGAAGG TCAAGATGTT CTTTTGTTTA TTGATAATAT     700
TTTCCGTTTC ACTCAAGCTG GTTCTGAAGT GTCAGCCCTT CTTGGTCGTA     750
TGCCATCAGC TGTTGGTTAC CAACCAACCT TGGCTACTGA AATGGGGCAA     800
TTACAAGAAC GTATTACATC AACGAAAAAA GGTTCTGTTA CCTCAA         846
```

2) INFORMATION FOR SEQ ID NO: 387

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus salivarius*
(B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

GCAGCTGGTG ATAAACTTCC TGAGATTAAC AATGCATTGG TCGTTTATAC 50
TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG 100
GAGAAGGTGT GGTTCGTACC ATTGCCATGG AATCTACTGA TGGATTGACT 150
CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG 200
TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT 250
TGGAAGCACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA 300
GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG 350
GATTAAAGTT ATCGACTTGC TAGCCCCTTA CCTTAAGGGT GGTAAAGTCG 400
GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCTTAT TCAAGAGTTG 450
ATTCACAACA TTGCCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT 500
TGGTGAACGT ACACGTGAAG GTAATGACCT TTACTGGGAA ATGAAAGAAT 550
CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA 600
CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA 650
CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT 700
TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG 750
CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT 800
GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT 843

2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus suis*
(B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT 50
AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAACT 100
TGGTGATGGC GTTGTACGGA CCATTGCCAT GGAATCAACG GATGGATTGA 150
CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCCAGTC 200
GGTAAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA 250
CCTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA 300
AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA 350
GGGATTAAGG TTATCGACCT CCTAGCACCT TATCTAAAAG GTGGTAAGGT 400

TGGTCTCTTC GGTGGTGCTG GTGTTGGTAA AACCGTTCTT ATCCAAGAAT 450
TGATTCACAA TATTGCCCAA GAACACGGTG GTATCTCTGT ATTTACCGGA 500
GTTGGCGAGC GTACCCGTGA AGGGAACGAT CTTTACTGGG AAATGAAAGA 550
ATCAGGTGTT ATTGAAAAAA CGGCCATGGT ATTTGGTCAG ATGAATGAGC 600
CACCAGGAGC CCGTATGCGT GTTGCTCTTA CTGGTTTGAC TATTGCGGAA 650
TACTTCCGTG ATGTGGAAGG GCAGGATGTT CTTCTGTTCA TCGATAATAT 700
CTTCCGTTTC ACACAGGCTG GTTCAGAAGT GTCTGCCCTC TTGGGTCGTA 750
TGCCATCAGC CGTTGGTTAT CAGCCAACAC TTGCGACGGA GATGGGACAA 800
TTGCAGGAGC GTATTACCTC AACCAAGAAG GGTTCTGTTA C 841

2) INFORMATION FOR SEQ ID NO: 389

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 844 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus uberis*
(B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

GCAAACGGTG AAAAATTACC AGAGATTAAT AATGCATTGA TAGTTTATAA 50
AGGTAGCGAT AAAAAACAAA AGATTGTTCT TGAAGTTGCT TTGGAACTTG 100
GGGACGGAAT GGTTCGTACA ATCGCTATGG AATCAACTGA TGGGCTTACA 150
CGTGGATTAG AAGTTTTAGA TACTGGCCGT GCCATTAGTG TACCAGTCGG 200
AAAAGAAACT TTGGGTCGTG TTTTCAATGT GCTTGGTGAA ACCATTGATT 250
TGGATGAACC ATTTGCCGCT GATGCTGCAA GAGAACCCAT CCATAAAAAA 300
GCCCCAGCAT TTGATGAACT ATCAACGTCT TCAGAAATTC TTGAAACCGG 350
AATAAAAGTT ATTGACTTAT TAGCCCCTTA TCTCAAAGGT GGTAAAGTTG 400
GTTTATTTGG TGGTGCCGGA GTAGGTAAAA CGGTTTTAAT TCAAGAATTA 450
ATTCATAATA TTGCACAAGA ACATGGTGGT ATTTCAGTAT TTACCGGTGT 500
TGGTGAAAGA ACTCGTGAAG GTAATGACCT TTATTGGGAA ATGAAAGAAT 550
CTGGCGTTAT TGAAAAAACA GCCATGGTAT TTGGACAAAT GAACGAACCA 600
CCAGGAGCAC GTATGCGCGT TGCTTTAACA GGTTTAACCA TTGCTGAATA 650
TTTCCGGGAT GTTGAAGGTC AAGATGTTTT GCTCTTTATT GACAACATTT 700
TCCGTTTCAC GCAAGCTGGT TCAGAAGTTT CAGCCCTATT GGGTCGTATG 750
CCTTCAGCGG TAGGATACCA ACCAACACTT GCTACCGAAA TGGGACAATT 800
GCAAGAAAGA ATTACCTCAA CTAACAAGGG ATCTGTTACT TCTA 844

2) INFORMATION FOR SEQ ID NO: 390

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 896 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Tatumella ptyseos*

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

```
TTCCCTCAGG ACGCTGTACC ACAGGTGTAC AACGCTCTTG AGGTTGAAAA      50
TGGTGATACC CGTCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGTGGTG     100
TCGTTCGTAC GATTGCAATG GGAACCTCTG ACGGCCTGAA ACGTGGCCTT     150
AAGGTGACCG ATCTGCAAAA ACCGATTCAG GTACCGGTCG GTAAAGCGAC     200
GCTGGGCCGT ATCATGAACG TACTGGGTCA GCCAATCGAT ATGAAAGGCG     250
ACCTGAAGAA CGAAGATGGT AGCAATGTTG AGGTGAACTC TATTCACCGT     300
GCAGCGCCAA GCTACGAAGA ACTGGCTAAC TCTACTGAGC TGCTGGAAAC     350
GGGTATCAAG GTTATCGACC TGATCTGTCC GTTTGCAAAA GGCGGTAAAG     400
TGGGTCTGTT CGGTGGTGCG GGTGTAGGTA AGACCGTCAA CATGATGGAA     450
CTGATCCGTA ACATCGCTAT CGAGCACTCT GGTTACTCTG TATTTGCAGG     500
GGTGGGTGAG CGTACCCGTG AAGGTAACGA CTTCTACCAC GAAATGACCG     550
AGTCTAACGT TCTGGATAAA GTTGCTCTGG TTTATGGCCA GATGAACGAG     600
CCACCAGGAA ACCGTCTGCG CGTTGCGCTG ACCGGTCTGA CTATGGCTGA     650
AAAATTCCGT GACGAAGGCC GTGACGTACT GCTGTTCGTT GATAACATCT     700
ATCGTTATAC CCTGGCCGGT ACTGAAGTTT CAGCACTGCT GGGTCGTATG     750
CCTTCTGCGG TAGGTTATCA GCCAACACTG GCCGAAGAAA TGGGTGTTCT     800
TCAGGAACGT ATCACGTCAA CCAAAACCGG TTCAATCACT TCCGTA         896
```

2) INFORMATION FOR SEQ ID NO: 391

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trabulsiella guamensis*
(B) STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

```
TTCCCTCAGG ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTTATGAA      50
TGGTAGTGAG CGTCTGGTGC TGGAAGTTCA GCAGCAGCTC GGTGGTGGTA     100
TCGTACGTAC TATCGCCATG GGTTCTTCCG ACGGTCTGCG TCGTGGTCTG     150
GATGTAAAAG ATCTCGAGCA TCCGATCGAA GTCCCGGTAG GTAAAGCAAC     200
GCTGGGTCGT ATCATGAACG TGCTGGGTCA GCCGATCGAT ATGAAAGGCG     250
ACATCGGCGA AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCGTCCTAC     300
GAAGAGCTGT CCAGCTCTCA GGAACTGCTG GAAACCGGCA TCAAAGTTAT     350
CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG     400
GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTGAT TCGTAACATC     450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAACGTAC     500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTCTGG     550
ACAAAGTATC CCTGGTGTAT GGACAGATGA ACGAGCCGCC GGGAAACCGT     600
CTGCGCGTTG CACTGACCGG TCTGACCATG GCTGAGAAGT TCCGTGACGA     650
AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTACCGT TACACCCTGG     700
CGGGTACTGA AGTATCTGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT     750
TACCAGCCGA CCCTGGCGGA AGAGATGGGT GTTCTTCAGG AACGTATCAC     800
CTCAACCAAA ACCGGTTCTA TCACCTCCG                            829
```

2) INFORMATION FOR SEQ ID NO: 392

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia bercovieri*
(B) STRAIN: ATCC 43970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

CGAATTCCCC CAAGACGCTG TACCAAAAGT GTACAACGCC CTTGAGGTTG 50
AAGGCACAGC TCAGAAGCTG GTGCTGGAAG TTCAGCAACA GCTGGGCGGT 100
GGTGTTGTTC GTTGTATCGC AATGGGCTCT TCCGATGGTC TGAGCCGCGG 150
GTTGAAAGTC ATCAACCTGG AACACCCAAT TGAAGTGCCG GTGGGTAAAT 200
CAACTCTGGG CCGTATCATG AACGTATTGG GTGACCCAAT CGACATGAAA 250
GGTCCTATCG GTGAAGAAGA GCGTTGGGCA ATCCACCGCG AAGCGCCTTC 300
TTACGAAGAG CTTGCCAGCT CGCAAGATCT GTTAGAAACC GGTATCAAGG 350
TAATGGATCT GATTTGTCCG TTCGCTAAGG GCGGTAAAGT CGGTCTGTTC 400
GGTGGTGCGG GTGTGGGTAA AACAGTCAAC ATGATGGAGC TGATTCGTAA 450
TATTGCGATT GAGCACTCAG GTTATTCTGT ATTTGCCGGT GTGGGTGAGC 500
GTACTCGTGA GGGTAACGAC TTCTACCACG AGATGACTGA CTCCAACGTT 550
CTGGACAAAG TATCCTTGGT TTATGGCCAG ATGAATGAGC CACCAGGTAA 600
CCGTCTGCGC GTTGCACTGA CCGGCTTGAC CATGGCGGAG AAATTCCGTG 650
ATGAAGGTCG TGATGTACTG TTATTCATCG ATAACATCTA TCGTTATACC 700
CTGGCCGGTA CAGAGGTATC TGCACTGCTA GGTCGTATGC CATCAGCGGT 750
AGGCTATCAG CCAACGCTGG CAGAAGAGAT GGGTGTGTTG CAGGAACGTA 800
TCACTTCCAC CAAGACGGGT TCAATCACCT CCGTA 835

2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia enterocolitica*
(B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTTGAAGGCG CAGCTGAGAA 50
GCTGGTGCTG GAAGTTCAGC AACAGCTGGG CGGTGGTGTT GTTCGTTGTA 100
TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTTGAA AGTCATCAAC 150
CTGGAACACC CAATTGAAGT GCCTGTGGGC AAGTCAACTC TGGGCCGTAT 200
CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGCGAAG 250
AAGAGCGTTG GGCAATCCAT CGTGAAGCGC CTTCTTACGA AGATCTTGCC 300
AGCTCGCAAG ACTTGTTAGA AACCGGTATC AAGGTAATGG ACTTGATTTG 350
TCCGTTCGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400

GTAAAACGGT AAACATGATG GAGCTTATTC GTAACATTGC GATTGAGCAC 450
TCAGGTTATT CCGTATTTGC TGGCGTGGGT GAGCGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT 550
TGGTTTATGG CCAAATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA 600
CTGACCGGCT TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
ATTGCTGTTC ATCGATAACA TCTATCGCTA TACCTTAGCC GGTACGGAAG 700
TTTCCGCACT GCTGGGTCGT ATGCCATCTG CCGTAGGTTA CCAGCCAACG 750
CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACCAAGAC 800
GGGTTCAATC AC 812

2) INFORMATION FOR SEQ ID NO: 394

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 802 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia frederiksenii*
(B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

AAAGTGTACA ACGCCCTTGA GGTTGAAGGT ACTGCTGAGA AGTTAGTACT 50
GGAAGTTCAG CAACAGCTGG GCGGTGGTGT TGCTCGTTGT ATCGCCATGG 100
GCTCTTCCGA TGGTTTGAGC CGCGGGTTGA AAGTTGTCAA CCTGGAACAC 150
CCAATTGAAG TACCGGTTGG TAAATCAACT CTGGGCCGTA TCATGAACGT 200
ATTGGGTGAC CCAATCGACA TGAAAGGTCC TATCGGTGAA GAAGAGCGTT 250
GGGCAATCCA CCGCGAAGCG CCTTCTTACG AAGAGCTTGC CAGCTCGCAA 300
GATCTGTTAG AAACCGGTAT CAAGGTAATG GATCTGATTT GCCCGTTCGC 350
TAAAGGCGGT AAAGTCGGTC TGTTCGGTGG TGCGGGTGTA GGTAAAACGG 400
TAAACATGAT GGAGCTGATC CGTAATATCG CGATCGAGCA CTCAGGTTAT 450
TCCGTATTTG CGGGTGTTGG TGAACGTACC CGTGAGGGTA ACGACTTCTA 500
CCACGAGATG ACTGACTCCA ACGTTCTGGA CAAAGTATCC TTGGTTTATG 550
GCCAGATGAA TGAGCCACCA GGTAACCGTC TTCGCGTTGC ACTGACCGGT 600
CTGACCATGG CGGAGAAATT CCGTGATGAA GGTCGTGACG TATTGCTGTT 650
CATCGATAAC ATCTATCGTT ATACCTTGGC CGGTACGGAA GTATCCGCAC 700
TGCTGGGTCG TATGCCATCT GCGGTAGGCT ATCAGCCAAC GCTGGCAGAA 750
GAGATGGGTG TGTTGCAGGA ACGTATTACT TCCACCAAGA CGGGTTCAAT 800
CA 802

2) INFORMATION FOR SEQ ID NO: 395

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia intermedia*

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

```
GCTGTACCAA GAGTGTACAA CGCCCTTGAG GTTGAAGGCA CTGCTGAGAA      50
GCTGGTGCTG GAAGTTCAGC AACAGCTAGG CGGTGGTGTT GTTCGTTGTA     100
TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GCGGGTTGAA AGTCATCAAC     150
CTGGAACACC CAATTGAAGT GCCGGTTGGT AAATCAACTC TGGGCCGTAT     200
CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGTGAAG     250
AAGAGCGTTG GGCAATCCAC CGCGAAGCGC CTTCTTACGA AGAGCTTGCC     300
AGCTCACAAG ATTTGTTAGA AACCGGTATC AAAGTAATGG ACTTGATTTG     350
CCCGTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG     400
GTAAAACAGT AAACATGATG GAGCTTATTC GTAACATCGC GATTGAGCAC     450
TCAGGTTATT CTGTATTTGC TGGTGTGGGT GAGCGTACTC GTGAGGGTAA     500
CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT     550
TGGTGTATGG CCAGATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA     600
CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT     650
ACTGTTGTTC ATCGATAACA TCTATCGCTA TACCTTGGCC GGTACGGAAG     700
TATCCGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCAACG     750
CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACGT CCACCAAGAC     800
GGGTTC                                                    806
```

2) INFORMATION FOR SEQ ID NO: 396

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia pseudotuberculosis*
(B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

```
GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTAGAAGGCA CAACTGAAAA      50
GTTAGTGCTG GAAGTTCAGC AACAGTTGGG CGGTGGTGTT GTTCGTTGTA     100
TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTTGAA AGTAACCAAC     150
CTGGAACACC CGATCGAAGT ACCGGTTGGT AAAGCGACCC TTGGCCGTAT     200
CATGAACGTA TTGGGTGAAC CAATCGACAT GAAAGGTCCT ATCGGTGAAG     250
AAGAGCGTTG GGCAATCCAT CGCGAAGCGC CTTCTTATGA AGAGCTTGCT     300
AGCTCACAAG ATCTGTTAGA AACCGGTATC AAGGTTATGG ACCTGATTTG     350
TCCGTTTGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG     400
GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC     450
TCTGGGTATT CTGTATTTGC CGGTGTAGGT GAGCGTACCC GTGAGGGTAA     500
TGACTTCTAC CATGAAATGA CTGACTCCAA CGTTTTGGAC AAAGTATCCT     550
TGGTTTACGG CCAGATGAAT GAGCCACCAG GTAACCGTCT ACGCGTTGCA     600
CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT     650
ACTGCTGTTC ATCGATAATA TCTATCGTTA TACCCTAGCT GGTACGGAAG     700
TATCCGCATT GCTGGGTCGT ATGCCATCAG CGGTAGGTTA TCAGCCAACA     750
CTGGCTGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACTAAGAC     800
GGGTTC                                                    806
```

2) INFORMATION FOR SEQ ID NO: 397

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yersinia rohdei*
(B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

TTCCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG 50
TGCAGCTGAG AAGCTTGTGC TGGAAGTTCA GCAGCAGCTG GGCGGTGGTG 100
TTGTTCGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG 150
AAAGTTATCA ACCTGGAACA CCCAATTGAA GTGCCAGTTG GTAAATCAAC 200
TCTGGGCCGT ATCATGAACG TATTGGGTGA CCCAATCGAC ATGAAAGGCC 250
CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC 300
GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT 350
GGATCTGATT TGTCCGTTCG CTAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC 450
GCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC 500
TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG 550
ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT 600
CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA 650
AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG 700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGC 750
TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC 800
TTCCACTAAG ACGGGTTCAA TCACCTCCG 829

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yokenella regensburgei*
(B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAAAA TGGTAACGAG 50
AAACTGGTGC TGGAAGCTCA GCAGCAGCTC GGCGGCGGTA TCGTGCGTAC 100
TATCGCCATG GGTTCTTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG 150
ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC CCTGGGCCGT 200
ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA 250
AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT 300
CCAGCTCTCA GGAACTGCTG GAAACCGGTA TCAAAGTAAT GGATCTGATC 350
TGCCCGTTCG CTAAGGGTGG TAAAGTCGGT CTGTTCGGTG GTGCGGGTGT 400

AGGTAAAACT GTAAACATGA TGGAGCTTAT CCGTAACATC GCGATTGAGC 450
ACTCCGGTTA CTCTGTGTTT GCAGGCGTGG GTGAACGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG ATAAAGTATC 550
CCTGGTGTAC GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
CGCTGACCGG CCTGACCATG GCTGAGAAAT TCCGTGACGA AGGCCGTGAC 650
GTTCTGCTGT TCGTCGATAA CATCTACCGT TATACCCTGG CCGGTACGGA 700
AGTATCCGCA CTGCTGGGTC GTATGCCTTC TGCGGTAGGT TATCAGCCAA 750
CTCTGGCGGA AGAGATGGGT GTTCTTCAGG AACGTATCAC CTCTACCAAA 800
ACCGGTTCTA TCACCTCCG 819

2) INFORMATION FOR SEQ ID NO: 399

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1097 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Yarrowia lipolytica*
(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

AAGCTTAAGG CTGAGCGAGA GCGAGGTATC ACCATTGATA TCGCTCTCTG 50
GAAGTTCCAG ACCCCTAAGT ACTACGTCAC CGTTATTGAT GCTCCCGGTC 100
ACCGAGATTT CATCAAGAAC ATGATTACCG GTACTTCCCA GGCTGACTGC 150
GCCATCCTCA TCATTGCTGG TGGTGTTGGT GAGTTCGAGG CTGGTATCTC 200
CAAGGATGGT CAGACCCGAG AGCACGCCCT GCTCGCTTTC ACCCTCGGTG 250
TTAAGCAGCT CATTGTTGCT ATCAACAAGA TGGACTCCGT CAAGTGGTCT 300
CAGGATCGAT ACCTCGAGAT TTGCAAGGAG ACTGCCAACT TCGTCAAGAA 350
GGTCGGTTAC AACCCCAAGG CTGTCCCCTT CGTCCCCATT TCCGGATGGA 400
ACGGTGACAA CATGATCGAG CCCTCTACCA ACTGTGACTG GTACAAGGGA 450
TGGACCAAGG AGACCAAGGC CGGCGAGATC AAGGGTAAGA CCCTCCTCGA 500
GGCCATTGAT GCCATTGAGC CCCCCGTGCG ACCCCACGAC AAGCCCCTCC 550
GACTTCCCCT CCAGGATGTC TACAAGATCG GTGGTATCGG CACAGTGCCC 600
GTTGGCCGAG TCGAGACCGG TGTTATCAAG GCCGGTATGG KTGTTACCTT 650
CGCTCCCGCC AACGTGACCA CTGAGGTCAA GTCTGTCGAG ATGCACCACG 700
AGATCCTCCC CGATGGAGGT TTCCCCGGTG ACAACGTCGG TTTCAACGTC 750
AAGAACGTTT CCGTCAAGGA TATCCGACGA GGTAACGTTG CTGGTGACTC 800
CAAGAACGAC CCCCCCAAGG GCTGCGACTC TTTCAACGCT CAGGTCATTG 850
TTCTTAACCA CCCCGGTCAG ATCGGTGCTG GTTACGCTCC CGTCCTTGAT 900
TGCCACACTG CCCACATTGC TTGCAAGTTC GACACCCTGA TCGAGAAGAT 950
CGACCGACGA ACCGGTAAGA AGATGGAGGA CTCCCCCAAG TTCATCAAGT 1000
CTGGTGATGC TGCCATTGTC AAGATGGTTC CCTCCAAGCC CATGTGTGTC 1050
GAGGCCTTCA CTGAGTACCC CCCTCTTGGT CGATTCGCCG TCCGAGA 1097

2) INFORMATION FOR SEQ ID NO: 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1233 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Absidia corymbifera*
(B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

```
CAAGCTTAAG GCTGAACGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT      50
GGAAGTTCGA GACTCCCAAG TACCACGTTA CCGTCATTGA TGCCCCTGGC     100
CATCGTGATT TCATCAAGAA CATGATTACT GGTACTTCCC AAGCTGACTG     150
CGGTATCTTG ATTATTGCTG CTGGTACTGG TGAATTCGAA GCTGGTATCT     200
CCAAGGATGG TCAAACCCGT GAACACGCTT TGCTTGCTTT CACCCTTGGT     250
GTCCGTCAAT TGATTGTCGC TATCAACAAG ATGGATTCCA CCAAGTACTC     300
TGAGGCCCGT TACAACGAAA TTGTCAAGGA AGTCTCCACC TTCATCAAGA     350
AGATTGGTTT CAACCCCAAG TCCGTTCCTT TCGTCCCTAT CTCTGGCTGG     400
AACGGTGACA ACATGTTGGA GGARTCCACC AACATGCCTT GGTTCAAGGG     450
ATGGAACAAG GAGACTAAGG CTGGTGCCAA GACYGGCAAG ACCCTTCTTG     500
AAGCCATTGA CAACATTGAT CCCCCTGTTC GTCCTTCCGA CAAGCCCCTT     550
CGTCTTCCCC TTCAAGATGT CTACAAGATC GGTGGTATTG GTACAGTTCC     600
TGTCGGTCGT GTTGAGACTG GTGTCATCAA GCCTGGTATG GTTGTCACCT     650
TCGCTCCCGC TAACGTCACC ACTGAAGTCA AGTCCGTYGA AATGCACCAC     700
GAGCAACTTG CTGAAGGTGT TCCCGGTGAC AACGTCGGTT TCAACGTCAA     750
GAACGTTTCC GTCAAGGATA TCCGCCGTGG TAACGTYTGC TCTGACTCCA     800
AGAACGACCC CGCCAAGGAA TCCGCTTCCT TCACCGCTCA AGTTATTGTC     850
TTGAACCACC CTGGTCARAT TGGTGCTGGT TACTCTCCTG TCTTGGATTG     900
CCACACTGCT CACATTGCAT GCAAGTTCTY TKAGCTTCTT KAGAAGATCG     950
ATYGTCGTTC CGGTAAGTAA ATANTTTGGT TTRGGATATG GGTATTGGGC    1000
TTAATCTYTG GATTTTGCCT CAATTGCTCC TTCCTTGATC TTTCTCGATT    1050
ACTTTTTGAT CATTTGCTAA TCCAAACCCT TTCCATTTYA TTGAAAACAG    1100
GTAAGAAGTT GGAAGACTCC CCCAAGTTCG TCAAGWSYGG TGACTCTGCY    1150
ATCGTCAAGA TGGTTCCTTC CAAGCCCATG TGCGTTGAAG CCTACACTGA    1200
ATATCCTCCT CTTGGTCGTT TCGCTGTCCG TGA                      1233
```

2) INFORMATION FOR SEQ ID NO: 401

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1151 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Alternaria alternata*
(B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

```
CAAGTTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTCT      50
GGAAGTTCGA GACTCCCAAG GTTAGTACCC CTCTGCCTAC TACATCAAGT     100
TCTTTACAAT GCTAACATGT TGTACTCAGT ACTATGTCAC CGTCATTGAC     150
GCCCCCGGTC ACCGTGATTT CATCAAGAAC ATGATCACTG GTACCTCCCA     200
GGCCGACTGC GCTATTCTCA TCATTGCCGC CGGTACTGGT GAGTTCGAGG     250
CTGGTATCTC CAAGGATGGC CAGACTCGTG AGCACGCTCT CCTCGCTTAC     300
ACCCTCGGTG TCAAGCAGCT CATCGTTGCC ATCAACAAGA TGGACACCAC     350
```

```
CAAGTGGTCC GAGGAGCGTT ACCAGGAGAT CATCAAGGAG ACCTCCAACT'     400
TCATCAAGAA GGTCGGCTAC AACCCCAAGC ACGTTCCCTT CGTCCCCATC     450
TCCGGTTTCA ACGGTGACAA CATGATTGAG GCCTCATCCA ACTGCCCCTG     500
GTACAAGGGT TGGGAGAAGG AGACCAAGGC CAAGGCCACT GGTAAGACCC     550
TCCTCGAGGC CATCGACGCC ATCGACCCTY CCAGCCGTCC CACCGACAAG     600
CCCCTCCGTC TTCCCCTYCA GGATGTTTAC AAGATTGGTG GTATTGGCAC     650
GGTGCCCGTC GGTCGTGTCG AGACCGGTAT CATCAAGGCC GGTATGGTCG     700
TCACCTTCGC CCCCGCTGGT GTCACCACTG AAGTCAAGTC CGTCGAGATG     750
CACCACGAGC AGCTCACCGA GGGTGTCCCC GGTGACAACG TCGGCTTCAA     800
CGTCAAGAAC GTCTCCGTCA AGGAGATCCG TCGTGGTAAC GTTGCCGGTG     850
ACTCCAAGAA CGACCCCCCC AAGGGTGCCG AGTCCTTCAA CGCCCAGGTC     900
ATCGTCCTCA ACCACCCTGG TCAGGTCGGT GCTGGTTACG CCCCAGTCCT     950
CGACTGCCAC ACCGCCCACA TTGCTTGCAA GTTCTCTGAG CTCCTCGAGA    1000
AGATTGACCG CCGTACCGGA AAGTCTGTTG AGAACTCTCC CAAGTTCATC    1050
AAGTCCGGTG ACGCCGCCAT CGTCAAGATG GTTCCCTCCA AGCCCATGTG    1100
CGTTGAGGCT TTCACTGACT ACCCTCCTCT CGGTCGTTTC GCTGTCCGTG    1150
A                                                        1151
```

2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1283 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aspergillus flavus*
- (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

```
CAAGCTCAAG TCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCCTCT      50
GGAAGTTCCA GACCTCCAAG TATGAGGTCA CCGTCATTGG TAAGCATTTG     100
AGTTCCAACC TACGTTGCCC AACATTTACA GTCATCTAAC AAAGTTCAAT     150
AGATGCCCCC GGTCACCGTG ACTTCATCAA GAACATGATC ACTGGTACTT     200
CCCAGGCTGA CTGCGCTATC CTCATCATTG CCTCCGGTAC TGGTGAATTC     250
GAGGCTGGTA TCTCCAAGGA TGGTCAGACC CGTGAGCACG CTCTGCTCGC     300
TTTCACCCTC GGTGTCCGTC AGCTCATCGT TGCCCTCAAC AAGATGGACA     350
CCTGCAAGTG GTCTCAGGAT CGTTACAACG AAATCGTTAA GGAGACTTCC     400
AACTTCATCA AGAAGGTCGG ATACAACCCC AAGAGCGTTC CTTTCGTCCC     450
CATCTCCGGT TTCAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC     500
CCTGGTACAA GGGTTGGGAG AAGGAGACCA AGGCTGGCAA GTCCACCGGT     550
AAGACCCTTC TCGAGGCCAT CGATGCCATC GAGCCCCCCG TCCGTCCCAC     600
CGACAAGCCT CTCCGTCTTC CCCTYCAGGA TGTCTACAAG ATCTCTGGTA     650
TCGGTACTGT GCCCGTCGGT CGTGTCGAGA CTGGTGTCAT CAAGCCTGGT     700
ATGGTCGTTA CTTTCGCTCC TGCCAACGTG ACCACTGAAG TCAAGTCCGT     750
TGAAATGCAC CACCAGCAGC TCCAGGCCGG TAACCCCGGT GACAACGTTG     800
GTTTCAACGT CAAGAACGTC TCCGTCAAGG AAGTCCGCCG TGGTAACGTT     850
GCCGGTGACT CCAAGAACGA CCCCCCTGCT GGCTGCGATT CCTTCAACGC     900
CCAGGTCATC GTCCTTAACC ACCCCGGTCA GGTCGGCAAC GGTTACGCTC     950
CCGTCCTGGA CTGCCACACC GCTCACATTG CTTGCAAGTT CGCTGAGCTC    1000
CTTGAGAAGA TTGACCGCCG TACCGGTAAA TCTGTTGAGG ACAAGCCCAA    1050
GTTCATCAAG TCTGGTGATG CTGCCATCGT CAAGATGATT CCCTCCAAGC    1100
CCATGTGTGT GGAGTCTTTC ACTGACTTCC CCCCTCTTGG TCGTTTCGCT    1150
GTCCGTGACG TAAGTTTTTC CCTCTTGACT ATCTTCACAA TTTTTCACAT    1200
```

ATTTTCACGC CTCGTCCCAC TCTTTTTCCT CCCTTCCTCT TTGGTTCCCC 1250
TTTTTGCCTG CAAGTTCTCT ATAGCTAACA TGA 1283

2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1103 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: DAL95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50
GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT 100
ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTCACCGT 150
GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200
CCTCATCATT GCCTCCGGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250
ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300
CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350
TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG 400
GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCAACGGT 450
GACAACATGC TTGAGCCCTC CTCCAACTGC CCCTGGTACA AGGGATGGGA 500
GAAGGAGACC AAGGCCGGCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA 550
TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600
CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCGG 650
CCGTGTCGAG ACCGGTATCA TCAAGCCCGG CATGGTCGTC ACCTTCGCCC 700
CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750
CTCCAGGAGG GTGTCCCCGG TGACAACGTC GGTTTCAACG TCAAGAACGT 800
TTCCGTCAAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850
ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900
CACCCCGGTC AGGTCGGCGC TGGTTACGCC CCCGTCCTCG ACTGCCACAC 950
TGCCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000
GTACCGGCAA GTCTGTTGAG AACAACCCCA AGTTCATCAA GTCCGGTGAT 1050
GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100
CAC 1103

2) INFORMATION FOR SEQ ID NO: 404

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1149 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

```
AAGCTCAAGT CCGAGCGTGA GCGTGGTATC ACCATCGACA TTGCCCTCTG      50
GAAGTTCCAG ACTCCCAAGT ATGAGGTCAC TGTCATCGGT AAGCTCGACT     100
CGCCCCGATA TGTTTTGGTG CTGTAGCTAA CACGATCTGA AGATGCCCCC     150
GGTCACCGTG ACTTCATCAA GAACATGATC ACTGGTACCT CCCAGGCTGA     200
CTGCGCTATC CTCATCATTG CCTCCGGTAC TGGTGAGTTC GAGGCTGGTA     250
TCTCCAAGGA TGGCCAGACC CGTGAGCACG CTCTGCTGGC TTTCACCCTC     300
GGTGTCAAGC AGCTCATCGT CGCCCTCAAC AAGATGGACA CCTGCAAGTG     350
GTCCGAGGAT CGTTACAACG AAATTGTCAA GGAAACCTCC AACTTCATCA     400
AGAAGGTCGG CTACAACCCC AAGGCCGTTC CCTTCGTCCC CATCTCTGGC     450
TTCAACGGTG ACAACATGCT TGAGCCCTCC TCCAACTGCC CCTGGTACAA     500
GGGATGGGAG AAGGAGACCA AGGCCGGCAA GGTCACTGGT AAGACCCTCA     550
TCGAGGCCAT CGACGCCATT GAGCCCCCTG TCCGTCCCTC CAACAAGCCC     600
CTCCGTCTTC CCCTCCAGGA TGTCTACAAG ATCTCTGGTA TCGGAACGGT     650
CCCTGTCGGC CGTGTCGAGA CCGGTATCAT CAAGCCCGGC ATGGTCGTCA     700
CCTTCGCCCC CGCCAACGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC     750
CACCAGCAGC TCCAGGAGGG TGTCCCCGGT GACAACGTCG GTTTCAACGT     800
CAAGAACGTT TCCGTCAAGG AAGTCCGCCG TGGTAACGTC TGCGGTGACT     850
CCAAGAACGA TCCCCCTCAG GGTGCTGCCT CCTTCAACGC CCAGGTCATC     900
GTCCTCAACC ACCCCGGTCA GGTCGGCGCT GGTTACGCCC CCGTCCTCGA     950
CTGCCACACT GCCCACATTG CTTGCAAGTT CTCTGAGCTG CTTGAGAAGA    1000
TTGACCGCCG TACCGGCAAG TCTGTTGAGA ACAACCCCAA GTTCATCAAG    1050
TCCGGTGATG CCGCCATCGT GAAGATGGTT CCTTCCAAGC CCATGTGTGT    1100
CGAGTCCTTC ACTGACTACC CCCCTCTGGG TCGTTTCGCC GTCCGTGAC     1149
```

2) INFORMATION FOR SEQ ID NO: 405

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1151 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aspergillus niger*
- (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

```
CAAGCTCAAG TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT      50
GGAAGTTCCA GACTGGCAAG TATGAGGTCA CCGTCATTGG TATGTACTCA     100
CAGAGTTCTC TTTTCATCAA AGCAATATAC TAACGTCCAT CATAGACGCC     150
CCCGGTCACC GTGACTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC     200
TGACTGCGCT ATCCTCATCA TTGCCTCCGG TACTGGTGAG TTCGAGGCTG     250
GTATCTCCAA GGATGGCCAG ACTCGTGAGC ACGCTCTGCT TGCTTTCACC     300
CTCGGTGTCC GCCAGCTCAT CGTTGCCCTC AACAAGATGG ACACCTGCAA     350
GTGGTCCGAG GACCGTTACA ACGAAATCGT TAAGGAGACC TCCAACTTCA     400
TCAAGAAGGT CGGATACAAC CCCAAGGGTG TTCCTTTCGT CCCCATCTCC     450
GGTTTCAACG GTGACAACAT GCTCGAGCCC TCCCCCAACT GCCCCTGGTA     500
CAAGGGTTGG GAGAAGGAGA CCAAGGCCGG CAAGGTCACC GGTAAGACCC     550
TCCTTGAGGC CATCGACGCC ATCGAGCCCC CCGTCCGTCC CTCCAACAAG     600
CCCCTCCGTC TTCCCCTCCA GGATGTCTAC AAGATCTCCG GTATTGGAAC     650
TGTTCCCGTC GGTCGTGTCG AGACCGGTAT CATTGCCCCT GGTATGGTCG     700
TGACCTTCGC TCCCGCCAAC GTCACCACTG AAGTCAAGTC CGTTGAGATG     750
```

CACCACCAGC AGCTCAAGGA AGGTGTCCCC GGTGACAACG TTGGTTTCAA 800
CGTCAAGAAC GTTTCCGTCA AGGAGGTTCG CCGTGGTAAC GTTGCCGGTG 850
ACTCCAAGAA CGACCCCCCT CTTGGCTGTG AGAGCTTCAC CGCCCAGGTC 900
ATCGTCCTCA ACCACCCCGG TCAGGTCGGC GCTGGTTACG CTCCCGTCCT 950
GGACTGCCAC ACTGCTCACA TTGCTTGCAA GTTCGCTGAG CTCCTTGAGA 1000
AGATTGACCG CCGTACCGGA AAGTCTGTTG AATCTTCCCC CAAGTTCATC 1050
AAGTCCGGTG ACGCTGCCAT CGTCAAGATG ATTCCCTCCA AGCCCATGTG 1100
TGTTGAGGCT TTCACTGACT ACCCCCCTCT TGGTCGTTTC GCCGTCCGCG 1150
A 1151

2) INFORMATION FOR SEQ ID NO: 406

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1093 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Blastoschizomyces capitatus*
(B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

GCTTAAAGCT GAACGTGAAC GTGGTATCAC CATTGATATC GCTCTCTGGA 50
AGTTCGAAAC TCCTAAGTAC TACGTTACTG TTATTGATGC TCCAGGTCAC 100
CGTGATTTCA TCAAGAACAT GATTACTGGT ACTTCCCAAG CCGATTGCGC 150
CATTCTTATC ATTGCTGCCG GTGTCGGTGA ATTCGAAGCT GGTATCTCCA 200
AGGAAGGTCA AACCAGAGAA CACGCTCTTC TCGCTTTCAC CCTTGGTGTC 250
AGACAACTTA TCATTGCCAT CAACAAGATG GACTCTGTCA AGTGGGACCA 300
AAAGAGATAC GAAGAAATCG TCAAGGAGGC TTCCAACTTC GTCAAGAAGG 350
TTGGTTACAA CCCCAAGTCT GTTCCATTCG TTCCTATCTC TGGTTGGAAC 400
GGTGACAACA TGTTGGAACC TACCACCAAC GCCCCATGGT ACAAGGGATG 450
GACCAAGGAA ACCAAGGCTG GTGCCACTAA GGGTATGACT CTTATTGAAG 500
CCATTGACGC CATTGAACCA CCAGTAAGAC CATCCGACAA GCCACTCCGT 550
CTCCCACTCC AAGATGTTTA CAAGATTGGT GGTATCGGAA CTGTGCCAGT 600
CGGCCGTGTC GAAACCGGTA TCATCAAGGC CGGTATGGTC GTTACCTTTG 650
CTCCACCAAT GGTCACAACT GAAGTTAAGT CCGTTGAAAT GCACCACGAA 700
CAACTTGCTC AAGGTAACCC AGGTGACAAC GTTGGTTTCA ACGTCAAGAA 750
CGTTTCCGTT AAGGAAATCA GACGTGGTAA CGTCTGTGGT GACTCCAAGA 800
ACGATCCACC AAAGGGCTGC GAATCTTTCA ACGCTCAAGT TATCGTCTTG 850
AACCACCCTG GTCAAATCTC TGCTGGTTAC TCTCCAGTTC TCGATTGCCA 900
CACTGCCCAC ATTGCCTGCA GATTCGACGA ACTCCTTGAA AAGATCGACC 950
GTCGTTCTGG TAAGAAGATT GAAGACTCTC CAAAGTTTGT CAAGTCTGGT 1000
GATGCCGCTA TCGTCAAGAT GATCCCAACC AAGCCAATGT GCGTTGAAAC 1050
CTTCACTGAA TACCCACCAC TTGGTCGTTT CGCCGTCCGT GAT 1093

2) INFORMATION FOR SEQ ID NO: 407

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 10231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

```
CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT     100
CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC     150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG     200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT     250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA     300
ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACTTCG     350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTYGT TCCAATCTCT     400
GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA     450
CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT     500
TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA     550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC     600
TGTGCCAGTC GGTAGAGTTG AAACTGGTAT CATCAAAGCC GGTATGGTTG     650
TTACTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG     700
CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA     750
CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG     800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC     850
ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT     900
GGATTGTCAC ACTGCCCACA TTGCTTGTAA ATTCGACACT TTGGTTGAAA     950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC    1000
AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG    1050
TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG    1100
A                                                        1101
```

2) INFORMATION FOR SEQ ID NO: 408

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1089 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

```
GAAGGCTGAA AGAGAAAGAG GTATCACCAT TGATATCGCT TTGTGGAAAT      50
TCGAAACTCC AAAATACCAC GTTACCGTCA TTGATGCTCC AGGTCACAGA     100
GATTTCATCA AGAATATGAT CACTGGTACT TCTCAAGCTG ATTGTGCTAT     150
TTTGATTATT GCTGGTGGTA CTGGTGAATT CGAAGCCGGT ATTTCTAAGG     200
ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACTTT GGGTGTCAAA     250
CAATTGATTG TTGCTGTCAA CAAGATGGAC TCTGTCAAAT GGGACAAAAA     300
CAGATTTGAA GAAATCATCA AGGAAACCTC CAACTTCGTC AAGAAGGTTG     350
GTTACAACCC AAAGACTGTT CCATTCGTTC CAATCTCTGG TTGGAATGGT     400
GACAACATGA TTGAACCATC CACCAACTGT CCATGGTACA AGGGTTGGGA     450
```

AAAGGAAACC AAATCCGGTA AAGTTACTGG TAAGACCTTG TTAGAAGCTA 500
TTGACGCTAT TGAACCACCA ACCAGACCAA CCGACAAACC ATTGAGATTG 550
CCATTGCAAG ATGTTTACAA GATCGGTGGT ATTGGTACTG TGCCAGTCGG 600
TAGAGTTGAA ACTGGTATCA TCAAAGCCGG TATGGTTGTT ACTTTCGCCC 650
CAGCTGGTGT TACCACTGAA GTCAAATCCG TTGAAATGCA TCACGAACAA 700
TTGGCTGAAG GTGTTCCAGG TGACAATGTT GGTTTCAACG TTAAGAACGT 750
TTCCGTTAAA GAAATTAGAA GAGGTAACGT TTGTGGTGAC TCCAAGAACG 800
ATCCACCAAA GGGTTGTGAC TCTTTCAATG CCCAAGTCAT TGTTTTGAAC 850
CATCCAGGTC AAATCTCTGC TGGTTACTCT CCAGTCTTGG ATTGTCACAC 900
TGCCCACATT GCTTGTAAAT TCGACACTTT GGTTGAAAAG ATTGACAGAA 950
GAACTGGTAA GAAATTGGAA GAAAATCCAA AATTCGTCAA ATCCGGTGAT 1000
GCTGCTATCG TCAAGATGGT CCCAACCAAA CCAATGTGTG TTGAAGCTTT 1050
CACTGACTAC CCACCATTAG GTAGATTCGC TGTCAGAGA 1089

2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 56884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC 150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT 400
GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAACTGGTAT CATCAAAGCC GGTATGGTTG 650
TTACTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
GGATTGTCAC ACTGCCCACA TTGCTTGTAA ATTCGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
A 1101

2) INFORMATION FOR SEQ ID NO: 410

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1102 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 60193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC 150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT 400
GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAACTGGTAT CATCAAAGCC GGTATGGTTG 650
TTACTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
GGATTGTCAC ACTGCCCACA TTGCTTGTAA ATTCGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
AT 1102

2) INFORMATION FOR SEQ ID NO: 411

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1102 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 90028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC 150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200

GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT 400
GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAACTGGTAT CATCAAAGCC GGTATGGTTG 650
TTACTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
GGATTGTCAC ACTGCCCACA TTGCTTGTAA ATTCGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
AT 1102

2) INFORMATION FOR SEQ ID NO: 412

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida dubliniensis*
(B) STRAIN: NCPF 3108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

CTTGGATAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT 400
GGTTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAGGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAACTGGTGT CATTAAAGCC GGTATGGTTG 650
TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAT GTTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
GGATTGTCAC ACTGCCCACA TTGCTTGTAA ATTCGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100

A 1101

2) INFORMATION FOR SEQ ID NO: 413

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida catenulata*
(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT 50
TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC 100
GGTCACAGAG ATTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA 150
CTGTGCTATC TTGATCATTG CTTCCGGTGT CGGTGAGTTC GAGGCTGGTA 200
TCTCCAAGGA CGGTCAGACC CGTGAGCACG CCTTGTTGGC CTACACCTTG 250
GGTGTCAAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG 300
GGACAAGAAC AGATTCGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA 350
AGAAGGTTGG TTACAACCCC AAGGCTGTCC CCTTCGTCCC CATCTCTGGC 400
TGGAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC CCTGGTACAA 450
GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT 500
TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC 550
TTGAGATTGC CCTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT 600
GCCCGTCGGC CGTGTCGAGA CCGGTGTCAT CAAGCCCGGT ATGGTCGTCA 650
CCTTCGCCCC CGCTGGTGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC 700
CACGAGCAGT TGTCCGAGGG TGTCCCCGGT GACAACGTTG GTTTCAACGT 750
CAAGAACGTC TCTGTTAAGG AGATCAGACG TGGTAACGTC TGCGGTGACT 800
CCAAGAACGA CCCCCCCATG GGTTGCTCTT CTTTCAACGC CCAGGTTATC 850
GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTTACTCTC CCGTCTTGGA 900
CTGCCACACC GCCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA 950
TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG 1000
TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT 1050
TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCGCC GTCAGAGA 1098

2) INFORMATION FOR SEQ ID NO: 414

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1102 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida dubliniensis*
(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

CTTGGATAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTCG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT 400
GGTTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAGGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAACTGGTGT CATTAAAGCC GGTATGGTTG 650
TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGTTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAT GTTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTAYT CTCCAGTCTT 900
GGATTGTCAC ACTGCCCACA TTGCTTGTAA ATTCGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
AT 1102

2) INFORMATION FOR SEQ ID NO: 415

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1102 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida dubliniensis*
(B) STRAIN: CBS 7987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

CTTGGATAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTYG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT 400
GGTTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAGGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAACTGGTGT CATTAAAGCC GGTATGGTTG 650
TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGTTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAT GTTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850

ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTAYT CTCCAGTCTT 900
GGATTGTCAC ACTGCCCACA TTGCTTGTAA ATTCGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
AT 1102

2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1094 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida famata*
(B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

AATTGAAGGC TGAAAGAGAA AGAGGTATCA CCATTGATAT CGCTTTATGG 50
AAATTCGAAA CTCCAAAATA CCACGTTACC GTTATTGATG CTCCAGGTCA 100
CAGAGATTTC ATCAAGAACA TGATTACTGG TACTTCTCAA GCTGATTGTG 150
CTATTTTRAT TATTGCTGGT GGTGTCGGTG AATTCGAAGC CGGTATCTCT 200
AAGGATGGTC AAACCAGAGA ACACGCTTTA TTGGCTTACA CCTTAGGTGT 250
TAGACAATTG ATTGTTGCCG TCAACAAGAT GGACTCTGTT AAATGGGACA 300
AGGCTAGATT CGAAGAAATC ATCAAGGAAA CCTCTAACTT CGTCAAGAAG 350
GTTGGTTACA ACCCTAAGAC TGTTCCTTTC GTYCCAATTT CTGGATGGAA 400
CGGTGACAAC ATGATTGAAG CCTCCACCAA CTGTCCATGG TACAAGGGTT 450
GGGAAAAGGA AACCAAGGCT GGTAAATCTA CTGGTAAGAC TTTGTTAGAA 500
GCCATTGATG CCATTGAACC ACCAACCAGA CCAACCGAAA AGCCATTGAG 550
ATTACCATTA CAAGATGTCT ACAAGATCGG TGGTATTGGT ACTGTGCCAG 600
TCGGTAGAGT TGAAACCGGT GTTATCAAGG GTGGTATGGT TGTTACCTTT 650
GCCCCAGCCG GTGTCACTAC CGAAGTCAAA TCCGTTGAAA TGCACCACGA 700
ACAATTAGCT GAAGGTGTTC CAGGTGACAA TGTTGGTTTC AACGTCAAGA 750
ACGTTTCCGT TAAGGAAATC AGAAGAGGTA ACGTTTGTGG TGACTCCAAG 800
AACGACCCAC CAAAGGGTGC TGAATCTTTC ACCGCTCAAG TTATTGTCTT 850
GAACCACCCA GGTCARATCT CTGCTGGTTA CTCTCCAGTC TTAGATTGTC 900
ACACCGCCCA CATTGCTTGT AAATTCGATG CTTTACTCGA AAAGATTGAC 950
AGAAGATCCG GTAAGAAATT AGAAGACGAA CCAAAATTCG TCAAGTCCGG 1000
TGATGCTGCT ATCGTCAAGA TGGTCCCAAC CAAACCAATG TGTGTTGAAG 1050
CTTTCACTGA ATACCCACCA TTAGGTAGAT TCGCTGTTAG AGAT 1094

2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida glabrata*
(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

TTTGGACAAG TTGAAGGCTG AAAGAGAAAG AGGTATCACT ATCGATATCG 50
CTTTGTGGAA GTTCGAAACT CCAAAGTACC ACGTYACCGT TATCGATGCY 100
CCAGGTCACA GAGATTTCAT CAAGAACATG ATTACTGGTA CTTCTCAAGC 150
TGACTGTGCT ATCTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCYG 200
GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTCTATT GGCTTTCACC 250
CTAGGTGTTA GACAATTGAT TGTYGCTGTC AACAAGATGG ACTCTGTCAA 300
GTGGGATGAA TCCAGATTCG CTGAAATCGT TAAGGAAACC TCCAACTTCA 350
TCAAGAAGGT CGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT 400
GGTTGGAACG GTGACAACAT GATTGAAGCC ACCACCAACG CTTCCTGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAAGGCTGG TGTCGTCAAG GGTAAGACCT 500
TGTTGGAAGC CATTGACGCT ATCGAACCAC CAACCAGACC AACTGACAAG 550
CCATTGAGAT TGCCATTGCA AGATGTCTAC AAGATCGGTG GTATCGGTAC 600
GGTGCCAGTC GGTAGAGTCG AAACCGGTGT CATCAAGCCA GGTATGGTTG 650
TTACCTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG 700
CACCACGAAC AATTGACTGA AGGTTTGCCA GGTGACAACG TTGGTTTCAA 750
CGTTAAGAAC GTTTCCGTTA AGGAAATCAG AAGAGGTAAT GTCTGTGGTG 800
ACTCCAAGAA CGACCCACCA AAGGCTGCTG CTTCTTTCAA CGCTACCGTC 850
ATTGTCTTGA ACCACCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTTTT 900
GGACTGTCAC ACCGCCCACA TTGCTTGTAA GTTCGAAGAA TTGTTGGAAA 950
AGAACGACAG AAGATCCGGT AAGAAGTTGG AAGACTCTCC AAAGTTCTTG 1000
AAGTCCGGTG ACGCTGCTTT GGTTAAGTTC GTTCCATCCA AGCCAATGTG 1050
TGTCGAAGCT TTCTCCGACT ACCCACCATT GGGTAGATTC GCTGTCAGAG 1100
A 1101

2) INFORMATION FOR SEQ ID NO: 418

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida guilliermondii*
(B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

AGAGAAAGAG GTATCACCAT TGACATTGCT TTGTGGAAAT TCGAGACTCC 50
AAAGTACCAC GTTACYGTCA TTGATGCCCC AGGTCACAGA GATTTCATCA 100
AGAACATGAT CACTGGTACT TCTCAAGCTG ACTGTGCTAT TTTGATTATT 150
GCTGGTGGTA CCGGTGAATT CGAAGCTGGT ATCTCTAAGG ATGGTCAAAC 200
CAGAGAGCAC GCTTTGTTGG CTTACACCTT GGGTGTTAGA CAATTGATTG 250
TTGCTGTCAA CAAGATGGAC TCCGTCAART GGGACAAGAA CAGATTYGAG 300
GAAATCATCA AGGAAACCTC TAACTTCGTC AAGAAGGTTG GTTACAACCC 350
TAAGACTGTG CCATTCGTTC CTATCTCTGG ATGGAAYGGT GACAACATGA 400
TTGAGGCTTC TACCAACTGT CCTTGGTACA AGGGATGGGA GAAGGAGACC 450
AAGGCTGGTA AGTCCACCGG TAAGACTTTG TTGGAGGCCA TTGACGCCAT 500
TGAGCCACCT CAAAGACCAA CCGACAAGCC ATTGAGATTG CCATTGCAAG 550
ATGTYTACAA GATTGGTGGT ATTGGAACGG TGCCAGTCGG TAGAGTTGAA 600

ACCGGTATCA TYAAGGCCGG TATGGTTGTT ACCTTTGCCC CAGCTGGTGT 650
YACCACTGAA GTCAAGTCCG TGGAAATGCA CCACGAACAA TTGGTTGAAG 700
GTGTTCCAGG TGACAATGTT GGTTTCAACG TTAAGAACGT TTCCGTTAAG 750
GAAATTAGAA GAGGTAACGT TTGTGGTGAC TCCAAGAACG ACCCACCAAA 800
GGGTTGTGAC TCTTTCACCG CTCAAGTTAT TGTGTTGAAC CACCCTGGTC 850
AAATCTCTGC TGGTTACTCT CCAGTTTTGG ACTGTCACAC CGCCCACATT 900
GCTTGTAAAT TCGACACCTT GTTGGAGAAG ATTGACAGAA GAACCGGTAA 950
GAAGATGGAG GACAACCCCA AGTTTGTCAA GTCCGGTGAC GCTTCTATCG 1000
TCAAGATGGT GCCATCCAAG CCAATGTGTG TTGAGGCTTT CACCGACTAC 1050
CCACCATTGG GAAGATTCGC CGTCAGAGAC 1080

2) INFORMATION FOR SEQ ID NO: 419

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida haemulonii*
(B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

TCTGTCAAGT GGGACAAGGC CAGATACGAG GAAATCGTCA AGGAGACCTC 50
TAACTTCGTC AAGAAGGTTG GTTACAACCC TAAGACTGTT CCATTCGTCC 100
CAATCTCTGG TTGGAACGGT GACAACATGA TTGAGGCTTC TACCAACTGT 150
GACTGGTACA AGGGTTGGGA GAAGGAGACC AAGTCTGGTA AGTCCACCGG 200
TAAGACCTTG TTGGAGGCCA TTGACGCCAT TGAGCCACCA ACCAGACCAA 250
CCGACAAGCC ATTGAGATTG CCATTGCAGG ATGTCTACAA GATTGGTGGT 300
ATCGGAACTG TGCCAGTCGG CAGAGTTGAG ACCGGTGTTA TCAAGGCCGG 350
TATGGTTGTC ACCTTCGCCC CAGCTGGTGT CACCACTGAA GTCAAGTCTG 400
TCGAGATGCA CCACGAGCAG TTGCCAGAGG GTGTCCCAGG TGACAACGTT 450
GGTTTCAACG TCAAGAACGT TTCCGTTAAG GAAATCAGAA GAGGTAACGT 500
CTGTGGTGAC TCCAAGCAGG ACCCACCAAA GGGCTGTGAC TCTTTCACCG 550
CTCAGGTTAT TGTGTTGAAC CACCCAGGTC AGATCTCTTC TGGTTACTCT 600
CCAGTTTTGG ACTGTCACAC TGCCCACATT GCTTGTAAGT TCGACACCTT 650
GGTTGAGAAG ATCGACAGAA GAACCGGTAA GAAGTTGGAA GATGAGCCAA 700
AGTTCATCAA GTCCGGTGAC GCTGCTATCG TCAAGATGGT CCCAACCAAG 750
C 751

2) INFORMATION FOR SEQ ID NO: 420

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1102 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida inconspicua*

(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

```
TCTTGACAAG TTAAAGGCTG AAAGAGAAAG AGGTATCACT ATTGATATTG      50
CTTTATGGAA ATTCGAAACT CCAAAGTATC ACGTTACCGT CATTGATGCT     100
CCAGGTCACA GAGATTTCAT TAAGAACATG ATTACTGGTA CTTCTCAAGC     150
AGATTGTGCT ATTTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG     200
GTATTTCCAA GGATGGTCAA ACTAGAGAAC ACGCTTTATT AGCATTCACC     250
TTAGGTGTTA AGCAATTGAT TGTTGCTATC AACAAGATGG ATTCTGTTAA     300
GTGGGATGAA AAGAGATTTG AAGAAATTGT CAAGGAAACC CAAAACTTCA     350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATTTCT     400
GGTTGGAATG GTGACAACAT GATTGAACCA TCTTCTAACT GTCCATGGTA     450
CAAGGGTTGG ACTAAGGAAA CCAAGGCAGG TGTTGTCAAG GGTAAGACCT     500
TATTAGAAGC TATTGATGCT ATTGAACCAC CTGTCAGACC AACTGATAAG     550
CCATTAAGAT TACCATTACA AGATGTTTAC AAGATTGGTG GTATTGGTAC     600
TGTGCCAGTC GGTAGAGTTG AAACCGGTAT TATTAAGCCA GGTATGGTTG     650
TTGTTTTCGC ACCATCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG     700
CACCATGAAC AATTAGAAGA AGGTGTCCCA GGTGACAATG TTGGTTTCAA     750
CGTCAAGAAC GTCTCTGTTA AGGATATCAA GAGAGGTAAC GTTTGTGGTG     800
ACTCCAAGAA TGACCCACCA CAAGGTTGTG CTTCCTTCAA TGCTCAAGTC     850
ATTGTCTTGA ACCACCCTGG TCAAATTTCT GCTGGTTACT CTCCAGTTTT     900
AGATTGTCAC ACTGCCCACA TTGCATGTAA ATTCGATGAA TTAATTGAAA     950
AGATTGACAG AAGAACTGGT AAGTCCGTTG AAGACCATCC AAAGTCTGTT    1000
AAGTCTGGTG ATGCAGCTAT CGTTAAGATG GTTCCAACCA AGCCAATGTG    1050
TGTTGAAGCT TTCACTGAAT ACCCACCATT AGGTAGATTC GCAGTCAGAG    1100
AT                                                       1102
```

2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida kefyr*
(B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

```
TGGACAAGTT AAAGGCTGAA AGAGAAAGAG GTATCACCAT CGATATCGCT      50
TTGTGGAAGT TCGAAACTCC AAAGTACCAA GTTACCGTTA TCGATGCTCC     100
AGGTCACAGA GATTTCATCA AGAACATGAT TACTGGTACT TCTCAAGCTG     150
ACTGTGCTAT CTTGATTATT GCTGGTGGTG TCGGTGAATT CGAAGCCGGT     200
ATCTCCAAGG ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACCTT     250
GGGTGTTAGA CAATTGATTG TTGCTATCAA CAAGATGGAC TCTGTTAAGT     300
GGGATGAATC TCGTTACCAA GAAATTGTTA AGGAAACCTC CAACTTCATC     350
AAGAAGGTCG GTTACAACCC AAAGAATGTT CCATTCGTCC CAATCTCTGG     400
TTGGAACGGT GACAACATGA TTGAAGCCAC CACCAACGCT CCATGGTACA     450
AGGGTTGGGA AAAGGAAACC AAGGCTGGTA CCGTCAAGGG TAAGACCTTG     500
TTGGAAGCTA TTGACGCTAT CGAACCACCA ACCAGACCAA CTGACAAGCC     550
ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT ATTGGTACTG     600
TGCCAGTCGG TAGAGTCGAA ACCGGTGTCA TCAAGCCAGG TATGGTTGTT     650
ACCTTCGCCC CAGCCGGTGT CACTACCGAA GTTAAGTCCG TCGAAATGCA     700
```

CCACGAACAA TTGGAAGAAG GTCTACCAGG TGACAACGTC GGTTTCAACG 750
TCAAGAACGT TTCCGTTAAG GAAATCAGAA GAGGTAACGT CTGTGGTGAC 800
TCCAAGAACG ATCCACCAAA GGCTGCTGCT TCTTTCAACG CCACTGTTAT 850
CGTCTTGAAC CACCCAGGTC AAATCTCTGC TGGTTACTCT CCAGTTTTGG 900
ATTGTCACAC TGCTCACATT GCTTGTAAGT TCGACGAATT GTTGGAAAAG 950
AACGACAGAA GATCCGGTAA GAAGTTGGAA GACTCTCCAA AGTTCTTGAA 1000
GTCTGGTGAC GCTGCTTTGG TTAAGTTCGT TCCATCTAAG CCAATGTGTG 1050
TTGAAGCATT CTCTGACTAC CCACCATTGG GTAGATTCGC TGTCAGAGA 1099

2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida krusei*
(B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

AAGTTAAAGG CAGAAAGAGA AAGAGGTATC ACTATTGATA TTGCTTTATG 50
GAAGTTYGAA ACTCCAAART ACCACGTTAC CGTTATTGAT GCTCCAGGTC 100
ACAGAGATTT CATCAAGAAC ATGATTACCG GTACTTCTCA AGCTGATTGT 150
GCTATTTTGA TTATTGCTGG TGGTGTCGGT GAATTCGAAG CTGGTATCTC 200
CAAGGATGGT CAAACTAGAG AACACGCTCT ATTGGCTTTC ACCTTAGGTG 250
TTAGACAATT GATTGTTGCT ATCAACAAGA TGGATTCCGT TAARTGGGAT 300
GAAAACAGAT TTGAAGAAAT TGTCAAGGAA ACCCAAAACT TCATCAAGAA 350
GGTTGGTTAC AACCCAAAGA CTGTTCCATT CGTTCCAATY TCTGGTTGGA 400
ATGGTGACAA CATGATTGAA GCATCCACCA ACTGTCCATG GTACAAGGGT 450
TGGACTAAGG AAACCAAGGC AGGTGTTGTT AAGGGTAAGA CCTTATTAGA 500
AGCAATCGAT GCTATTGAAC CACCTGTCAG ACCAACCGAA AAGCCATTAA 550
GATTACCATT ACAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA 600
GTCGGTAGAG TCGAAACCGG TGTCATTAAG CCAGGTATGG TTGTCACTTT 650
TGCTCCAGCA GGTGTCACCA CCGAAGTCAA GTCCGTTGAA ATGCACCATG 700
AACAATTAGA ACAAGGTGTT CCAGGTGATA ACGTTGGTTT CAACGTTAAG 750
AACGTTTCTG TCAAGGATAT CAAGAGAGGT AACGTTTGTG GTGACTCCAA 800
GAACGACCCA CCAATGGGTG CAGCTTCCTT CAATGCTCAA GTCATTGTCT 850
TGAACCACCC TGGTCAAATT TCCGCTGGTT ACTCTCCAGT CTTGGATTGT 900
CACACTGCCC ACATTGCATG TAAGTTCGAC GAATTAATCG AAAAGATTGA 950
CAGAAGAACT GGTAAGTCTG TTGAAGACCA TCCAAAGTCY GTCAAGTCTG 1000
GTGATGCAGC TATCGTCAAG ATGGTCCCAA CCAAGCCAAT GTGTGTTGAA 1050
GCTTTCACTG AATAYCCACC ATTAGGTAGA TTCGCAGTCA GAGAT 1095

2) INFORMATION FOR SEQ ID NO: 423

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1104 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida lambica*
(B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

CTTGGACAAG CTTAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTATGGAA GTTCGAAACT CCAAAGTACC ACGTTACCGT CATTGACGCT 100
CCAGGTCACA GAGATTTCAT CAAGAACATG ATTACTGGTA CCTCTCAAGC 150
AGATTGTGCT ATTTTRATYA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG 200
GTATCTCTAA GGATGGTCAA ACCAGAGAAC ACGCTCTTCT TGCATTCACT 250
CTTGGTGTTA GACAATTGAT TGTTGCTATC AACAAGATGG ACTCTGTCAA 300
GTGGGACGAA TCCAGATTCG ATGAAATTTG TAAGGAAACC GCWAACTTCA 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT 400
GGTTGGAACG GTGACAACAT GATTGAACCA TCTGCTAACT GTCCATGGTA 450
CAAGGGATGG ACTAAGGAAA CCAAGGCTTC CGGTGTCGTC AAGGGTAAGA 500
CCCTTCTTGA AGCAATTGAT GCTATTGAGC CACCTGTCAG ACCAACTGAC 550
AAGGCTTTGA GATTGCCATT RCAAGATGTC TACAAGATTG GTGGTATTGG 600
TACTGTGCCA GTCGGTAGAG TTGAAACCGG TATCATCAAG CCAGGTATGA 650
TTGTCGTTTT CGCTCCAACC GGTGTTACTA CTGAAGTTAA GTCCGTTGAA 700
ATGCACCATG AACAATTAGA AGAAGGTGTC CCAGGTGACA ATGTTGGTTT 750
CAACGTCAAG AACGTCTCTG TTAAGGATAT TAAGAGAGGT AACGTCTGTG 800
GTGACTCCAA GAACGACCCA CCAATGGGTT GTGCTTCCTT CAATGCTCAA 850
GTCATTGTTC TTAACCACCC AGGTCAAATT TCTGCTGGTT ACTCACCAGT 900
TCTTGACTGT CACACTGCCC ACATTGCATG TAAGTTCGAY GAATTACTCG 950
AAAAGATTGA CAGAAGAACC GGTAAGGCTA CTGAAGACCA TCCAAAGTCT 1000
GTCAAGTCTG GTGATGCAGC TATCGTCAAG ATGGTTCCAA CCAAGCCAAT 1050
GTGTGTYGAA GCTTTCACTG ACTACCCACC ATTAGGTAGA TTCGCTGTYA 1100
GAGA 1104

2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida lusitaniae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

GGACAAGTTG AAGGCTGAGA GAGAAAGAGG TATCACCATC GATATCGCTT 50
TGTGGAAGTT CGAGACTCCA AAGTACCACG TTACCGTCAT TGACGCTCCA 100
GGTCACAGAG ATTTCATCAA GAACATGATC ACTGGTACTT CCCAAGCTGA 150
CTGTGCTATC TTGATTATCG CTGGTGGTGT CGGTGAGTTC GAAGCCGGTA 200
TCTCTAAGGA CGGTCAAACC AGAGAGCACG CTTTGTTGGC TTACACCTTG 250
GGTGTCAAGC AGTTGATTGT TGCTGTCAAC AAGATGGACT CCGTCAAGTG 300
GGACCAATCT AGATTCGAGG AAATCATCAA GGAAACCTCT AACTTCGTCA 350
AGAAGGTTGG TTACAACCCT AAGACTGTTC CATTCGTCCC AATCTCTGGT 400
TGGAACGGTG ACAACATGAT TGAGCCATCY ACCAACTGCC CATGGTACAA 450
GGGTTGGGAG AAGGAGACCA AGTCYGGTAA GTCCACCGGT AAGACCTTGT 500

```
TGGAGGCCAT TGACGCCATT GAGCCACCTT CGAGACCAAC CGACAAGCCA      550
TTGAGATTGC CATTGCAAGA TGTCTACAAG ATYGGTGGTA TTGGTACTGT      600
GCCAGTCGGT AGAGTTGAGA CCGGTGTCAT CAAGGCCGGT ATGGTTGTCA      650
CCTTTGCTCC AGCTGGTGTC ACCACTGAAG TCAAGTCCGT GGAAATGCAC      700
CACGAACAAT TGGCTGAGGG TGTCCCAGGT GACAACGTTG GTTTCAACGT      750
CAAGAACGTT TCCGTCAAGG AAATCAGAAG AGGTAACGTC TGTGGTGACT      800
CCAAGAACGA CCCACCAAAG GCTGCTGCTT CYTTCACTGC TCAAGTYATY      850
GTCTTGAACC ACCCAGGTCA AATCTCCTCY GGTTACTCTC CAGTYTTGGA      900
CTGTCACACT GCYCACATTG CTTGTAAGTT CGACACCTTG ATTGAGAAGA      950
TCGACAGAAG AACYGGTAAG AAGTTGGAAG AAGAGCCAAA GTTCATCAAG     1000
TCYGGTGACG CTGCTATCGT CAAGATGGTC CCAACCAAGC CAATGTGYGT     1050
YGAAGCTTTC ACCGACTACC CACCATTGGG TAGATTCGCT GTCAGAGA       1098
```

2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida norvegensis*
(B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

```
TCTTGACAAG TTAAAGGCTG AAAGAGAAAG AGGTATCACT ATTGATATTG       50
CTTTATGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT TATTGATGCT      100
CCAGGTCACA GAGATTTCAT TAAGAACATG ATTACTGGTA CTTCCCAAGC      150
TGATTGTGCT ATCTTAATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTTTATT AGCATTCACC      250
TTAGGTGTTA AGCAATTAAT TGTTGCTATC AACAAGATGG ACTCTGTTAA      300
GTGGGATGAA AAGAGATTTG AAGAAATTGT CAAGGAAACC CAAAACTTCA      350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATTTCT      400
GGTTGGAATG GTGACAACAT GATTGAACCA TCTACTAACT GTCCATGGTA      450
CAAGGGTTGG ACTAAGGAAA CCAAGGCAGG TGTTGTTAAG GGTAAGACCT      500
TATTAGAAGC TATTGATGCT ATTGAACCAC CTGTCAGACC AACTGACAAG      550
CCATTAAGAT TACCATTACA AGATGTTTAC AAGATTGGTG GTATTGGTAC      600
TGTGCCAGTC GGTAGAGTTG AAACCGGTGT TATTAAGCCA GGTATGGTTG      650
TTGTTTTCGC ACCATCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
CACCATGAAC AATTAGAACA AGGTGTCCCA GGTGACAATG TTGGTTTCAA      750
CGTCAAGAAC GTCTCTGTTA AGGATATTAA GAGAGGTAAC GTTTGTGGTG      800
ACTCCAAGAA CGACCCACCA CAAGGTTGTG CTTCCTTCAA TGCTCAAGTC      850
ATTGTCTTGA ACCACCCTGG TCAAATTTCT GCAGGTTACT CTCCAGTTTT      900
AGATTGTCAC ACTGCCCACA TTGCATGTAA GTTCGATGAA TTAATCGAAA      950
AGATTGACAG AAGAACTGGT AAGTCCGTTG AAGACCATCC AAAGTCTGTT     1000
AAGTCTGGTG ATGCAGCTAT CGTTAAGATG GTTCCAACCA AGCCAATGTG     1050
TGTTGAAGCT TTCACTGAAT ACCCACCATT AGGTAGATTC GCAGTCAGAG     1100
A                                                         1101
```

2) INFORMATION FOR SEQ ID NO: 426

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida parapsilosis*
(B) STRAIN: ATCC 90018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

```
CAAATTGAAG GCTGAAAGAG AAAGAGGTAT CACCATTGAT ATCGCTTTGT      50
GGAAATTCGA AACTCCAAAA TACCATGTTA CTGTTATTGA TGCTCCAGGT     100
CACAGAGATT TCATCAAGAA TATGATTACT GGTACTTCTC AAGCTGATTG     150
TGCTATTTTG ATTATTGCTG GTGGTACTGG TGAATTCGAA GCTGGTATCT     200
CTAAGGATGG TCAAACCAGA GAACACGCTT TGTTGGCTTA CACCTTGGGT     250
GTTAAGCAAT TGATTGTTGC CATCAACAAG ATGGACTCAG TCAAATGGGA     300
CAAGAACAGA TACGAAGAAA TTGTCAAGGA AACTTCCAAC TTCGTCAAGA     350
AGGTTGGTTA CAACCCTAAA GCTGTCCCAT TCGTCCCAAT CTCTGGTTGG     400
AACGGTGACA ATATGATTGA ACCATCAACC AACTGTCCAT GGTACAAGGG     450
TTGGGAAAAG GAAACTAAAG CTGGTAAGGT TACCGGTAAG ACCTTGTTGG     500
AAGCTATCGA TGCTATCGAA CCACCAACCA GACCAACTGA CAAGCCATTG     550
AGATTGCCAT TGCAAGATGT CTACAAGATT GGTGGTATTG GAACTGTGCC     600
AGTTGGTAGA GTTGAAACCG GTATCATCAA GGCTGGTATG GTTGTTACTT     650
TTGCCCCAGC TGGTGTTACC ACTGAAGTCA AGTCCGTTGA AATGCACCAC     700
GAACAATTGA CTGAAGGTGT CCCAGGTGAC AATGTTGGTT TCAACGTCAA     750
GAACGTTTCA GTTAAGGAAA TCAGAAGAGG TAACGTTTGT GGTGACTCCA     800
AGAACGATCC ACCAAAGGGA TGTGAYTCCT TCAATGCTCA AGTTATTGTC     850
TTGAACCACC CAGGTCAAAT CTCTGCTGGT TACTCACCAG TCTTGGATTG     900
TCACACTGCC CACATTGCTT GTAAATTCGA CACTTTGATT GAAAAGATTG     950
ACAGAAGAAC CGGTAAGAAA TTGGAAGATG AACCAAAATT CATCAAGTCC    1000
GGTGATGCTG CYATCGTCAA GATGGTCCCA ACCAAGCCAA TGTGTGTTGA    1050
AGCTTTCACT GACTACCCAC CATTGGGAAG ATTCGCTGTT AGAGA         1095
```

2) INFORMATION FOR SEQ ID NO: 427

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 752 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida rugosa*
(B) STRAIN: ATCC 96275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

```
CTCCGTCAAG TGGTCTCAGT CTCGTTTCGA GGAGATCGTC AAGGAGGTTT      50
CCAACTTCAT CAAGAAGGTT GGTTACAAGC CCGATGAGGT TCCTTTCGTC     100
CCCATCTCTG GCTGGAACGG CGACAACATG CTTGAGCCCT CCACCAACTG     150
CCCCTGGTAC AAGGGATGGA CCAAGAAGAC CAAGAAGGGT GAGGTCAAGG     200
GTAAGACTCT TCTCGAGGCC ATTGACGCCA TCGAGCCCCC CTCCCGTCCT     250
ACCGACAAGC CCCTCCGCTT GCCTCTTCAG GATGTCTACA AGATCGGCGG     300
```

TATCGGTACG GTACCTGTCG GCCGTGTCGA GACCGGTATC ATCAAGCCCG 350
GCATGGTCGT CACTTTCGCC CCCGCTGGTG TCACCACTGA AGTGAAGTCC 400
GTCGAGATGC ACCACGAGCA GATCCCCGAG GGTCTCCCCG GTGACAACGT 450
CGGTTTCAAC GTCAAGAACG TTACCGTCAA GGATATCCGC CGTGGTAACG 500
TCTGCGGTGA CTCCAAGAAC GACCCCCCCA AGGGCTGCTC TTCCTTCACT 550
GCCCAGGTCA TCGTTTTCAA CCACCCCGGT CAGATCTCCA ACGGTTACTC 600
CCCCGTTTTG GACTGCCACA CCGCCCACAT TGCCTGCCGC TTCGACGAGA 650
TCCAGTCCAA GATGGACCGT CGTACTGGTA AGACCCTTGA GGAGAACCCC 700
AAGTTCATCA AGGCTGGTGA CTCCGCTATC GTCAAGATGG TTCCCTCCAA 750
GC 752

2) INFORMATION FOR SEQ ID NO: 428

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1093 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida sphaerica*
(B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

AGTTAAAGGC TGAAAGAGAA AGAGGTATCA CCATCGATAT CGCTTTGTGG 50
AAGTTCGAAA CTCCAAAGTA CCAAGTTACC GTTATCGATG CTCCAGGTCA 100
CAGAGATTTC ATCAAGAACA TGATTACTGG TACTTCTCAA GCTGACTGTG 150
CTATCTTGAT TATTGCTGGT GGTGTCGGTG AATTCGAAGC CGGTATCTCC 200
AAGGATGGTC AAACCAGAGA ACACGCTTTG TTGGCTTTCA CCTTGGGTGT 250
TAGACAATTG ATTGTTGCTG TTAACAAGAT GGATTCCGTT AAGTGGGATG 300
AATCTCGTTT CCAAGAAATT GTCAAGGAAA CCTCTAACTT CATCAAGAAG 350
GTCGGTTACA ACCCAAAGAC TGTTCCATTC GTCCCAATCT CTGGTTGGAA 400
CGGTGACAAC ATGATTGAAG CCACCACCAA TGCTTCATGG TACAAGGGTT 450
GGGAAAAGGA AACCAAGTCC GGTGTCGTCA AGGGTAAGAC CTTGTTGGAA 500
GCTATTGACG CTATCGAACC ACCATCCAGA CCAACTGACA AGCCATTGAG 550
ATTGCCATTG CAAGATGTCT ACAAGATTGG TGGTATCGGA ACTGTGCCAG 600
TCGGTAGAGT CGAAACCGGT GTTATCAAGC CAGGTATGAT TGTTACCTTT 650
GCCCCAGCCG GTGTTACTAC TGAAGTTAAG TCCGTCGAAA TGCACCACGA 700
ACAATTGGAA GAAGGTCTAC CAGGTGACAA CGTCGGTTTC AACGTCAAGA 750
ACGTTTCCGT TAAGGAAATC AGAAGAGGTA ACGTCTGTGG TGACTCCAAG 800
AACGATCCAC CAAAGGCTGC TGCTTCTTTC AACGCCACTG TTATCGTCTT 850
GAACCATCCA GGTCAAATCT CTGCTGGTTA CTCTCCAGTT TTGGATTGTC 900
ACACTGCTCA CATTGCTTGT AAGTTCGACG AATTGTTGGA AAAGAACGAT 950
AGAAGATCCG GTAAGAAGTT GGAAGACTCT CCAAAGTTCT TGAAGTCCGG 1000
TGATGCTGCT TTGGTTAAGT TCGTTCCATC TAAGCCAATG TGTGTTGAAG 1050
CCTTCTCTGA CTACCCACCT CTAGGTAGAT TCGCTGTCAG AGA 1093

2) INFORMATION FOR SEQ ID NO: 429

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1094 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida tropicalis*
(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG 50
GAAATTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC 100
ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT 150
GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCGAAG CTGGTATTTC 200
TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG 250
TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC 300
AAAAACAGAT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA 350
GGTTGGTTAC AACCCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTGGA 400
ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT 450
TGGGAAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTTGGA 500
AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA 550
GATTGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA 600
GTCGGTAGAG TTGAAACTGG TGTCATCAAA GCCGGTATGG TTGTTACTTT 650
CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG 700
AACAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTTAAG 750
AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA 800
GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT 850
TGAACCACCC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT CTTGGATTGT 900
CACACTGCTC ATATTGCTTG TAAATTCGAC ACCTTGGTTG AAAAGATTGA 950
CAGAAGAACT GGTAAGAAAT TGGAAGAAAA TCCAAAATTC GTCAAATCCG 1000
GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA 1050
GCTTTCACTG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA 1094

2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida utilis*
(B) STRAIN: Csp 388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT 50
GGAAGTTCGA GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT 100
CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG 150
TGCTATTCTT ATCATTGCCG GTGGTGTTGG TGAGTTCGAG GCTGGTATCT 200
CTAAGGATGG TCAGACCAGA GAGCACGCTT TGCTCGCTTT CACCCTTGGT 250
GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGGA 300
CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA 350
AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG 400
AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG 450

```
TTGGGAGAAG GAGACCAAGG CTGGTGTTGT CAAGGGTAAG ACCTTGCTCG      500
ATGCCATTGA CGCCATTGAG CCACCAACAA GACCAACTGA CAAGCCATTG      550
AGATTGCCAC TCCAGGATGT CTACAAGATT GGTGGTATCG GAACTGTTCC      600
AGTCGGTAGA GTCGAGACCG GTGTCATCAA GCCAGGTATG GTTGTTACCT      650
TTGCCCCATC CGGTGTCACC ACTGAGGTTA AGTCCGTCGA GATGCACCAC      700
GAGCAGCTTG CTGAGGGTAT CCCAGGTGAC AACGTTGGTT TCAACGTTAA      750
GAACGTCTCT GTTAAGGAGA TCAGAAGAGG TAACGTTGCC GGTGACTCCA      800
AGAACGACCC ACCACAGGGT GCTGAGTCCT TCAACGCTCA GGTCATTGTC      850
TTGAACCACC CAGGTCAGAT CTCTGCTGGT TACTCTCCAG TTTTGGACTG      900
TCACACCGCC CACATTGCTT GTAAGTTCTC TGAGCTTTTG GAGAAGATTG      950
ACAGAAGATC CGGTAAGTCC CTTGAGGCCT CTCCAAAGTT CGTCAAGTCT     1000
GGTGATGCCG CTATCGTCAA GATGGTTCCA TCCAAGCCAT TGTGTGTTGA     1050
GGCCTTCACT GACTACCCAC CACTCGGTAG ATTCGCTGTC AGAGA          1095
```

2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1085 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida viswanathii*
(B) STRAIN: ATCC 28269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

```
GCTGAAAGAG AAAGAGGTAT CACCATCGAT ATCGCTTTGT GGAAATTCGA       50
AACTCCAAAR TACCACGTTA CCGTCATTGA YGCTCCAGGT CACAGAGATT      100
TCATCAAGAA CATGATYACT GGTACTTCTC AAGCTGATTG TGCTATYTTG      150
ATTATCGCTG GTGGTACTGG TGAATTCGAA GCTGGTATYT CTAAGGATGG      200
TCAAACCAGA GAACACGCTT TGTTGGCCTA CACCTTGGGT GTCAAGCAAT      250
TGATTGTTGC TGTCAACAAG ATGGACTCTG TCAAATGGGA CAAGAACAGA      300
TTCGAAGAAA TCATCAAGGA AACCTCCAAC TTCGTCAAGA AGGTTGGTTA      350
CAACCCAAAG ACTGTTCCAT TCGTCCCAAT CTCTGGTTGG AACGGTGACA      400
ACATGATTGA AGCCTCCACC AACTGCCCAT GGTACAAGGG TTGGGAAAAG      450
GAAACCAAGG CTGGTAAGGT TACCGGTAAG ACTTTGTTGG AAGCCATTGA      500
CGCTATCGAA CCACCAACCA GACCAACTGA CAAGCCATTG AGATTGCCAT      550
TGCAAGATGT CTACAAGATT GGTGGTATCG GAACTGTGCC AGTCGGTAGA      600
GTTGAAACTG GTGTCATCAA GGCCGGTATG GTTGTCACTT TYGCCCCAGC      650
TGGTGTTACC ACTGAAGTCA AGTCCGTTGA AATGCACCAC GAACAATTGG      700
CTGAAGGTGT CCCAGGTGAC AACGTTGGTT TCAACGTCAA GAACGTTTCC      750
GTCAAGGAAA TCAGAAGAGG TAACGTCTGT GGTGACTCCA AGAACGACCC      800
ACCAAAGGGT TGTGASTCTT TCAACGCTCA AGTCATTGTC TTGAACCACC      850
CAGGTCAAAT CTCTGCTGGT TACTCTCCAG TCTTGGATTG TCACACTGCC      900
CACATTGCTT GTAAGTTTGA CACCTTGGTT GAAAAGATTG ACAGAAGAAC      950
CGGTAAGAAG TTGGAAGAAA ACCCAAAGTT TGTCAAGTCC GGTGACGCTG     1000
CTATCGTCAA GATGGTCCCA ACCAAGCCAA TGTGTGTTGA AGCYTTCACT     1050
GACTACCCAC CATTGGGTAG ATTCGCTGTC AGAGA                     1085
```

2) INFORMATION FOR SEQ ID NO: 432

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1072 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida zeylanoides*
(B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

AGGTATTACC ATTGACATTG CCTTGTGGAA GTTCGAGACC CCCAAGTACC 50
AGGTCACCGT CATTGACGCT CCTGGCCACA GAGATTTCAT TAAGAACATG 100
ATCACTGGTA CCTCCCAGGC TGACTGTGCC ATCTTGATCA TTGCTGGTGG 150
TGTTGGTGAG TTCGAGGCTG GTATCTCCAA GGATGGCCAG ACCAGAGAGC 200
ACGCCTTGCT TGCCTACACC TTGGGTGTCA AGCAATTGAT TGTTGCTGTC 250
AACAAGATGG ACTCCGTCAA GTGGGACAAG AACAGATTCG AGGAGATTGT 300
CAAGGAGACC TCCAACTTCG TCAAGAAGGT TGGCTACAAC CCCAAGACTG 350
TCCCCTTCGT TCCCATCTCC GGTTGGAACG GTGACAACAT GATTGAGGCC 400
TCCACCAACT GCCCTTGGTA CAAGGGTTGG GAGAAGGAGA CCAAGGCCGG 450
TAAGGTCACT GGTAAGACCT TGTTGGAGGC TATTGACGCC ATTGAGCCCC 500
CCACCAGACC CACCGACAAG CCCTTGAGAT TGCCCTTGCA GGATGTCTAC 550
AAGATTGGTG GTATTGGAAC GGTGCCCGTT GGCAGAGTTG AGACCGGCAT 600
CATCAAGGCC GGTATGGTTG TCACCTTTGC CCCCGCTGGT GTCACTACTG 650
AAGTGAAGTC TGTCGAGATG CACCACGAGC AATTGGCTGA GGGTGTCCCA 700
GGTGACAATG TTGGTTTCAA CGTGAAGAAC GTTTCCGTTA AGGAGATCAG 750
AAGAGGTAAC GTTTGCGGTG ACTCCAAGAA CGACCCCCCC AAGGCTGCTG 800
CTTCTTTCAA CGCCCAGGTT ATCGTCTTAA ACCACCCCGG TCAAATCTCT 850
GCTGGTTACT CTCCGGTTTT GGATTGCCAC ACTGCCCACA TTGCTTGCAG 900
ATTCGACCAG TTGATTGAGA AGATCGACAG AAGAACCGGT AAGAAGATGG 950
AGGACGACCC TAAGTTCATC AAGTCCGGTG ACGCTGCCAT CGTCAAGATG 1000
GTTCCTTCCA AGCCCATGTG TGTTGAGGCC TTCACTGACT ACCCTCCCTT 1050
GGGTCGTTTC GCTGTCAGAG AC 1072

2) INFORMATION FOR SEQ ID NO: 433

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Coccidioides immitis*
(B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

AGCACCAACT GGTCCGAGCC TCGTTTCAAC GAAATCGTCA AGGAAGTCTC 50
CAACTTCATC AAGAAGGTCG GATACAACCC CAAGGCTGTT CCATTCGTCC 100
CCATCTCTGG TTTCGAAGGT GACAACATGA TTCAACCCTC CACCAACGCT 150
CCTTGGTACA AGGGCTGGAA CAAGGAGACC GCCTCTGGCA AGCACACTGG 200
CAAGACCCTC CTCGACGCCA TTGATGCCAT CGACCCCCCA ACCCGCCCCA 250
CCGAGAAGCC CCTCCGTCTC CCACTTCAGG ATGTGTACAA GATCTCTGGT 300

ATCGGAACAG TCCCAGTCGG CCGTGTCGAA ACCGGTGTTA TCAAGCCTGG 350
TATGGTTGTG ACCTTCGCTC CTTCCAACGT CACCACTGAA GTCAAGTCCG 400
TCGAAATGCA CCACCAGCAG CTCACCCAGG GTAACCCTGG TGACAACGTT 450
GGCTTCAACG TCAAGAACGT CTCTGTCAAG GAAGTCCGCC GCGGTAACGT 500
CGCTGGTGAC TCCAAGAACG ACCCACCAAA GGGCTGCGAC TCCTTCAACG 550
CCCAGGTCAT CGTCCTCAAC CACCCTGGTC AAGTCGGTGC TGGTTATGCC 600
CCAGTCCTTG ACTGCCACAC TGCCCACATT GCTTGCAAGT TCTCCGAGCT 650
CCTCGAGAAG ATCGACCGCC GTACCGGTAA ATCCGTTGAG AACAACCCCA 700
AGTTCATCAA GTCTGGTGAT GCCGCTATCG TCAAGATGGT TCCATCCAAG 750
C 751

2) INFORMATION FOR SEQ ID NO: 434

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1146 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptococcus albidus*
(B) STRAIN: ATCC 66030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

AAGCTCAAGG CCGAGCGAGA GCGAGGTATC ACCATCGACA TCGCCTTGTG 50
GAAGTTCGAG ACCCCCAAGT ACAATGTCAC CGTCATTGAC GCCCCCGGTC 100
ACCGAGACTT CATCAAGAAC ATGATCACCG GTACCTCGCA GGCCGACTGT 150
GCCATCCTCA TCATCGCCTC CGGTATCGGA GAGTTCGAGG CTGGTATCTC 200
CAAGGACGGT CAGACCCGAG AGCACGCCCT TTTGGCCTTC ACCCTCGGTG 250
TCCGACAGCT CATCATTGCC ATCAACAAGA TGGACACCTG CAAGGTTAGT 300
TCGCAGGTCC TGGTCTCTGT ACGAATCTTG CTGACCCCTT TTACAGTGGT 350
CCGAAGACCG ATACAACGAA ATCGTCAAGG AGGCTTCCGG TTTCATCAAG 400
AAGGTCGGAT ACAACCCCAA GACCGTTCCC TTCGTCCCCA TCTCCGGATG 450
GCACGGAGAC AACATGTTGG AGGAGTCCAC CAACATGCCC TGGTACAAGG 500
GATGGCACAA GGAGTCCAAG GCCGGTGTTG TCAAGGGAAA GACCTTGCTC 550
GAGGCCATCG ACGCCATCGA GCCCCCTACC CGACCTTCCG ACAAGCCCTT 600
GCGATTGCCC CTCCAGGATG TCTACAAGAT CGGTGGTATC GGTACGGTGC 650
CCGTCGGTCG AGTCGAGACC GGTGTCATCA AGGCTGGTAT GGTCGTCACC 700
TTCGCCCCTG CCAACGTCAC CACCGAAGTC AAGTCCGTCG AAATGCACCA 750
CGAACAGCTC GCTGAGGGTG TTCCCGGTGA CAACGTCGGT TTCAACGTCA 800
AGAACGTTTC CGTCAAGGAC ATCCGACGAG GAAACGTCTG CTCCGACTCG 850
AAGAACGACC CCGCTATGGA GTCTGCTTCC TTCAACGCTC AGGTCATTGT 900
CTTGAACCAC CCGGGTCAGA TCGGTGCCGG CTACTCCCCC GTTTTGGACT 950
GCCACACCGC TCACATTGCC TGCAAGTTCG CTGAGCTCGT TGAGAAGATC 1000
GACCGACGAA CCGGTAAGGT CATGGAGGCC GCCCCCAAGT TCGTCAAGTC 1050
CGGTGACGCC GCCATCGTCA AGTTGATCCC GTCCAAGCCC ATGTGTGTCG 1100
AGTCCTACTC CGAGTACCCC CCCTTGGGTC GATTCGCCGT CCGAGA 1146

2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Exophiala jeanselmei*
(B) STRAIN: ATCC 64755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435

```
CAAGCTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCTTGT      50
GGAAGTTCGA GACTCCCAAG TACTATGTCA CTGTCATCGA CGCCCCTGGT     100
CATCGTGACT TTATCAAGAA CATGATCACT GGTACTTCCC AGGCTGACTG     150
CGCCATTCTC ATCATTGCCG CCGGTACTGG TGAATTCGAA GCCGGTATCT     200
CCAAGGATGG TCAGACTCGT GAGCACGCTC TGCTCGCCTA CACCCTGGGT     250
GTCAAGCAGC TCATTGTCGC CATCAACAAG ATGGACACCA CCAAGTGGTC     300
CGAGGATCGT TTCAACGAAA TCATCAAGGA GACTTCCAGC TTCATCAAGA     350
AGGTCGGCTA CAACCCCAAG TCCGTTCCTT TCGTCCCCAT CTCCGGCTTC     400
AACGGTGACA ACATGATCGA TGTCTCCACC AACTGCCCCT GGTACAAGGG     450
CTGGGAGAAG GAGACCAAGG CTGGCAAGGC CTCTGGCAAG ACTCTCCTCG     500
AGGCCATCGA CGCCATCGAC CCCCCCACTC GTCCCACCGA CAAGCCTCTC     550
CGTCTTCCTC TCCAGGATGT CTACAAGATC TCTGGTATCG GAACGGTGCC     600
CGTCGGTCGT GTTGAGACTG GTGTCATCAA GGCCGGTATG GTCGTTACCT     650
TCGCTCCTGC CAACGTCACC ACTGAAGTCA AGTCCGTCGA AATGCACCAC     700
GAACAACTCG CCGAGGGTGT TCCAGGTGAC AACGTTGGTT TCAACGTCAA     750
GAACGTCTCC GTCAAGGAGG TTCGTCGTGG AAACGTCTGC GGTGACTCCA     800
AGAACGACCC ACCCAAGGGT GCTGATTCCT TCAACGCCCA GGTCATCGTC     850
TTGAACCACC CTGGTCAAGT CGGTGCTGGC TACGCCCCAG TGTTGGATTG     900
CCACACTGCC CACATTGCTT GCAAGTTCTC TGAGCTTCTC GAGAAGATTG     950
ACCGCCGTAC CGGTAAATCC ATCGAAAACA ACCCCAAGTT CATCAAGTCT    1000
GGTGACGCTG CCATCGTCAA GATGGTTCCC AGCAAGCCCA TGTGTGTTGA    1050
GGCCTTCACT GACTACCCAC CTCTTGGTCG TTTCGCCGTC CGTGA         1095
```

2) INFORMATION FOR SEQ ID NO: 436

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436

```
AAGCTCAAGG CCGAGCGTGA GCGTGGTATC ACCATCGATA TTGCTCTCTG      50
GAAGTTCGAG ACTCCTCGCT ACTATGTCAC CGTCATTGGT ATGTTGTCGC     100
TCATGCTTCA TTCTACTTCT CTTCGTACTA ACACATCACT CAGACGCTCC     150
CGGTCACCGT GATTTCATCA AGAACATGAT CACTGGTACT TCCCAGGCCG     200
ATTGCGCCAT TCTCATCATT GCCGCCGGTA CTGGTGAGTT CGAGGCTGGT     250
ATCTCCAAGG ATGGCCAGAC CCGTGAGCAC GCTCTTCTTG CCTACACCCT     300
TGGTGTCAAG AACCTCATCG TCGCCATCAA CAAGATGGAC ACCACCAAGT     350
GGTCTGAGGC CCGTTACCAG GAGATCATCA AGGAGACCTC CTCTTTCATC     400
```

AAGAAGGTCG GCTACAACCC CAAGGCTGTC GCTTTCGTCC CCATCTCCGG 450
TTTCAACGGT GACAACATGC TTACCCCCTC CACCAACTGC CCCTGGTACA 500
AGGGTTGGGA GCGTGAGATC AAGTCCGGCA AGCTCACTGG CAAGACCCTC 550
CTCGAGGCCA TTGACTCCAT CGAGCCCCCC AAGCGTCCCG TTGACAAGCC 600
CCTTCGTCTT CCCCTTCAGG ATGTCTACAA GATCGGTGGT ATTGGAACGG 650
TTCCCGTCGG CCGTATCGAG ACTGGTGTCA TCAAGCCCGG TATGGTCGTT 700
ACCTTCGCTC CTTCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA 750
CCACGAGCAA CTCACTGAGG GCCAGCCCGG TGACAACGTT GGTTTCAACG 800
TGAAGAACGT CTCCGTCAAG GACATCCGAC GTGGTAACGT CGCTGGTGAC 850
TCCAAGAACG ACCCCCCTAT GGGTGCCGCT TCTTTCACCG CCCAGGTCAT 900
CGTCCTCAAC CACCCCGGTC AGGTCGGTGC TGGTTACGCT CCCGTCCTCG 950
ATTGTCACAC TGCCCACATT GCCTGCAAGT TCGCCGAGAT CCAGGAGAAG 1000
ATCGACCGCC GAACCGGTAA GGCTACTGAG GCCGCCCCCA AGTTCATCAA 1050
GTCTGGTGAC TCCGCCATCG TCAAGATGGT TCCCTCCAAG CCCATGTGTG 1100
TTGAGGCTTT CAC 1113

2) INFORMATION FOR SEQ ID NO: 437

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 726 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Geotrichum* spp.
(B) STRAIN: LEV-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

GGTCCGAGGA CAGATTCAAC GAGATTGTCA AGGAGACTTC CAACTTCATC 50
AAGAAGGTTG GTTAYAACCC CAAGACTGTT GCTTTCGTCC CCATCTCTGG 100
TTGGAACGGT GACAACATGA TTGAGCCCTC CACCAACTGC CCCTGGTACA 150
AGGGATGGCA GAAGGAGACC AAGGCTGGTG TCACTAAGGG TAAGACCCTC 200
CTTGAGGCCA TCGATGCCAT TGAGCCCCCT GTCAGACCTT CCGACAAGCC 250
CCTCCGTCTT CCCCTCCAGG ATGTCTACAA GATCGGTGGT ATCGGAACTG 300
TGCCCGTCGG CCGTGTCGAA ACCGGTGTCA TCAAGGCCGG TATGGTCGTC 350
ACCTTCGCCC CCGCTGGTGT CACCACTGAA GTCAAGTCCG TCGAGATGCA 400
CCACGAGCTC CTCACTGAGG GTCTCCCCGG TGACAACGTT GGTTTCAACG 450
TCAAGAACGT CTCCGTTAAG GATATCAGAC GTGGTAACGT CTGCGGTGAC 500
TCCAAGAACG ATCCCCCCAA GGCTTGCGCT TCTTTCAACG CCCAGGTCAT 550
TATCTTCAAC CACCCTGGTC AGATCTCTGC TGGATACTCT CCCGTCCTTG 600
ATTGCCACAC CGCCCATATT GCTTGCAAGT TCGACACTTT GATCGAGAAG 650
ATTGACCGTC GTACTGGTAA GAAGACTGAG GACTCCCCCA AGTTCGTCAA 700
GGCCGGTGAT GCTGCTATCG TCAAGA 726

2) INFORMATION FOR SEQ ID NO: 438

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

```
CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
CCAACTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG     100
CCAATCTCTG GTTTCGAGGG TGACAACATG ATTGAACCCT CCCCCAACTG     150
CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCTCTGGC AAGTCTTCTG     200
GTAAAACCCT TCTCGATGCC ATTGACGCCA TTGAACCCCC AACCCGTCCT     250
ACCGATAAGC CCCTCCGTCT TCCCCTCCAG GATGTGTACA AAATCTCTGG     300
TATTGGCACT GTTCCCGTCG GACGTGTTGA GACTGGTGTC ATCAAGCCCG     350
GTATGGTCGT GACTTTCGCT CCCTCCAACG TCACCACTGA AGTCAAGTCC     400
GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTTACCCTG GCGACAACGT     450
CGGCTTCAAC GTCAAGAACG TTTCAGTCAA GGAAGTCCGC CGTGGCAACG     500
TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT     550
GCCCAGGTCA TCGTCCTTAA CCACCCCGGC CAGGTTGGCG CTGGTTATGC     600
CCCAGTCCTC GACTGCCACA CTGCCCACAT TGCTTGCAAG TTCTCTGAGC     650
TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC     700
AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA     750
GCCC                                                      754
```

2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 743 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Issatchenkia orientalis*
(B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

```
TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCGTT CCAATCTCTG     100
GTTGGAATGG TGACAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC     150
AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT     200
ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC     250
CATTAAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT     300
GTGCCAGTCG GTAGAGTCGA AACCGGTGTC ATTAAGCCAG GTATGGTTGT     350
CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC     400
ACCATGAACA ATTAGAACAA GGTGTTCCAG GTGATAACGT TGGTTTCAAC     450
GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGGTGA     500
CTCCAAGAAC GACCCACCAA TGGGTGCAGC TTCYTTCAAT GCTCAAGTCA     550
TTGTCTTGAA CCACCCTGGT CAAATTTCCG CTGGTTACTC TCCAGTCTTG     600
GATTGTCACA CTGCCCACAT TGCATGTAAG TTCGACGAAT TAATCGAAAA     650
GATTGACAGA AGAACTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA     700
AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCCAACCAA GCC            743
```

2) INFORMATION FOR SEQ ID NO: 440

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1091 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Malassezia furfur*
(B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

```
CAAGCTCAAG GCTGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTGT      50
GGAAGTTCGA GACCCCTAAG TACCACGTTA CCGTCATTGA CGCTCCTGGT     100
CACCGTGACT TCATCAAGAA CATGATTACG GGTACCTCGC AGGCTGACTG     150
CGCTATCCTC ATCATTGCCG GTGGTACCGG TGAGTTCGAG GCTGGTATCT     200
CGAAGGACGG TCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTGGGT     250
GTGCGTCAGC TCATTGTGGC CGTCAACAAG ATGGACACCA CCAAGTACTC     300
GGAGGACCGC TTCAACGAGA TTGTCCGCGA AGTGTCGAAC TTCATCAAGA     350
AGGTCGGTTT CAACCCCAAG ACTGTTGCCT TCGTCCCCAT CTCGGGCTGG     400
CACGGTGACA ACATGATCGA GGCCACCACC AACATGCCTT GGTACAAGGG     450
CTGGGAGAAG GAGACCAAGT CGGGCAAGGT CACTGGTAAG ACTCTGCTGG     500
ACGCCATCGA CGCCATCGAG CCCCCGACCC GCCCCACTGA CAAGCCCCTG     550
CGTCTCCCTC TGCAGGATGT GTACAAGATC GGTGGTATCG GTACTGTCCC     600
TGTCGGTCGT GTTGAGACCG GTGTGATCAA GCCCGGTATG GTTGTGACCT     650
TCGCTCCCTC GAACGTCACC ACTGAAGTTA AGTCGGTTGA GATGCACCAC     700
GAGTCGCTCC CTGAGGGTCT CCCCGGTGAC AACGTTGGTT TCAACGTGAA     750
GAACGTCTCG GTTAAGGACA TTCGCCGTGG TAACGTTGCC TCGGACTCGA     800
AGAACGACCC CGCTCAGGAG GCTGCTTCGT TCAACGCGCA GGTCATTGTC     850
ATGAACCACC CTGGTCAGAT CAGCAACGGT TACTCGCCCG TGCTTGACTG     900
CCACACTGCG CACATTGCCT GCCGCTTCAA CAACATCCTC CAGAAGATCG     950
ACCGTCGCTC GGGTAAGGTG CTTGAGGAGA ACCCCAAGTT CATCAAGTCG    1000
GGTGACGCTG CCATGGTGGA GATGATCCCC ACCAAGCCCA TGTGTGTGGA    1050
GTCGTTCAAC GAGTACCCCC CTCTGGGTCG TTTCGCTGTG C             1091
```

2) INFORMATION FOR SEQ ID NO: 441

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 749 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Malassezia pachydermatis*
(B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

```
ACCACCAAGT ACTCGGAGGA CCGCTTCAAC GAGATTATTC GCGAGACTTC      50
GAACTTCATC AAGAAGGTCG GTTACAACCC GAAGACTGTT GCCTTCGTCC     100
```

CGATCTCGGG CTGGCACGGT GACAACATGA TTGAGGCGAC CACCAACATG 150
CCGTGGTACA AGGGCTGGGA GAAGGAGACC AAGTCGGGCA AGGCCACTGG 200
TAAGACCCTT CTGGACGCTA TTGACGCCAT TGAGCCGCCG ACGCGCCCGA 250
CCGACAAGCC TCTCCGTCTT CCTCTCCAGG ATGTGTACAA GATCGGTGGT 300
ATCGGTACYG TCCCGGTCGG CCGTGTTGAG ACCGGTGTTA TCAAGCCCGG 350
TATGGTTGTG ACCTTCGCTC CGTCGAACGT CACSACTGAA GTTAAGTCGG 400
TCGAGATGCA CCACGAGCAG ATCCCTGAGG GTCTTCCGGG TGACAACGTT 450
GGTTTCAACG TGAAGAACGT GTCGGTCAAG GACATTCGCC GTGGTAACGT 500
CGCCTCGGAC TCGAAGAACG ACCCGGCTCA GGAGGCTGCC TCGTTCAATG 550
CTCAGGTCAT TGTGATGAAC CACCCTGGTC AGATCAGCAA CGGTTACTCG 600
CCRGTGCTCG ACTGCCACAC TGCTCACATT GCCTGCCGCT TCAACAACAT 650
CCTCCAGAAG ATCGACCGTC GTTCGGGTAA GGTTCTYGAA GAGAACCCCA 700
AGTTCATCAA GTCGGGTGAC GCTGCCATGG TTGAGATGAT CCCGACCAA 749

2) INFORMATION FOR SEQ ID NO: 442

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Malbranchea filamentosa*
(B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

ACTGAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA 50
AGTTCGAGAC CCCCAAGTAC CATGTCACCG TCATTGGTAC GTTCGACATG 100
TTCGACCTTT TGCCTAGTGT CCCCTTCTAA CCACAGTTTA TAGACGCCCC 150
TGGCCATCGT GATTTCGTCA AGAACATGAT CACTGGTACT TCCCAGGCTG 200
ATTGCGCTAT CCTCATCATT GCTTCCGGCA CTGGTGAATT CGAGGCTGGT 250
ATCTCCAAGG ATGGCCAGAC CCGTGAGCAC GCTCTGCTTT CCTTCACCCT 300
CGGTGTTAGG CAGCTCATTG TCGCCCTCAA CAAGATGGAC ACTGTCAACT 350
TCGCTGAGGC CCGTTACAAC GAGATTGTCA AGGAAGTCTC CAACTTCATC 400
AAGAAGGTCG GCTACAACCC CAAGGCCGTT CCTTTCGTCC CCATCTCCGG 450
TTTCGAGGGT GACAACATGA TCGAGGCCTC CACCCGCATT CCTTGGTACA 500
AGGGCTGGAA CAAGGAGACC GCCAGTGGCA AGAGCACCGG CAAGACCCTY 550
CTCGAGGCCA TTGATGCCAT CGAACCCCCG GTCCGTCCCA CCGACAAGCC 600
CCTYCGTCTC CCTCTTCAGG ATGTGTACAA GATCTCCGGT ATTGGCACTG 650
TTCCTGTCGG TCGTGTTGAG ACTGGTGTCA TCAAGCCTGG TATGGTCGTT 700
ACTTTCGCCC CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA 750
CCACCAGCAG CTCCAGGCCG GTAACCCCGG TGACAACGTC GGCTTCAACG 800
TCAAGAACGT TTCCGTCAAG GAAGTCCGCC GTGGCAACGT TGCCTCCGAC 850
TCCAAGAACG ACCCCGCCAA GGGCTGCGAC TCCTTCAACG CCCAGGTCAT 900
CGTCCTTAAC CACCCCGGTC AGGTCGGTGC TGGATACGCT CCCGTCCTCG 950
ATTGCCACAC TGCCCACATT GCTTGCAAGT TCTCTGAGCT TCTTGAGAAG 1000
ATCGATCGCC GTACCGGTAA ATCCGTTGAG GACCACCCCA AGTTCATCAA 1050
GTCTGGTGAT GCCGCTATCG TCAAGATGGT TCCCTCCAAG CCTATGTGCG 1100
TTGAGGCTTT CACTGACTAC CCTCCCCTTG GTCGTTTCGC CGTCCGTGAC 1150

2) INFORMATION FOR SEQ ID NO: 443

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Metschnikowia pulcherrima*
(B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

GGACAAGTTG AAGGCTGAGA GAGAGAGAGG TATCACCATC GACATTGCCT 50
TGTGGAAGTT CGAGACTCCT AAGTACCACG TCACCGTYAT TGACGCCCCA 100
GGTCACAGAG ATTTCATCAA GAACATGATC ACTGGTACTT CCCAGGCTGA 150
CTGTGCYATC TTGATTATCG CYGGTGGTGT TGGTGAGTTC GAGGCTGGTA 200
TCTCCAAGGA TGGCCAGACC AGAGAGCACG CTTTGTTGGC YTACACCTTG 250
GGTGTTAGAC ARTTGATTGT TGCCGTCAAC AAGATGGACT CTGTCAAGTG 300
GGACAAGAAC AGATTTGAGG AGATCATCAA GGAGACCTCT AACTTCGTCA 350
AGAAGGTTGG TTACAACCCT AAGACYGTGC CATTCGTGCC AATYTCTGGT 400
TGGAACGGTG ACAACATGAT TGAGGCYTCC ACTAACTGCC CATGGTACAA 450
GGGTTGGGAG AAGGAGACCA AGGCCGGTAA GTCTWCCGGT AAGACCTTGT 500
TGGAGGCCAT TGACGCCATT GAGCCACCAA CCAGACCTAC CGACAAGGCC 550
TTGAGATTGC CTTTGCAGGA TGTCTACAAG ATCGGTGGTA TCGGAACGGT 600
GCCAGTCGGC CGTGTCGAGA CCGGTGTCAT TAAGGCCGGT ATGGTTGTYA 650
CCTTYGCCCC AGCTGGTGTC ACCACTGAGG TCAAGTCCGT CGAGATGCAC 700
CACGAGCAGT TGGTCGAGGG TCTTCCAGGT GACAAYGTTG GTTTCAACGT 750
CAAGAACGTC TCCGTTAAGG AGATCAGAAG AGGTAACGTC TGTGGTGACT 800
CCAAGCAGGA CCCACCAAAG GGTGCCGCTT CTTTCACCGC YCAGGTTATT 850
GTGTTGAACC ACCCTGGTCA GATCTCCTCT GGTTACTCTC CAGTGTTGGA 900
CTGYCACACC GCCCACATTG CCTGTAARTT CGACACCTTG TTGGAGAAGA 950
TTGACAGAAG AACTGGTAAG TCCTTGGAGT CYGAGCCTAA GTTCGTCAAG 1000
TCYGGTGACG CCGCCATTGT CAAGATGGTG CCAACCAAGC CAATGTGTGT 1050
TGAGGCTTTC ACCGACTACC CACCTTTGGG TAGATTCGCC GTCAGAGAC 1099

2) INFORMATION FOR SEQ ID NO: 444

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1153 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Paecilomyces lilacinus*
(B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT 50
GGAAGTTCGA GACTCCCAAG TACTATGTCA CCGTCATTGG TACGTCGACT 100
CGCGCGAGAC TGGTCGCAAT TTCCACGTCG CTAACGTGCT TGAACAGACG 150
CTCCCGGCCA CCGTGACTTC ATCAAGAACA TGATCACTGG TACCTCCCAG 200
GCTGACTGCG CTATCCTCAT TATCGCTGCC GGCACTGGTG AGTTCGAGGC 250

TGGTATCTCC AAGGATGGCC AGACCCGTGA GCACGCTCTG CTCGCCTACA 300
CCCTCGGTGT TAAGCAGCTC ATCGTCGCTA TCAACAAGAT GGACACCACC 350
AAGTGGTCTG AGGCCCGTTT CCAGGAGATC ATCAAGGAGA CCTCCAACTT 400
CATCAAGAAG GTCGGCTACA ACCCCAAGAC CGTCGCTTTC GTCCCCATCT 450
CTGGTTTCCA CGGCGACAAC ATGCTTTCCC CCTCCACCAA CTGCCCCTGG 500
TACAAGGGCT GGGAGAAGGA GACCAAGGCT GGCAAGTCCA CCGGCAAGAC 550
CCTCCTTGAG GCCATCGACT CCATCGAGCC CCCCAAGCGC CCCAGCGACA 600
AGCCCCTCCG CCTTCCCCTT CAGGATGTGT ACAAGATCGG CGGTATCGGC 650
ACAGTCCCTG TCGGCCGTAT CGAGACTGGT GTCATCAAGC CCGGCATGGT 700
CGTGACCTTC GCTCCTTCCA ACGTCACCAC CGAAGTCAAG TCCGTTGAGA 750
TGCACCACGA GCAGCTCTCC GAGGGTGTCC CCGGTGACAA CGTCGGCTTC 800
AACGTCAAGA ACGTCTCCGT CAAGGAGATC CGTCGTGGCA ACGTCGCCGG 850
TGACTCCAAG AACGACCCCC CTCTGGGTGC CGCTTCTTTC GATGCCCAGG 900
TCATCGTCCT CAACCACCCC GGCCAGGTCG GTGCTGGCTA CGCCCCCGTC 950
CTCGACTGCC ACACCGCCCA CATTGCCTGC AAGTTCGCCG AGATCAAGGA 1000
GAAGATCGAC CGCCGTACCG GCAAGTCTGT CGAGTCCGCC CCCAAGTTCA 1050
TCAAGTCTGG CGACTCTGCC ATCGTCAAGA TGATTCCCTC CAAGCCCATG 1100
TGCGTTGAGG CTTTCACCGA CTACCCTCCT CTGGGCCGCT TCGCCGTCCG 1150
TGA 1153

2) INFORMATION FOR SEQ ID NO: 445

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 763 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Paracoccidioides brasiliensis*
(B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

TACCACTAAG TGGTCCGAGA CCCGATTCAA TGAAATTATC AAGGAAGTCA 50
CCAATTTCAT TAAGAAGGTC GGATATAACC CCAAGACTGT TCCTTTCGTT 100
CCCATTTCTG GTTTCGAGGG TGACAACATG ATCGAGCCCT CTGCCAACTG 150
CCCATGGTAC AAGGGCTGGT CCAAGGAGAC TGCTCAGGGC AAGTACTCTG 200
GCAAGACCCT TCTTGAGGCC ATCGACGCCA TTGAGCCCCC CACCCGTCCT 250
ACCGATAAAC CTCTCCGTCT TCCCCTCCAG GATGTCTACA AGATCTCCGG 300
TATTGGCACT GTTCCTGTCG GACGTGTTGA GACTGGAGTC ATCAAGCCCG 350
GTATGGTCGT GACCTTCGCT CCCGCCAACG TCACCACTGA AGTCAAGTCC 400
GTCGAAATGC ACCACCAGCA GCTTACCGCC GGTAACCCCG GTGACAACGT 450
CGGCTTCAAC GTCAAGAATG TTTCCGTCAA AGAAGTCCGC CGTGGTAACG 500
TTGCCGGTGA CTCTAAGAAT GATCCCCCAA AGGGCTGCGA TTCCTTCAAT 550
GCCCAGGTCA TCGTCCTCAA CCACCCTGGT CAGGTTGGCG CTGGTTATGC 600
CCCAGTCCTC GACTGCCATA CTGCCCACAT TGCCTGCAAA TTCGCTGAGC 650
TCCTTGAGAA GATTGATCGA CGAACCGGAA AGTCTGTTGA GAACAACCCC 700
AAGTTCATCA AGTCCGGTGA TGCTGCTATC GTCAAGATGA TTCCTTCCAA 750
GCCCATGTGC GTC 763

2) INFORMATION FOR SEQ ID NO: 446

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1346 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

AAGCTCAAGG CTGAGCGTGA GCGTGGTATC ACCATCGATA TTGCTCTCTG 50
GAAGTTCCAG ACTGCCAAGT ACGAGGTTAC CGTCATTGAC GCCCCCGGTC 100
ACCGTGATTT CATCAAGAAC ATGATCACTG GTACCTCCCA GGCCGATTGC 150
GCTATTCTCA TCATTGCCTC TGGTACTGGT GAATTCGAGG CTGGTATCTC 200
CAAGGATGGC CAGACTCGTG AGCACGCTCT TTTGGCTTTC ACCCTCGGTG 250
TCCGTCAGCT CATTGTTGCC CTCAACAAGA TGGACACTTG CAAGTGGTCT 300
CAGGGTGAGT ACTCGTACCT GCGTTTGGCC TTGAATATCT TACTAATGCA 350
CCATAGATCG TTACAACGAA ATTGTCAAGG AGACTTCCAA CTTCATCAAG 400
AAGGTCGGAT ACAACCCCAA GAACGTTCCT TTCGTTCCTA TCTCCGGTTT 450
CAACGGTGAC AACATGCTTG AGCCCTCCCC CAACTGCCCC TGGTACAAGG 500
GTTGGGAGAA GGAGACCAAG GCCGGTAAGG TCACTGGTAA GACCCTCCTC 550
GAGGCCATCG ACGCCATTGA GCCCCCTACC CGTCCCGCCA ACAAGGTTAG 600
TCCCTCCTCG ACTACTCAAA CCCTCCTCAT AAGTTCAGAT TACTGACTCG 650
TTCACAGCCC CTCCGTCTTC CCCTCCAGRA TGTCTACAAG ATCGGTGGTA 700
TTGGAACGGT TCCCGTCGGT CGTGTTGAGA CTGGTACCAT CGTTCCTGGT 750
ATGGTTGTCA CCTTGTAAGT CACTCTCCTC GCTTATCCTA CCTGAAATCA 800
TCATGTGCTA ACTTGACACT CAGCGCTCCC GCCAACGTCA CCACTGAAGT 850
CAAGAGTGTT GAAATGCACC ACCAGCAGCT CACTGCCGGT CAGCCCGGTG 900
ACAACGTTGG TTTCAACGTG AAGAACGTCT CCGTCAAGGA AATCCGTCGT 950
GGTAACGTTG CTGGTGACAG CAAGAACGAC CCCCCTGCCG GTGCTGCCTC 1000
CTTCAACGCC CAGGTCATCG TCCTCAACCA CCCCGGTCAG GTCGGTGCTG 1050
GTTACGCCCC AGTCCTCGAT TGCCACACTG CCCACATTGC TTGCAAGTTC 1100
GCTGAGCTCC TCGAGAAGAT TGACCGTCGT ACCGGAAAGT CTGTTGAGGA 1150
CCACCCCAAG TTCATCAAGT CCGGTGACGC TGCCATCGTC AAGATGATTC 1200
CTTCCAAGCC CATGTGTGTT GAGGCTTTCA CCGAGTACCC TCCTCTCGGT 1250
CGTTTCGCCG TTCGCGAGTA AGTTTTATCT CCGTTGTCTA TTTTCCATCC 1300
TTCCCTTCTC CTCCGTCTTC CATATATACT TTTTCAGTTA TATGTG 1346

2) INFORMATION FOR SEQ ID NO: 447

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1094 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

AAGTTAAAAG CTGAACGTGA AAGAGGTATC ACTATTGATA TTGCTTTATG 50

GAAATTCGAA ACTCCAAAAT ACCATGTTAC CGTTATTGAT GCTCCAGGTC 100
ACAGAGATTT CATCAAAAAT ATGATTACTG GTACTTCCCA AGCTGATTGT 150
GCTATYTTAA TTATTGCCGG TGGTATTGGT GAATTCGAAG CTGGTATCTC 200
AAAAGATGGT CAAACCAGAG AACACGCTTT NTTAGCTTAC ACCTTAGGTG 250
TTAAACAATT GATTGTTGCT ATCAACAAGA TGGATTCCGT TAAATGGGAT 300
GAATCTCGTT TCGAAGAAAT TGTCAAGGAA ACYTCAAACT TTATCAAGAA 350
AGTTGGTTAC AACCCAAAAA CTGTTCCATT CGTTCCAATC TCAGGTTGGA 400
ATGGTGATAA CATGATTGAA CCATCAWCTA ACTGTCCATG GTACAAAGGT 450
TGGAAAAAAG AAACCAAAGC TGGTGAAGCT AAAGGTAAAA CTTTATTAGA 500
AGCCATTGAT GCTATTGACC CACCATCAAG ACCAACTGAT AAACCATTAC 550
GTTTACCATT ACAAGATGTT TACAARATTG GTGGTATTGG TACTGTGCCA 600
GTCGGTAGAG TTGAAACCGG TGTTATCAAA CCAGGTATGG TTGTTACCTT 650
TGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCTGTTGAA ATGCATCATG 700
AACAATTGAC TGAAGGTTTA CCAGGTGACA ATGTTGGTTT CAACGTTAAG 750
AATGTTTCTG TTAAAGAAAT CCGTCGTGGT AACGTCTGTG GTGACTCTAA 800
AAACGATCCA CCAAAAGCTG CTGAATCATT CAATGCTCAA GTTATTGTCT 850
TAAACCATCC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT TTTAGATTGT 900
CACACTGCTC ACATTGCTTG TAAATTTGAC ACTTTAATTG AAAAAATTGA 950
CAGACGTACT GGTAAGAAAT TAGAAGAAGC TCCAAAATTC ATCAAATCAG 1000
GTGATGCTGC TATTGTTAAA TTTGTTCCAT CAAAACCATT ATCAGTTGAA 1050
GCTTTCACTG ACTACCCACC ATTAGGTCGT TTCGCTGTCA GAGA 1094

2) INFORMATION FOR SEQ ID NO: 448

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1100 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

CTTAGATAAG TTAAAAGCTG AACGTGAAAG AGGTATCACT ATTGATATTG 50
CTTTATGGAA ATTCGAAACT CCAAAATACC ATGTTACCGT TATTGATGCT 100
CCAGGTCACA GAGATTTCAT CAAAAATATG ATTACTGGTA CTTCCCAAGC 150
TGATTGTGCT ATMTTAATTA TTGCCGGTGG TATTGGTGAA TTCGAAGCTG 200
GTATCTCAAA AGATGGTCAA ACCAGAGAAC ACGCTTTRTT AGCTTACACC 250
TTAGGTGTTA AACAATTGAT TGTTGCTATC AACAAGATGG ATTCCGTTAA 300
ATGGGATGAA TCTCGTTTCG AAGAAATTGT CAAGGAAACY TCAAACTTTA 350
TCAAGAAAGT TGGTACAACC CAAAAACTGT TCCATTCGTT CCAATCTCAG 400
GTTGGAATGG TGATAACATG ATTGAACCAT CAACTAACTG TCCATGGTAC 450
AAAGGTTGGA AAAAAGAAAC CAAAGCTGGT GAAGCTAAAG GTAAAACTTT 500
ATTAGAAGCC ATTGATGCTA TTGATCCACC ATCAAGACCA ACTGATAAAC 550
CATTACGTTT ACCATTACAA GATGTTTACA ARATTGGTGG TATTGGTACT 600
GTGCCAGTCG GTAGAGTTGA AACCGGTGTT ATCAAACCAG GTATGGTTGT 650
TACCTTTGCC CCAGCTGGTG TTACCACTGA AGTCAAATCT GTTGAAATGC 700
ATCATGAACA ATTGACTGAA GGTTTACCAG GTGACAATGT TGGTTTCAAC 750
GTTAAGAATG TTTCTGTTAA AGAAATCCGT CGTGGTAACG TCTGTGGTGA 800
CTCTAAAAAC GATCCACCAA AAGCTGCTGA ATCATTCAAT GCTCAAGTTA 850
TTGTCTTAAA CCATCCAGGT CAAATCTCTG CTGGTTACTC TCCAGTTTTA 900
GATTGTCACA CTGCTCACAT TGCTTGTAAA TTTGACACTT TAATTGAAAA 950
AATTGACAGA CGTACTGGTA AGAAATTAGA AGAAGCTCCA AAATTCATCA 1000

AATCAGGTGA TGCTGCTATT GTTAAATTTG TTCCATCAAA ACCATTATCA 1050
GTTGAAGCTT TCACTGACTA CCCACCATTA GGTCGTTTCG CTGTCAGAGA 1100

2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1201 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudallescheria boydii*
(B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCCTCT 50
GGAAGTTCGA GACCCCCAAG TACCAGGTCA CCGTCATTGG TATGTCTTTG 100
TGCTTTTTGT GCTTTTTGTG CCTGTGCCTC GCACAATTCC AGCCCTCGAT 150
AATTATGAAC CTCGTACTAA TATGTCGTTC TCCCACTACC CACAGACGCC 200
CCCGGCCATC GTGATTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC 250
TGATTGCGCC ATTCTCATCA TTGCCTCCGG TACTGGTGAG TTCGAGGCTG 300
GCATCTCCAA GGATGGCCAG ACCCGTGAGC ACGCTCTTCT CGCCTTCACC 350
CTCGGTGTCA AGAACCTCAT TGTTGCCATC AACAAGATGG ACACCAACAA 400
CTGGTCCGAG GACCGATACA AGGAGATCAT CAAGGAGACC TCCAACTTCA 450
TCAAGAAGGT CGGCTACAAC CCCAAGGCCG TTCCTTTCGT CCCCATCTCC 500
GGTTTCCACG GAGACAACAT GCTTACCCCC TCCACCAACT GCCCCTGGTA 550
CAAGGGTTGG GTCCGTGAGG TCAAGGGTAA CACCCTTACC GGCAAGACCC 600
TTCTCGAGGC CATCGACTYC ATCGAGCCCC CCAAGCGTCC CACCGAGAAG 650
CCCCTCCGTC TTCCCCTTCA GGACGTCTAC AAGATCGGTG GTATTGGCAC 700
TGTGCCCGTC GGCCGTATCG AGACCGGTAT CCTCAAGCCC GGTATGGTCG 750
TCACCTTCGC TCCCTCCAAC GTCACCACTG AAGTCAAGTC CGTCGAGATG 800
CACCACGAGC AGCTTACCGA GGGTGTCCCC GGTGACAACG TTGGTTTCAA 850
CGTGAAGAAC GTCTCCGTCA AGGATATCCG CCGTGGCAAC GTCTGCGGTG 900
ACTCCAAGAA CGACCCCCCC GCTGCTGCCG CCTCTTTCCA GGCCCAGGTC 950
ATTGTCCTCA ACCACCCCGG CCAGATCGGT GCTGGTTACG CTCCCGTTCT 1000
TGACTGCCAC ACTGCCCACA TTGCTTGCAA GTTCGCCGAG CTCCTTGAGA 1050
AGATCGACCG CCGTACCGGT AAGTCGGTCG AGAACAACCC CAAGTTCGTC 1100
AAGTCTGGTG ATGCCGCCAT CGTCAAGATG GTTCCCTCCA AGCCCATGTG 1150
TGTTGAGTCC TTCACCGAGT ACCCCCCTCT CGGTCGTTTC GCCGTCCGTG 1200
A 1201

2) INFORMATION FOR SEQ ID NO: 450

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhizopus oryzae*
(B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

```
CAAGCTTAAG GCTGAACGTG AACGTGGTAT CACCATCGAT ATTGCTCTCT       50
GGAAGTTCGA AACCCCCAAG TACCAAATTA CCGTTATTGA TGCTCCCGGT      100
CACCGTGATT TCATCAAGAA CATGATTACC GGTACTTCTC AAGCCGATTG      150
TGCTATTCTT ATCATTGCTG GTGGTACTGG TGAATTCGAA GCTGGTATCT      200
CCAAGGATGG TCAAACCCGT GAACACGCCC TTTTGGCTTT CACTCTCGGT      250
GTCCGTCAAT TGATTGTTGC TGTCAACAAG ATGGATACCA CCAAGTGGTC      300
CGAAGCTCGT TTCAACGAAA TYGTCAAGGA AGTTTCTTCC TTCATCAAGA      350
AGATTGGTTA CAACCCCAAG TCTGTTCCCT TCGTCCCCAT CTCTGGTTGG      400
CACGGTGACA ACATGTTGGA AGAATCTACC AACATGCCCT GGTACAAGGG      450
ATGGAACAAG GAAACCAAGG CTGGTGCCAA GTCTGGTAAG ACCCTCTTGG      500
ATGCCATTGA CAACATTGAC CCTCCTACCC GTCCTGTTGA CAAGCCTCTC      550
CGTCTTCCTC TTCAAGATGT TTACAAGATT GGTGGTATCG GTACTGTCCC      600
CGTCGGTCGT GTCGAAACTG GTGTCATCAA GGCTGGTATG GTTGTCACCT      650
TCGCTCCTGC TGCTGTCACC ACTGAAGTTA AGTCCGTCGA AATGCACCAC      700
GAAACCCTCA CTGAAGGTCT CCCCGGTGAC AACGTCGGTT TCAACGTCAA      750
GAACGTCTCC GTCAAGGATA TCCGTCGTGG TAACGTCTGT TCTGACTCCA      800
AGAACGACCC CGCCAAGGAA GCCGGTTCCT TCACCGCTCA AGTCATTATC      850
TTGAACCACC CTGGTCAAAT TGGTGCTGGT TACGCTCCYG TTTTGGATTG      900
TCACACTGCT CACATTGCCT GTAAGTTCGC TGAATTGATC GAAAAGATTG      950
ACAGACGTTC CGGTAAGTCC TTGGAAGCTA CTCCCAAGTT CGTCAAGTCT     1000
GGTGACTCTG CCATCGTCAA GATGATCCCC TCCAAGCCCA TGTGTGTTGA     1050
AGCTTACACT GACTACCCTC CTCTCGGTCG TTTCGCTGTT CGTGA          1095
```

2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Rhodotorula minuta*
(B) STRAIN: ATCC 10658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

```
GCTGAAGGCC GAGCGAGAGC GTGGTATCAC CATCGATATC GCTCTATGGA       50
AGTTCGAGAC CCCCAAGTAC AACGTCACCG TCATTGACGC TCCAGGACAT      100
CGTGATTTCA TCAAGAGTGA GTTAACCATA ACATCAAACA GTGTTGCAAA      150
CATCAGCTAA TGCATGTTAT GCGTCCAGAC ATGATTACTG GTACTTCCCA      200
GGCCGATTGC GCTATTCTCA TCATCGCCAC CGGTGTTGGT GAGTTCGAGG      250
CTGGTATCTC CAAGGATGGC CAGACCCGAG AGCACGCCCT TCTCGCCTTC      300
ACCCTCGGTG TCAGACAGCT CATCGTTGCC TTGAACAAGA TGGACTCGGT      350
CAAGGTAGGC TAACTTCACA ACGTCGGCTT CCCATCATTC ATTCACTTAC      400
CTGTCTTGTC TTCCACCCTC CAGTTCTCCG AGTCCCGATA CGATGAAATC      450
GTCAAGGAGA CATCCGGTTT CATCAAGAAG GTCGGATTCG ACCCCAAGGG      500
TGTTCCCTTC GTCCCCATCT CAGGATGGCA CGGAGACAAC ATGATCGAGG      550
AGTCCACCAA CATGCCTTGG TACAAGGGAT GGAAGAAGAC CACCAAGACC      600
GGCGAGTACA AGGGAAAGAC CCTGCTCGAG GCCATCGACT CCATCGAGCC      650
CCCCACCCGT CCTACCGACA AGCCTCTCCG ACTTCCCCTC CAGGATGTCT      700
```

ACAAGATTGG TGGTATCGGA ACAGTGCCAG TCGGACGAGT CGAGACTGGT 750
ACCATCAAGG CTGGTATGGT CGTCACCTTC GCTCCTTCAG CTGTCACCAC 800
CGAAGTCAAG TCTGTTGAGA TGCACCACGA GCAGCTCGAG GCTGGTCTTC 850
CAGGTGACAA CGTCGGATTC AACATCAAGA ACGTTTCAGT CAAGGATATC 900
CGAAGAGGAA ACGTCTGCGG TGACTCCAAG AACGATCCCC CCAAGGAGGC 950
TGCTTCCTTC ACCGCCCAGG TCATTGTCCT CAACCACCCC GGTCAAATCG 1000
GTAACGGATA CTCTCCAGTT CTCGATTGCC ACACTGGTGA GTCATTCTTC 1050
CATATTAGTT TGAACTCTTT TGAACAATAC TAACGTGAAT CATTATACTT 1100
TTCAGCCCAC ATTGCATGCA AGTTCGACAC CCTCCTAGAG AAGATTGACC 1150
GACGATCCGG AAAGTCCATC GAAGATACCC CCAAGTTCGT CAAGTCTGGT 1200
GACGCCGCCA TCGTCAAGAT GGTCCCCACC AAGCCAATGT GCGTTGAGGC 1250
TTTCACCGAC TACCCACCTC TTGGACGATT CGCCGTCCGT GA 1292

2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1289 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Sporobolomyces salmonicolor*
(B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

AAGCTCAAGG CCGAGCGTGA GCGTGGTATC ACCATCGATA TCGCTCTCTG 50
GAAGTTCGAG ACCCCCAAGG TGCGTTCTCA CCCCGGCTGA GGAGCACGCA 100
CGCGAGGGCT CACGCTGCGC CTCTTACAGT ACATGATCAC CGTCATCGAC 150
GCCCCGGGTC ACCGTGACTT CATCAAGAAC ATGATCACCG GTACCTCGCA 200
GGCCGACTGC GCCATCCTCA TCATCGCCGC CGGTACCGGT GAGTTCGAGG 250
CTGGTATCTC GAAGGACGGC CAGACCCGCG AGCACGCCCT CCTCGCCTTC 300
ACCCTCGGTG TCCGTCAGCT CATCGTCGCC ATCAACAAGA TGGACACGAC 350
CAAGTACTCG GAGGCCCGTT TCGAGGAGAT CATCAAGGAG ACCTCCAACT 400
TCATCAAGAA GGTCGGCTTC AACCCCAAGA ACGTCCCCTT CGTCCCCATC 450
TCGGGATGGC ACGGTGACAA CATGATTGAG GAGACCGCCA ACATGCCCTG 500
GTACAAGGGA TGGAAGAAGG AGACCAAGGC CGGTGAGGTC AAGGGCAAGA 550
CCCTCCTCGA CGCCATCGAC GCGATCGAGC CCCCTTCGCG CCCTACCGAC 600
AAGCCCCTCC GTCTTCCCCT CCAGGTTCGT TTCCCTGCTC GCGGTTTACG 650
CTGCTACTTC GAGCTGACCC GCGAGCTCTG CCCGAACAGG ATGTCTACAA 700
GATCGGTGGT ATCGGCACAG TCCCCGTCGG CCGTGTCGAG ACCGGCACGA 750
TCAAGGCCGG TATGGTCGTC GTCTTCGCCC CGGCCAACGT CACCACTGAG 800
GTCAAGTCGG TCGAGATGCA CCACGAGCAG CTCGAGGCTG GTCTCCCGGG 850
AGACAACGTC GGCTTCAAGT GCGTCTCATC ATGTTTTTGC TTCGCTCGGC 900
CATTTTTTCA GTCCTGACCC CGTTTTGCCC CTCGACAGCG TCAAGAACGT 950
TTCCGTTAAG GACATCCGTC GCGGTAACGT CTGCGGTGAC TCGAAGAACG 1000
ACCCCCCCAA GGAGGCCGCT TCCTTCAAGG CCCAGGTCAT CGTCATGAAC 1050
CACCCCGGTC AGATCGGCAA CGGTTACGCT CCCGTTCTCG ACTGCCACAC 1100
CGCCCACATT GCCTGCAAGT TCGACACCCT CCTCGAGAAG ATCGACCGTC 1150
GCTCGGGCAA GTCGATTGAG GACCTCCCCA AGTTCGTCAA GTCGGGTGAC 1200
GCCGCCATCG TCAAGATGGT TCCCTCCAAG CCGATGTGTG TCGAGTCGTT 1250
CGCCGAGTAC CCCCCTCTCG GACGTTTCGC CGTCCGTGA 1289

2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1070 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: WSA-148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTTCATCAA 100
GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
CGTGAGCACG CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
GAGCCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTCGGC CGTATCGAGA 600
CTGGTGTCCT GAAGCCCGGC ATGGTCGTCA CCTTTGCCCC GTCCAACGTC 650
ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCCTCG 800
GGCGCCGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGGCCA 850
GGTCGGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG 900
CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
CCCCTCTGGG CCGTTTCGCC 1070

2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stephanoascus ciferrii*
(B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
ATTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
GAGATTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC CGATCTTGCC 150

ATCCTTATCA TTGCTGGTGG TGTCGGTGAG TTCGAGGCTG GTATCTCCAA 200
GGACGGTCAG ACCAGAGAGC ACGCTCTTCT TTCTTTCACC CTTGGTGTCA 250
GAAACATGAT TGTTGCTGTC AACAAGATGG ACTCCGTCAA GTGGTCTGAG 300
GATCGTTTCA ACGAAATTGT CAAGGAGACC TCCAACTTCG TCAAGAAGGT 350
TGGTTACAAC CCTAAGAATA TTGCTTTCGT TCCTATCTCC GGTTGGAACG 400
GTGACAATAT GATTGAGCCA TCCACCAACT GCCCATGGTA CAAGGGTTGG 450
GAGCGTGAGA CCAAGAACGG TACTGCCAAG GGTAAGACCA TCTTGGAGGC 500
CATTGACTCT ATGGAGCCAC CTTCCAGACC AGTTGACAAG CCTCTCCGTC 550
TTCCTCTTCA GGACGTTTAC AAGATTGGTG GTATTGGTAC GGTGCCAGTT 600
GGTCGTGTTG AGACTGGTGT TATCAAGCCA GGTATGGTTG TTACCTTTGC 650
CCCAGCTGGT GTCACCACTG AAGTCAAGTC TGTCGAGATG CACCACGAAC 700
AGATCCCAGA AGGTACCCCA GGTGACAACG TTGGTTTCAA CGTCAAGAAC 750
GTCTCCGTCA AGGAAATCAG ACGTGGTAAC GTTACTGGTG ACTCCAAGAA 800
CGACCCACCA AAGGGCTGCG ACTCTTTCAA CGCTCAGGTC ATCATCTTCA 850
ACCACCCTGG TCAGATCTCT GCTGGTTACG CTCCAGTTTT GGACTGCCAC 900
ACTGCTCACA TTGCTTGCAA GTTTGAGGAG CTCATTGAGA AGATTGACAG 950
ACGTTCCGGT AAGAAGGTCG AAGACTCTCC TAAGTTCGTC AAGGCCGGTG 1000
ATGCCGCCAT TGTCAAGATG GTTCCATCCA AGCCAATGTG TGTTGAAACC 1050
TTCACTGAGT ACCCACCTCT TGGTCGTTTC GCCGTCCGTG AC 1092

2) INFORMATION FOR SEQ ID NO: 455

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1149 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trichophyton mentagrophytes*
(B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCCTCT GGAAGTTCGA 50
GACCCCCAAG TACAATGTCA CCGTCATTGG TATGTTTTCT CTTTACCTTT 100
CCCCTCCATC GTCTTGCTGT GCCATAACTA ACGAGAGTAG ACGCCCCCGG 150
TCACCGTGAC TTCATCAAGA ACATGATCAC TGGTACCTCC CAGGCCGACT 200
GTGCTATTCT CATCATTGCT GCCGGTACTG GTGAGTTCGA GGCTGGTATC 250
TCCAAGGATG GCCAGACCCG TGAGCACGCT CTGCTCGCCT TCACCCTTGG 300
TGTCAAGCAG CTCATCGTTG CCATCAACAA GATGGACACC ACCAACTGGT 350
CCGAGGACCG TTTCAAGGAA ATCATCAAGG AAGTCACCAA CTTCATCAAG 400
AAGGTTGGCT ACGACCCCAA GGGTGTTCCA TTCGTTCCAA TCTCTGGTTT 450
CAACGGTGAC AACATGATTG AGGCCTCCAC CAACTGCCCA TGGTACAAGG 500
GATGGAACAA GGAGACTAAG GCCGGTGGTG CCAAGACTGG CAAGACCCTC 550
CTCGAGGCCA TCGATGCCAT CGACATGCCA ACCCGTCCTA CCGACAAGCC 600
CCTCCGTCTC CCACTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACTG 650
TACCAGTCGG TCGTGTTGAG ACCGGTATCA TCAAGCCCGG TATGGTCGTC 700
ACCTTCGCCC CTGCCAACGT CACCACTGAA GTCAAGTCCG TCGAAATGCA 750
CCACCAGCAG CTTCAGCAGG GTGTCCCCGG TGACAACGTC GGCTTCAACG 800
TCAAGAACGT TTCCGTCAAG GAAGTCCGCC GTGGTAACGT TGCCGGTGAC 850
TCCAAGAACG ACCCACCATC CGGCTGTGCC TCCTTCAACG CCCAGGTCAT 900
CGTCCTCAAC CACCCCGGCC AGATCGGTGC TGGTTACGCC CCAGTCCTCG 950
ACTGCCACAC TGCTCACATT GCTTGCAAGT TCGCTGAGCT CCTCGAGAAG 1000
ATTGACCGCC GTACCGGTAA ATCCGTCGAA GCCAACCCCA AGTTCGTCAA 1050
GTCTGGTGAT GCCGCTATCG CCAAGATGGT TCCCTCCAAG CCTATGTGCG 1100

TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC CGTCCGTGA 1149

2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trichosporon cutaneum*
(B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

TCTTGACAAG CTTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50
CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100
CCAGGTCACC GTGATTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150
CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCGGTGAA TTCGAAGCTG 200
GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250
CTTGGTGTCA GACAACTTAT CATTGCCATC AACAAGATGG ACTCTGTCAA 300
GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCCAAGTCTG TTCCATTCGT TCCTATCTCT 400
GGTTGGAACG GTGACAACAT GTTGGAACCT ACCACCAACG CCCCATGGTA 450
CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500
TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550
CCACTCCGTC TCCCACTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600
TGTGCCAGTC GGCCGTGTCG AAACCGGTAT CATCAAGGCC GGTATGGTCG 650
TCACCTTTGC TCCACCAATG GTCACAACTG AAGTTAAGTC CGTTGAAATG 700
CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750
CGTCAAGAAC GTTTCCGTTA AGGAAATCAG ACGTGGTAAC GTCTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850
ATCGTCTTGA ACCACCCTGG TCAAATCTCT GCTGGTTACT CTCCAGTTCT 900
CGATTGCCAC ACTGCCCACA TTGCCTGCAG ATTCGACGAA CTCCTTGAAA 950
AGATCGACCG TCGTTCCGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTC 1000
AAGTCTGGTG ATGCCGCTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050
CGTTGAAACC TTCACTGAAT ACCCACCACT TGGTCGTTTC GCCGTCCGTG 1100
A 1101

2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1085 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Wangiella dermatitidis*
(B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

```
GTTGAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA      50
AGTTCGAGAC CCCCAAGTAC TATGTCACCG TCATCGACGC CCCGGGTCAT     100
CGTGACTTTA TCAAGAACAT GATCACTGGT ACCTCGCAGG CCGACTGCGC     150
CATCTTGATC ATTGCCGCCG GTACCGGTGA ATTCGAAGCC GGTATCTCCA     200
AGGATGGTCA GACCCGTGAG CACGCTCTGC TCGCCTACAC CTTGGGTGTC     250
AAGCAGCTCA TCGTCGCCAT CAACAAGATG GACACCACCA AGTGGTCCGA     300
GGAGCGTTTC AACGAAATCA TCAAGGAGAC TTCCAACTTC ATCAAGAAGG     350
TCGGCTACAA CCCCAAGGCC GTTCCTTTCG TCCCCATCTC CGGCTTCAAC     400
GGTGACAACA TGATTGAGGT CTCCACCAAC TGCCCGTGGT ACAAGGGATG     450
GGAGAAGGAG TCCAAGGCTG GCAAGGCCAC CGGCAAGACC CTCCTCGAGG     500
CCATTGACGC CATCGACCCA CCCACCCGTC CCACCGACAA GCCTCTCCGT     550
CTCCCTCTCC AGGATGTCTA CAAGATCTCT GGTATCGGAA CGGTTCCTGT     600
CGGTCGTGTC GAGACCGGTA CCATCAAGGC CGGTATGGTC GTCACCTTCG     650
CTCCGGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAAAT GCACCACGAG     700
CAGCTCGCCG AGGGTCTGCC AGGTGACAAC GTTGGCTTCA ACGTCAAGAA     750
CGTCTCCGTC AAGGAGGTTC GTCGTGGTAA CGTTGCCGGT GACTCCAAGA     800
ACGACCCGCC CAAGGGTGCC GAGTCCTTCA ACGCCCAGGT CATTGTCCTC     850
AACCACCCTG GTCAGATCGG TGCCGGCTAC GCTCCAGTCT TGGATTGCCA     900
CACTGCCCAC ATTGCTTGCA AGTTCGCCGA GTTGCTCGAG AAGATCGACC     950
GTCGTACCGG AAAGTCCATC GAGAACAACC CCAAGTTCAT CAAGTCTGGT    1000
GATGCTGCCA TCGTCAAGAT GATTCCCAGC AAGCCCATGT GTGTCGAGGC    1050
TTTCACCGAC TATCCTCCTC TGGGTCGTTT CGCTG                    1085
```

2) INFORMATION FOR SEQ ID NO: 458

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: DAL-95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

```
TGTCTTCATC CGGAATTGAT TGTGAGTCGT TCCACATGCT CACCTAGTTT      50
TCGCTCGATC TTTTCACTAA CGCAAACCAT GTAGAACAAC ATTGCCAAGG     100
CCCACGGTGG TTACTCCGTC TTCACTGGTG TTGGTGAGCG TACTCGTGAG     150
GGTAACGATC TGTACCACGA AATGCAGGAG ACTGGTGTCA TTCAGCTCGA     200
GGGTGAATCC AAGGTCGCAC TGGTGTTCGG ACAGATGAAC GAGCCCCCCG     250
GTGCCCGTGC CCGTGTCGCC CTTACCGGTC TGACCATTGC CGAGTACTTC     300
CGTGACGAGG AGGGTCAGGA CGTGCTGCTC TTCATTGACA ACATTTTCCG     350
TTTCACCCAG GCCGGTTCTG AGGTGTCTGC CCTTCTCGGT CGTATCCCCT     400
CTGCCGTCGG TTACCAGCCC ACCCTGGCCG TCGACATGGG TGGTATGCAG     450
GAGCGTATCA CCACCACCAA GAAGGGTTCT ATTACCTCCG TC            492
```

2) INFORMATION FOR SEQ ID NO: 459

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1154 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Blastoschizomyces capitatus*
(B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

GTCCGTGGTC AAGAAGTTAT TGACACTGGT GCCCCAATTA CCATTCCTGT 50
TGGTCGTGGT ACTCTTGGTA GAATTATCAA CGTCATTGGT GAACCAATTG 100
ACGAACGTGG TCCTATCAAG GCTTCTAAGT ATGCTCCTAT CCATACTGAA 150
CCACCAACCT TTGCTGAACA ATCTACTTCT GCTGAAGTTC TTGAAACTGG 200
TATCAAGGTT GTCGATCTTC TTGCTCCTTA CGCCCGTGGT GGTAAGATTG 250
GTCTTTTCGG TGGTGCTGGT GTCGGTAAGA CTGTCTTCAT TCAAGAACTT 300
ATTAACAACA TTGCCAAGGC TCACGGTGGT TTCTCTGTCT TCACTGGTGT 350
CGGTGAAAGA ACCCGTGAAG GTAACGATCT TTACCGTGAA ATGAAGGAAA 400
CTGGTGTCAT CAACCTCGAA GGTGACTCCA AGGTCGCTCT CGTTTTCGGT 450
CAAATGAACG AACCTCCAGG TGCCCGTGCC CGTGTCGCTT TGACTGGTCT 500
TACCATTGCC GAATACTTCC GTGATGAAGA AGGACAAGAT GTCTTGCTTT 550
TCGTTGACAA CATTTTCAGA TTCACCCAAG CCGGTTCTGA AGTCTCTGCT 600
CTTTTGGGTC GTATTCCATC TGCCGTCGGT TACCAACCTA CCCTTGCTAC 650
CGATATGGGT GCCCTCCAAG AACGTATTAC CACCACCCAA AAGGGTTCCG 700
TCACATCTGT CCAAGCCGTC TATGTCCCAG CAGACGATTT GACTGATCCT 750
GCCCCAGCCA CCACTTTCGC TCACTTGGAC GCCACCACTG TCTTGTCTCG 800
TTCCATTTCC GAATTGGGTA TCTACCCAGC TGTCGATCCT CTCGATTCCA 850
AGTCTCGTCT TTTGGATCCT GAAGTTATTG GACACGAACA CTACGAAGTT 900
GCCACTCAAG TTCAACAAAC CCTCCAAGCT TACAAGTCTC TCCAAGATAT 950
CATTGCCATT TTGGGTATGG ATGAATTGTC TGAAGCTGAT AAGCTTACTG 1000
TCGAACGTGC CCGTAAGATC CAAAGATTCC TTTCCCAACC ATTCGCTGTT 1050
GCCGAAGTTT TCACTGGTAT CGAAGGTCGT CTCGTTCCAT TGAAGGAAAC 1100
CGTCAGATCT TTCAAGGAAA TCCTTGAAGG TAAGTACGAT CACCTTCCAG 1150
AAGC 1154

2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1295 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

CCAATTCGAC GAAGGAAACT TGCCAGCTAT TTTGAATGCT TTGACTTTGA 50
AGAACGGTGA CCAAGACTTG GTCTTGGAAG TTGCTCAACA TTTGGGTGAA 100
AACACCGTCA GAGCTATTGC TATGGATGGT ACTGAAGGTT TAGTCAGAGG 150
TACCGAAGTC AACGATACCG GTGCCCCAAT CTCCGTCCCA GTCGGTAGAG 200
GTACTTTAGG TAGAATCATC AATGTTGTTG GTGAACCAAT TGATGACAGA 250

GGTCCAATTG AATGTAAGGA AAAGAAACCA ATTCACGCTG AACCACCATC 300
ATTCGTTGAA CAATCCACTG CTGCCGARAT TTTGGAAACC GGTATCAAGG 350
TTGTCGACTT GTTGGCCCCA TACGCCAGAG GTGGTAARAT TGGTTTATTC 400
GGTGGTGCTG GTGTCGGTAA GACCGTCTTT ATCCAAGAAT TGATTAACAA 450
CATTGCCAAA GCCCATGGTG GTTTCTCTGT CTTTACCGGT GTYGGTGAAA 500
GAACCAGAGA AGGTAACGAT TTGTACCGTG AAATGAAAGA AACCGGTGTC 550
ATCAACTTGG AAGGTGACTC CAAGGTCGCT TTGGTCTTCG GTCAAATGAA 600
CGAACCACCA GGTGCTAGAG CTAGAGTTGC TTTGACTGGT TTGACCATTG 650
CTGAATACTT CAGAGATGAA GAAGGTCAAG ATGTCTTGTT GTTCATTGAT 700
AACATTTTCA GATTCACCCA AGCTGGTTCC GAAGTGTCTG CTTTGTTAGG 750
TCGTATTCCA TCTGCTGTCG GTTATCAACC AACCTTAGCC ACTGATATGG 800
GTCTTTTGCA AGAACGTATT ACCACCACCA AGAAAGGTTC CGTCACCTCT 850
GTCCAAGCTG TCTATGTCCC AGCTGATGAT TTGACCGATC CTGCTCCAGC 900
CACTACATTC GCCCATTTGG ATGCCACTAC TGTCTTGTCT AGAGGTATTT 950
CTGAATTGGG TATCTACCCA GCTGTCGATC CATTGGATTC CAAATCCAGA 1000
TTATTGGACG CTTCTGTTGT TGGTCAAGAA CATTACGATG TCGCTACTGG 1050
TGTTCAACAA ACTTTACAAG CTTACAAATC CTTACAAGAT ATCATTGCTA 1100
TTTTGGGTAT GGATGAATTG TCTGAAGCTG ATAAATTGAC TGTCGAAAGA 1150
GCCCGTAAGA TCCAAAGATT CTTGTCTCAA CCATTCGCTG TTGCTGAAGT 1200
TTTCACTGGT ATCCCAGGTA GATTAGTCAG ATTGCAAGAC ACTGTCAAAT 1250
CATTCAAGGA TGTTTTGGAA GGTAAATACG ATAACTTGCC AGAAA 1295

2) INFORMATION FOR SEQ ID NO: 461

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1277 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida dubliniensis*
(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

TAACTTGCCA GCTATTTTGA ATGCTTTGAC TTTGAAGAAC GGTGACCAAG 50
ATTTAGTTTT GGAAGTTGCT CAACATTTGG GTGAAAACAC CGTCAGAGCT 100
ATTGCTATGG ATGGTACTGA AGGTTTAGTC AGAGGTACTG AAGTCAACGA 150
TACCGGTGCC CCAATCTCCG TTCCAGTCGG TAGAGGTACC TTAGGTAGAA 200
TCATCAATGT TGTTGGTGAA CCAATTGATG ACAGAGGTCC AATTGAATGT 250
AAGGAAAAGA AACCAATTCA TGCAGAACCA CCATCCTTCG TTGAGCAATC 300
CACTGCTGCC GAAATTTTGG AAACCGGTAT CAAGGTTGTC GACTTATTGG 350
CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCGGTGG TGCTGGTGTC 400
GGTAAGACCG TCTTTATCCA AGAATTGATT AACAACATTG CTAAAGCCCA 450
TGGTGGTTTC TCCGTCTTTA CCGGTGTCGG TGAAAGAACC AGAGAAGGTA 500
ACGATTTGTA CCGTGAAATG AAAGAAACCG GTGTCATCAA CTTAGAAGGT 550
GACTCCAAGG TCGCTTTGGT CTTTGGACAA ATGAACGAAC CACCAGGTGC 600
TAGAGCTAGA GTTGCTTTGA CTGGTTTGAC TATTGCTGAA TACTTCAGAG 650
ATGAAGAAGG TCAAGATGTC TTGTTGTTCA TCGATAACAT TTTCAGATTC 700
ACCCAAGCTG GTTCCGAAGT GTCTGCTTTG TTAGGTCGTA TTCCATCTGC 750
CGTCGGTTAT CAACCAACCT TAGCTACTGA TATGGGTCTT TTGCAAGAAC 800
GTATTACCAC CACCAAGAAA GGTTCCGTCA CCTCTGTCCA AGCTGTCTAT 850
GTCCCAGCTG ATGATTTGAC CGATCCTGCT CCAGCCACCA CATTCGCCCA 900
TTTGGATGCC ACTACTGTCT TGTCTAGAGG TATTTCTGAA TTGGGTATTT 950
ACCCAGCTGT CGATCCATTG GATTCCAAAT CCAGATTATT GGACGCTGCC 1000

GTTGTTGGTC AAGAACATTA TGATGTCGCT ACTGGTGTTC AACAAACTTT 1050
GCAAGCTTAC AAATCCTTAC AAGATATCAT TGCTATTTTG GGTATGGATG 1100
AATTGTCTGA AGCTGATAAA TTGACTGTCG AAAGAGCCCG TAAGATTCAA 1150
AGATTCTTGT CTCAACCATT CGCCGTTGCT GAAGTTTTCA CTGGTATTCC 1200
AGGTAGATTA GTCAGATTGC AAGACACTGT CAAATCATTC AAGGATGTTT 1250
TGGAAGGTAA ATACGATCAC TTGCCAG 1277

2) INFORMATION FOR SEQ ID NO: 462

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida famata*
(B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

GTAACTTGCC AGCTATTTTG AACGCTTTGA CCTTGAAGAA CGGTGAAAAC 50
GACTTAGTTT TAGAAGTTGC CCAACATTTG GGTGAAAACA CCGTCAGAGC 100
TATTGCTATG GATGGTACTG AAGGTTTAGT TAGAGGTACT CCAGTTACCG 150
ATTCTGGTGC TCCAATTTCT GTCCCAGTCG GTAGAGGTAC TTTAGGTAGA 200
ATCTTGAACG TTATTGGTGA ACCAATTGAT GAACAAGGTC CAGTTGATGC 250
CAAGGAAACC AGACCAATTC ACCAAGACCC ACCAGCATTC GTTGATCAAT 300
CCACCAAGGC TGAAGTTTTG GAAACTGGTA TCAAGGTTGT CGATTTATTA 350
GCCCCTTACG CTAGAGGTGG TAAGATTGGT TTATTCGGTG GTGCCGGTGT 400
CGGTAAGACC GTCTTTATCC AAGAATTGAT TAACAACATT GCCAAGGCCC 450
ATGGTGGTTT CTCTGTTTTC ACTGGTGTCG GTGAAAGAAC CAGAGAAGGT 500
AACGATTTAT ATAGAGAAAT GAAGGAAACT GGTGTCATTA ACTTGGAAGG 550
TGACTCCAAG GTCGCCTTGG TTTTCGGTCA AATGAACGAA CCACCAGGTG 600
CTAGAGCTAG AGTTGCTTTA ACCGGTTTAA CCATTGCCGA ATACTTCAGA 650
GACGAAGAAG GTCAAGATGT GTTATTGTTC GTCGATAACA TTTTTAGATT 700
CACCCAAGCC GGTTCCGAAG TGTCTGCTTT GTTAGGTCGT ATTCCATCGG 750
CTGTCGGTTA TCAACCAACC TTAGCCACTG ATATGGGTCT TTTACAAGAA 800
AGAATTACCA CCACCACCAA GGGTTCCGTT ACTTCTGTCC AAGCTGTCTA 850
CGTCCCAGCC GATGATTTAA CCGATCCTGC TCCAGCTACC ACTTTCGCCC 900
ACTTGGATGC TACCACTGTG TTGTCTCGTG GTATCTCTGA ATTGGGTATT 950
TACCCAGCTG TCGATCCATT GGATTCCAAA TCCAGATTGT TAGATGCTGA 1000
TATCGTTGGT AAAGAACACT ACGAAGTTGC CACTGGTGTC CAACAAACCT 1050
TACAAGCTTA CAAATCTTTA CAAGATATCA TTGCTATTTT AGGTATGGAT 1100
GAATTGTCTG AAGCCGATAA ATTGACTGTC GAAAGAGCCA GAAAGATCCA 1150
AAGATTCTTG TCTCAACCAT TCGCCGTTGC CGAAGTTTTC ACCGGTATCC 1200
CAGGTAGATT AGTTAGATTG CAAGACACTG TTAAATCTTT CAAGGAAGTC 1250
TTAGAAGGTA AATATGATCA CTTACCAG 1278

2) INFORMATION FOR SEQ ID NO: 463

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1154 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida glabrata*
(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

```
TCTGGTCAGA GGCGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC      50
CTGTCGGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CGGTGAACCT     100
ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC     150
CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA     200
CAGGTATCAA GGTCGTCGAC TTGCTGGCCC CTTACGCCAG AGGTGGTAAG     250
ATCGGTCTGT TCGGTGGTGC CGGTGTCGGT AAGACCGTGT TCATCCAAGA     300
ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTCACAG     350
GTGTCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG     400
GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CCTTGGTCTT     450
CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG     500
GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG     550
CTGTTCGTCG ACAACATTTT CAGATTCACC CAAGCCGGTT CAGAAGTCTC     600
CGCTTTGCTA GGTCGTATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG     650
CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT     700
TCCGTCACTT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA     750
TCCTGCCCCT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT     800
CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCGA CCCATTGGAC     850
TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA     900
CGTCGCCACA AAGGTCCAAG AAACTTTACA AACTTACAAG TCTCTGCAAG     950
ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCCGAACA AGATAAGCTA    1000
ACTGTCGAAA GAGCAAGAAA GATCCAAAGA TTCTTGTCCC AACCATTCGC    1050
TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG    1100
ACACCATCTC CTCTTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT    1150
CCAG                                                     1154
```

2) INFORMATION FOR SEQ ID NO: 464

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1293 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida guilliermondii*
(B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

```
CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA      50
AGAACGGTGA CCAAAACTTG GTTTTGGAAG TTGCCCAGCA TTTGGGTGAA     100
AACACCGTCA GAACCATTGC TATGGATGGT ACTGAAGGTT TGGTTAGAGG     150
TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG     200
GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT     250
GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTCACGCTG AACCACCATC     300
GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGAAACC GGTATCAAGG     350
```

TTGTCGACTT GTTGGCTCCA TACGCCAGAG GTGGTAAGAT TGGATTGTTC 400
GGTGGTGCCG GTGTCGGTAA GACTGTGTTT ATCCAAGAGT TGATTAACAA 450
CATTGCCAAG GCTCACGGTG GTTTCTCCGT GTTCACCGGT GTCGGTGAAA 500
GAACCAGAGA AGGTAACGAT TTGTACCGTG AAATGAAGGA AACTGGTGTC 550
ATCAACTTGG AAGGTGAATC CAAGGTGGCC TTGGTGTTCG GTCAAATGAA 600
CGAACCTCCA GGAGCTAGAG CCAGAGTTGC CCTTACCGGT TTGACCATCG 650
CTGAATACTT CAGAGATGAG GAGGGTCAAG ATGTGTTGTT GTTCGTCGAC 700
AACATTTTCA GATTCACTCA AGCTGGTTCT GAAGTGTCGG CTTTGTTGGG 750
TCGTATTCCT TCGGCTGTCG GTTACCAACC TACTTTGGCC ACCGATATGG 800
GTTTGTTGCA AGAGCGTATT ACCACCACCA AGAAGGGTTC CGTCACCTCT 850
GTCCAAGCTG TCTATGTGCC AGCCGATGAT TTGACCGATC CTGCTCCTGC 900
TACTACTTTT GCTCACTTGG ATGCTACCAC TGTGTTGTCT AGAGGTATCT 950
CCGAGTTGGG TATTTACCCA GCTGTCGATC CTTTGGATTC CAAGTCGAGA 1000
TTGTTGGATG CCTCTGTTGT CGGTGAGGAG CACTACTCGG TTGCTTCTAA 1050
CGTTCAACAA ACCTTGCAAG CTTACAAGTC TTTGCAAGAT ATCATTGCCA 1100
TTTTGGGTAT GGACGAATTG TCGGAAGCTG ACAAGTTGAC CGTCGAGAGA 1150
GCCCGTAAGA TCGAGAGATT CTTGTCTCAA CCATTTGCTG TTGCCGAAGT 1200
TTTCACTGGT ATCAGTGGTA AGTTGGTCAG ATTGGAGGAC ACTATCAGAT 1250
CTTTCAAGGA AGTCTTGGAA GGTAAGTACG ATCACTTGCC AGA 1293

2) INFORMATION FOR SEQ ID NO: 465

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1293 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida haemulonii*
(B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

CACTTTGACG ATGGTAACTT GCCAGCCATT TTCAACGCCT TGAAGTTGAA 50
GAACGGTGAC CAGGACTTGG TCTTGGAGGT CGCCCAGCAC TTGGGTGAGA 100
ACACCGTCAG AACCATTGCC ATGGACGGTA CCGATGGTTT GGTCAGAGGC 150
GAGGCTGTCA CTGACACTGG TGCTCCAATC TCCGTGCCTG TTGGTCGTGA 200
GACTTTGGGT CGTATCATCA ACGTTATTGG TGAGCCAATT GACGAGAGAG 250
GACCAATCAA GTCCAAGAAG AGAAACCCAA TCCACACTGA CCCACCAACC 300
TTCGTTGAGC AGTCTACTTC TGCTGAGGTT TTGGAGACTG GTATTAAGGT 350
TGTCGACTTG TTGGCCCCTT ACGCCAGAGG TGGTAAGATT GGTTTGTTCG 400
GTGGTGCCGG TGTCGGTAAG ACCGTCTTTA TCCAAGAGTT GATTAACAAC 450
ATTGCCAAGG CCCACGGTGG TTTCTCTGTC TTTACCGGTG TCGGTGAGAG 500
AACCAGAGAA GGTAACGATT TGTACCGTGA AATGCAGGAG ACCGGTGTCA 550
TCAACTTCGA GGGTGACTCC AAGGTCGCCT TGGTCTTCGG TCAGATGAAC 600
GAGCCACCAG GAGCTAGAGC TAGAGTTGCT TTGACCGGTT TGACCATTGC 650
CGAATACTTC AGAGATGAAG AAGGTCAGGA TGTGTTGTTG TTCGTTGACA 700
ACATTTTCAG ATTCACTCAG GCTGGTTCCG AGGTGTCCGC CTTGTTGGGT 750
CGTATTCCAT CTGCTGTCGG TTACCAGCCA ACCTTGGCCA CCGATATGGG 800
TACCTTGCAA GAAAGAATTA CCACCACCAA GAAGGGTTCC GTCACCTCTG 850
TCCAGGCCGT TTACGTGCCA GCTGATGATT TGACCGATCC TGCCCCAGCT 900
ACCACTTTCG CTCACTTGGA TGCTACCACT GTGTTGTCTA GAGGTATTTC 950
CGAGTTGGGT ATCTACCCAG CTGTCGACCC ATTGGACTCC AAGTCTAGAT 1000
TGTTGGATGC CTCTGTTGTC GGTAAGGAGC ACTACGATGT TGCTACCAAC 1050
GTCCAGCAGA CCTTGCAGGC CTACAAGTCC TTGCAGGATA TCATTGCCAT 1100

TTTGGGTATG GATGAATTGT CCGAAGCCGA CAAGTTGACT GTCGAGAGAG 1150
CTAGAAAGAT TCAGAGATTC TTGTCCCAGC CATTCGCCGT CGCCGAGGTT 1200
TTCACTGGTA TCGAGGGTAA GTTGGTCAGA TTGGAGGAGA CCGTCAAGTC 1250
TTTCAAGGAG GTCTTGGATG GTAAGTACGA CCACTTGCCA GAG 1293

2) INFORMATION FOR SEQ ID NO: 466

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1111 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida inconspicua*
(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT CTAAGTTAGT CTTAGAAGTT GCTCAACATT TGGGTGAAAA 50
CACTGTCAGA ACCATTGCTA TGGATGGTAC TGAAGGTTTA GTTAGAGGTC 100
AACCAGTTAA TGATACTGGT GCTCCAATCT CTGTCCCAGT CGGTAGAGGT 150
ACTTTAGGTA GAATCTTAAA CGTTATTGGT GATCCAGTCG ATGAAAGAGG 200
TCCAATTGAT TGTAAGGAAA GAAAACCAAT TCATCAAGAT CCTCCTGCTT 250
TCGTTGAACA ATCTACTGAA GCTGAAGTTT TAGAAACCGG TATTAAGGTT 300
GTTGATTTAT TAGCTCCTTA CGCTAGAGGT GGTAAGATTG GTTTATTCGG 350
TGGTGCTGGT GTCGGTAAAA CCGTTTTCAT TCAAGAATTA ATTAACAATG 400
TTGCAAAGGC TCATGGTGGT TTCTCAGTTT TCACTGGTGT CGGTGAAAGA 450
ACCAGAGAAG GTAATGATTT ATACAGAGAA ATGAAGGAAA CTGGTGTTAT 500
TAACTTAGAA GGTGAATCTA AGGTCGCCTT AGTTTTCGGT CAAATGAATG 550
AACCACCAGG AGCAAGAGCA AGAGTTGCTT TAACCGGTTT AACTATTGCT 600
GAATACTTCA GAGATGAAGA AGGTCAAGAT GTCTTGTTAT TCATTGATAA 650
CATTTTCAGA TTTACTCAAG CAGGTTCTGA AGTTTCTGCA TTGTTAGGTA 700
GAATTCCATC CGCTGTCGGT TATCAACCAA CTTTAGCAAC TGATATGGGT 750
CTTTTACAAG AAAGAATTAC AACTACTAAG AAAGGTTCCG TTACTTCTGT 800
CCAAGCAGTT TATGTCCCAG CAGATGATTT AACTGATCCT GCTCCAGCAA 850
CTACTTTCGC CCACTTAGAT GCAACTACTG TCTTATCTAG AGGTATTTCC 900
GAATTAGGTA TTTACCCAGC TGTCGATCCA TTAGATTCTA AATCTAGATT 950
ATTAGATGTT GCTGTTGTTG GTCAAGAACA TTATGATGTT GCAACTCAAG 1000
TTCAAGAAAC TTTACAAGCA TACAAATCTT TACAAGATAT TATTGCTATT 1050
TTAGGTATGG ATGAATTATC TGAACAAGAT AAATTAACCG TTGAAAGAGC 1100
AAGAAAGATT C 1111

2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1283 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida kefyr*
(B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

```
TCGAACAAGG TCAATTGCCA GAAATTTTGA ACGCTTTGGA GATTGAWACT      50
CCTCAAGGTA AGTTGGTTTT GGAAGTTGCC CAACATTTGG GTGAAAACAC     100
CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTGGTC CGTGGTGAGA     150
AGGTTTTGGA CACTGGTGCT CCAATTTCCG TCCCAGTCGG TAGAGAAACT     200
TTGGGTAGAA TCATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGCCC     250
AATCAAGTCC AAGATGAGAA AGCCAATTCA CGCTGACCCT CCATCCTTTG     300
TTGAACAATC CACTGCTGCT GAAGTTTTGG AAACCGGTAT CAAGGTTGTC     350
GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCGGTGG     400
TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAGTTGATT AACAACATTG     450
CCAAGGCCCA TGGTGGTTTC TCCGTCTTCA CCGGTGTCGG TGAAAGAACC     500
AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACCG GTGTCATCAA     550
CTTGGAAGGT GACTCCAAGG TCGCCTTGGT CTTCGGTCAA ATGAACGAAC     600
CACCTGGAGC TAGAGCCAGA GTTGCCTTGA CCGGTTTGAC TATCGCTGAA     650
TACTTCAGAG ATGAAGAAGG TCAAGATGTG TTGTTGTTTA TCGACAACAT     700
TTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA     750
TTCCATCCGC TGTCGGTTAC CAACCTACTT TGGCCACCGA TATGGGTTTG     800
TTGCAAGAAA GAATTACCAC TACCAAGAAG GGTTCCGTTA CCTCCGTCCA     850
AGCTGTCTAC GTCCCTGCTG ATGATTTGAC TGATCCTGCT CCAGCTACYA     900
CTTTCGCCCA TTTGGACGCC ACCACCGTGT TGTCCAGAGG TATCTCCGAA     950
TTGGGTATCT ACCCAGCTGT CGATCCATTG GATTCCAAGT CTAGATTGTT    1000
GGACGCTGCC GTTGTCGGTC AAGAACATTA CGACGTCGCT ACTCAAGTTC    1050
AACAAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG    1100
GGTATGGATG AATTGTCTGA ACAAGACAAG TTGACTGTCG AAAGAGCCAG    1150
AAAGATCCAA AGATTCTTGT CTCAACCATT CGCCGTCGCC GAAGTTTTCA    1200
CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CGCTTCCTTC    1250
AAGGCTGTTT TGGAAGGTAA GTACGATCAC TTG                      1283
```

2) INFORMATION FOR SEQ ID NO: 468

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1287 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida krusei*
(B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

```
CTTCGAACAA GGCCAATTAC CACAAATTTT AAACGCTTTA GTTATGGATA      50
ATGGTGGTAA CAAGTTAGTT TTAGAAGTTG CTCAACATTT AGGTGAAAAC     100
ACTGTCAGAA CCATTGCTAT GGATGGTACT GAAGGTTTAG TTAGAGGTCA     150
AACCGTTAAC GATACCGGTG CTCCAATCTC TGTCCCAGTT GGTAGAGGTA     200
CCTTAGGTAG AATCTTGAAC GTCATTGGTG ATCCAGTCGA TGAAAGAGGT     250
CCAGTTGACT GTAAGGAAAG AAAGCCAATT CACGCTGATC CTCCAGCTTT     300
CGTTGAACAA TCCACTGAAG CTGAAGTTTT GGAAACTGGT ATTAAGGTTG     350
TCGATTTATT AGCACCTTAC GCAAGAGGTG GTAAGATTGG TTTATTCGGT     400
GGTGCTGGTG TTGGTAAGAC CGTTTTTATC CAAGAATTGA TCAACAATGT     450
YGCAAAGGCT CATGGTGGTT TCTCCGTTTT CACTGGTGTT GGTGAAAGAA     500
```

CCAGAGAAGG TAACGATTTA TACAGAGAAA TGAAGGAAAC TGGTGTTATT 550
AACTTGGAAG GTGAATCCAA GGTCGCCTTA GTTTTCGGTC AAATGAACGA 600
ACCACCAGGA GCTAGAGCAA GAGTTGCTTT AACTGGTTTG ACCATTGCAG 650
AATATTTCAG AGATGAAGAA GGTCAAGATG TCTTGTTATT CATTGATAAC 700
ATTTTCAGAT TCACCCAAGC AGGTTCTGAA GTCTCTGCAT TATTAGGTAG 750
AATTCCATCT GCTGTCGGTT ATCAACCAAC TTTAGCAACC GATATGGGTC 800
TTTTACAAGA AAGAATTACC ACCACCAAGA AGGGTTCCGT TACTTCTGTC 850
CAAGCTGTTT ATGTCCCAGC CGATGATTTA ACCGATCCTG CTCCAGCTAC 900
TACTTTCGCC CACTTGGATG CAACCACTGT CTTGTCYAGA GGTATTTCCG 950
AATTAGGTAT CTACCCAGCT GTCGATCCAT TAGATTCTAA GTCTAGATTA 1000
TTAGATGTTG CAGTTGTTGG TCAAGAACAT TATGAAGTTG CAACTCAAGT 1050
CCAAGAAACT TTACAAGCTT ACAAGTCTTT ACAAGATATT ATTGCTATTT 1100
TGGGTATGGA TGAATTATCT GAACAAGATA AGTTAACYGT TGAAAGAGCA 1150
AGAAAGATCC AAAGATTCTT ATCTCAACCA TTCTCTGTTG CAGAAGTTTT 1200
CACTGGTATT CCAGGTAAGT TAGTCAGATT AGAAGAAACC ATCAAGTCTT 1250
TCAGGGATGT TCTTGCAGGT AAGTACGATC ACTTACC 1287

2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1283 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida lambica*
(B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

TCGAACAAGG TCAATTACCA CCAATTCTTA ACGCTTTGGT CATGGAAAAC 50
GATGGTCAAA AGTTAGTTTT GGAAGTTGCT CAACATTTGG GTGAAAACAC 100
CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTAGTT AGAGGTCAAC 150
CTGTTAACGA CACTGGTGCT CCAATCTCTG TCCCAGTTGG TAGAGGTACT 200
CTTGGTAGAA TCTTGAACGT CACTGGTGAC CCAGTYGATG AAAGAGGTCC 250
TGTCGAMTGT AAGGAGAGAA GACCAATTCA CCAAGACCCA CCTGCTTTCG 300
TTGACCAATC CACTGAAGCT GAAGTTTTGG AAACCGGTAT TAAGGTTGTC 350
GATTTATTAG CACCTTACGC TAGAGGTGGT AAGATTGGTT TGTTCGGTGG 400
TGCTGGTGTC GGTAAGACCG TTTTCATCCA AGAATTGATT AACAATGTTG 450
CTAAGGCCCA CGGTGGTTTC TCCGTTTTCA CTGGTGTCGG TGAAAGAACC 500
AGAGAAGGTA ACGATTTATA CAGAGAAATG AAGGAAACCG GTGTTATTAA 550
CCTTGAAGGT GAATCTAAGG TCGCCCTCGT TTTCGGTCAA ATGAACGAAC 600
CACCAGGAGC AAGAGCTAGA GTTGCTCTTA CTGGTTTGAC CATTGCTGAA 650
TACTTCAGAG ATGAAGAAGG TCAAGATGTC TTGCTTTTCA TTGACAACAT 700
TTTCAGATTC ACCCAAGCAG GTTCCGAAGT GTCTGCTTTG TTAGGTAGAA 750
TTCCWTCTGC CGTTGGTTAC CAACCAACCT TAGCAACCGA TATGGGTTTG 800
TTACAAGAAA GAATTACCAC CACCAAGAAG GGTTCCGTCA CCTCCGTCCA 850
AGCTGTTTAC GTCCCAGCTG ATGATTTRAC TGACCCTGCA CCAGCAACCA 900
CTTTCGCCCA CTTGGATGCT ACCACCGTCT TGTCTAGAGG TATTTCCGAA 950
TTAGGTATTT ACCCAGCTGT CGATCCATTA GATTCTAAGT CTAGATTATT 1000
GGATGTCGCT GTTGTCGGTC AAGAACATTA TACCGTTGCA ACYCAAGTCC 1050
AAGAAACTTT ACAAGCTTAC AAGTCCTTAC AAGATATCAT TGCTATTTTG 1100
GGTATGGACG AATTATCTGA ACAAGATAAG CTTACTGTTG AAAGAGCAAG 1150
AAAGATCCAA AGATTCCTTT CCCAACCTTT CTCCGTCGCA GAAGTTTTCA 1200
CTGGTATCCC AGGTAAGCTT GTCAGATTAG AAGAAACCAT TATTTCTTTC 1250

AGAGATGTCC TCGATGGTAA GTACGACCAC TTA 1283

2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1140 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida lusitaniae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

AGGTGCCTCT GTCACTGACA CTGGTTCTCC AATCTCTGTC CCTGTTGGTC 50
GTGAAACCTT GGGTAGAATT ATCAACGTTG TTGGTGAGCC AATTGACGAG 100
AGAGGCCCAA TCAACTCCAA GAAGAGAAAC CCAATTCACA CTGAGCCACC 150
ATCGTTTGTT GAACAATCCA CTTCTGCTGA AGTTTTGGAG ACTGGTATCA 200
AGGTTGTCGA CTTGTTGGCC CCTTACGCCA GAGGTGGTAA GATTGGTTTG 250
TTCGGTGGTG CCGGTGTCGG TAAGACCGTT TTCATCCAAG AGTTGATTAA 300
CAACATTGCC AAGGCCCACG GTGGTTTCTC TGTTTTCACT GGTGTCGGTG 350
AAAGAACCAG AGAAGGTAAC GATTTGTACC GTGAAATGCA AGAGACCGGT 400
GTCATCAACT TCGAGGGTGA CTCCAAGGTC GCCTTGGTCT TCGGTCAAAT 450
GAACGAACCA CCAGGAGCCA GAGCTAGAGT TGCTTTGACC GGTTTGACTA 500
TTGCCGAGTA CTTCAGAGAC GAAGAGGGCC AAGATGTCTT GTTGTTCGTT 550
GACAACATTT TCAGATTCAC CCAGGCCGGT TCTGAAGTGT CTGCTTTGTT 600
GGGTCGTATT CCATCCGCTG TCGGTTACCA ACCAACCTTG GCCACCGATA 650
TGGGTGCTTT GCAAGAGAGA ATTACCACCA CCAAGAAGGG TTCCGTCACC 700
TCTGTCCAAG CCGTTTATGT TCCAGCTGAT GACTTGACTG ACCCTGCTCC 750
AGCCACCACC TTCGCCCACT TGGACGCCAC CACTGTGTTG TCCAGAGGTA 800
TCTCTGAATT GGGTATCTAC CCAGCTGTCG ACCCATTGGA CTCCAAGTCT 850
AGATTGTTGG ACGCTTCTAT TGTTGGTAAG GAGCACTACG AAGTTGCTTC 900
TAACGTTCAA CAAACTTTGC AAGCTTACAA GTCTTTGCAA GATATCATTG 950
CCATTTTGGG TATGGATGAA TTGTCTGAGG CTGACAAGTT GACCGTTGAG 1000
AGAGCCAGAA AGATCCAAAG ATTCTTGTCT CAACCATTCG CTGTTGCCGA 1050
GGTTTTCACT GGTATCCCAG GTAGATTGGT CAGATTGGAG GACACTGTCA 1100
GATCCTTCAA GGAAGTTTTG GACGGTAAGT ACGACCACTT 1140

2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1296 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida norvegensis*
(B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

```
TCAATTCGAA CAAGGTCAAT TACCACCAAT TTTAAACGCT TTAGTCATGG       50
ACAACGGTGG AACTAAGTTA GTTTTAGAAG TTGCTCAACA TTTAGGTGAA      100
AACACCGTCA GAACCATTGC TATGGATGGT ACTGAAGGTT TAGTTAGAGG      150
TCAACCAGTT AATGATACTG GTGCTCCAAT CTCTGTCCCA GTCGGTAGAG      200
GTACTTTAGG TAGAATCTTA AACGTTATTG GTGATCCAGT CGATGAAAGA      250
GGTCCAATCG ATTGTAAGGA AAGAAAACCA ATTCATCAAG ATCCTCCTGC      300
TTTCGTTGAA CAATCAACTG AAGCTGAAGT TTTAGAAACT GGTATTAAAG      350
TTGTCGATTT ATTAGCTCCT TACGCTAGAG GTGGTAAGAT TGGTTTATTC      400
GGTGGTGCAG GTGTTGGTAA AACCGTTTTT ATTCAAGAAT TAATTAACAA      450
TGTTGCAAAA GCTCATGGTG GTTTCTCCGT TTTCACTGGT GTCGGTGAAA      500
GAACTAGAGA AGGTAACGAT TTATACAGAG AAATGAAGGA AACTGGTGTT      550
ATTAATTTAG AAGGTGATTC TAAGGTCGCA TTAGTTTTCG GTCAAATGAA      600
CGAACCACCT GGAGCAAGAG CAAGAGTTGC TTTAACTGGT TTAACTATTG      650
CTGAATATTT CAGAGATGAA GAAGGTCAAG ATGTCTTGTT ATTCATTGAT      700
AACATTTTCA GATTTACTCA AGCAGGTTCT GAAGTTTCCG CTTTGTTAGG      750
TAGAATTCCA TCCGCTGTCG GTTATCAACC AACTTTAGCA ACTGATATGG      800
GTCTTTTACA AGAAAGAATT ACTACTACTA AGAAAGGTTC TGTTACTTCC      850
GTTCAAGCAG TTTATGTCCC AGCAGATGAT TTAACTGATC CTGCTCCAGC      900
AACTACTTTC GCCCACTTAG ATGCAACTAC TGTCTTATCT AGAGGTATTT      950
CCGAATTAGG TATTTACCCA GCTGTCGATC CATTAGATTC TAAATCTAGA     1000
TTATTAGATG TTGCAGTTGT TGGTCAAGAA CATTATGATG TTGCAACTCA     1050
AGTTCAAGAA ACTTTACAAG CTTACAAATC TTTACAAGAT ATTATTGCTA     1100
TTTTAGGTAT GGATGAATTA TCTGAACAAG ATAAATTAAC CGTTGAAAGA     1150
GCTAGAAAAA TTCAAAGATT CTTATCTCAA CCTTTCTCTG TCGCAGAAGT     1200
TTTCACTGGT ATCCCAGGTA AGCTTGTTAG ATTAGAAGAA ACTATTTCTT     1250
CATTCAGAGA TGTCTTAGCA GGTAAGTACG ATCACTTACC AGAAAA         1296
```

2) INFORMATION FOR SEQ ID NO: 472

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida parapsilosis*
- (B) STRAIN: ATCC 90018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

```
ACACTTCGAA GAAGGAAACT TGCCAGCTAT TTTGAACGCT TTGACCTTGA       50
AAAACGGTAA ACAAGACTTG GTCTTGGAAG TTGCCCAACA TTTGGGTGAA      100
AACACCGTCA GAGCAATTGC TATGGATGGT ACTGAAGGTT TAGTTAGAGG      150
TACTTCTGTC ACTGACACTG GTGCCCCAAT TTCTGTCCCA GTTGGTAGAG      200
GTACTTTGGG TAGAATCATC AATGTTACTG GTGACCCAAT TGATGAAAGA      250
GGTCCAATTG AATGTAAGAA GAGAAACCCA ATCCACGCTG AACCACCTTC      300
ATTCATTGAA CAATCCACTG CTGCTGAAGT TTTGGAAACC GGTATTAAGG      350
TTGTCGACTT GTTGGCTCCA TACGCTAGAG GTGGTAAGAT TGGTTTGTTC      400
GGTGGTGCCG GTGTCGGTAA AACCGTGTTT ATCCAAGAAT TGATCAACAA      450
CATTGCCAAG GCACATGGTG GTTTCTCGGT TTTCACTGGT GTTGGTGAAA      500
GAACCAGAGA AGGTAACGAT TTGTACCGTG AAATGAAGGA AACTGGTGTT      550
ATCAACTTGG AAGGTGACTC CAAGGTCGCT TTGGTTTTCG GTCAAATGAA      600
CGAACCACCT GGAGCTAGAG CTAGAGTTGC TTTGACTGGT TTGACCATTG      650
```

CTGAATACTT TAGAGATGAA GAAGGTCAAG ATGTCTTGTT GTTTATTGAC 700
AACATTTTCA GATTCACCCA AGCTGGTTCA GAAGTGTCTG CTTTGTTGGG 750
TCGTATTCCA TCCGCTGTCG GTTATCAACC AACCTTGGCC ACCGATATGG 800
GTCTTTTGCA AGAACGTATT ACCACTACCA AAAAGGGTTC AGTTACTTCA 850
GTCCAAGCCG TTTACGTGCC AGCTGATGAT TTAACCGATC CTGCTCCAGC 900
TACCACTTTC GCTCACTTGG ATGCCACCAC TGTGTTGTCT AGAGGTATTT 950
CGGAGTTGGG TATTTACCCA GCTGTCGATC CATTGGATTC CAAATCCAGA 1000
TTGTTGGATG CTGCCGTTGT TGGTCAAGAA CATTACGACG TTGCCACTGG 1050
TGTTCAACAA ACTTTACAAG CTTACAAGTC CTTGCAAGAT ATCATTGCTA 1100
TCTTGGGTAT GGATGAATTG TCCGAACAAG ATAAATTGAC TGTCGAAAGA 1150
GCTCGTAAGA TTCAAAGATT CTTGTCTCAA CCATTTGCTG TCGCTGAAGT 1200
TTTCACTGGT ATTCCAGGTA AATTGGTTAG ATTGTCTGAA ACTGTCAAGT 1250
CATTCAAGGA AGTCTTGGAA GGTAAGTACG ATAACTTGCC AGAAAAT 1297

2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1285 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida rugosa*
(B) STRAIN: ATCC 96275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

CCAGTTTGGC AACGACCTCC CTGCCATTTT GAACGCCCTC ACTCTTCAGC 50
GTGAAGACGG TAACAAGCTT GTTCTTGAGG TTGCCCAGCA TCTCGGTGAG 100
AACACCGTCC GTACCATTGC TATGGACGGT ACCGAGGGTT TGGTGCGTGG 150
CACTGGTGTC CACGACACCG GACACCCCAT CATGACTCCC GTCGGTGACG 200
GTACCCTGGG ACGTATTCTT AACGTCACCG GTGACCCTGT AGACGAGCGT 250
GGTCCCGTCA AGACTGACAA GTTCCGCCCC ATCCACGCCG AGGCCCCTGC 300
CTTCGATGAG CAGGCTACCA GTGCCGAGGT TCTTGAGACC GGTATCAAGG 350
TTGTCGACTT GCTCGCTCCT TACGCCAAGG GTGGTAAGAT TGGTTTGTTC 400
GGTGGTGCCG GTGTCGGCAA GACCGTCTTC ATCCAGGAGC TGATTAACAA 450
CATCGCCAAG GCCCACGGTG GTTACTCCGT GTTCACTGGT GTCGGTGAGC 500
GTACTCGTGA GGGTAACGAT TTGTACAAGG AAATGATCGA GTCCGGTGTC 550
ATCAACCTCG ATGGTGAGTC CAAGGTCGCC TTGGTGTTCG GTCAGATGAA 600
CGAGCCCCCT GGAGCCCGTG CCCGTGTCGC CCTTACCGGT CTTACCATCG 650
CTGAGTATTT CCGTGATGAG GAGGGTAAGG ATGTCTTGTT GTTCGTTGAC 700
AACATTTTCC GCTTCACTCA GGCCGGTTCT GAGGTGTCCG CCTTGCTTGG 750
TCGTATTCCT TCCGCTGTCG GTTACCAGCC TACCCTGGCC ACCGATATGG 800
GTGCCCTTCA GGAGCGTATC ACCACCACCA AGAAGGGTTC CGTTACATCC 850
GTCCAGGCCG TCTACGTCCC TGCCGATGAT TTGACTGATC CCGCCCCTGC 900
CACCACCTTC GCCCATTTGG ATGCCACCAC TGTCTTGTCT CGTGCCATCT 950
CTGAGTTGGG TATCTACCCC GCTGTCGACC CTCTCGACTC CAAGTCCCGT 1000
CTTCTTGACG CCGCTGTCGT TGGTCAGGAG CACTACGATA CTGCCACCTC 1050
CGTTCAGCAG ACTTTGCAGG CTTACAAGTC TTTGCAGGAT ATCATTGCCA 1100
TTCTTGGTAT GGATGAGTTG TCCGAGTCTG ACAAGCTCAC CGTCGAGCGT 1150
GCTCGTAAGA TCCAGCGTTT CCTCTCCCAG CCTTTCGCTG TTGCTGAGGT 1200
CTTCACTGGT ATTCAGGGCC GTCTTGTTCC TCTCAAGGAC ACTGTCCGCT 1250
CCTTCAAGGA GATTCTCGAA GGTAAGTACG ATGCT 1285

2) INFORMATION FOR SEQ ID NO: 474

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1283 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida sphaerica*
(B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

TTGAACAAGG TCAATTGCCA GCTATTTTGA ACGCTTTGGA AATCGACACT 50
CCAGAAGGAA AGTTGGTTTT GGAAGTCGCT CAACATTTGG GTGAAAACAC 100
TGTCAGAACC ATTGCTATGG ATGGTACTGA AGGTTTAGTC CGTGGTGAAA 150
ACGTTTCTGA CACTGGTGCT CCAATTTCCG TCCCAGTTGG TAGAGAAACC 200
TTGGGTAGAA TTATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGTCC 250
AATCAACTCC AAGATGAGAA AGCCAATTCA TGCTGATCCT CCATTATTCG 300
TTGAACAATC CACTGCTGCT GAAGTTTTGG AAACTGGTAT CAAGGTTGTC 350
GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCGGTGG 400
TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAATTGATT AACAACATTG 450
CCAAGGCTCA TGGTGGTTTC TCTGTCTTCA CTGGTGTCGG TGAAAGAACC 500
AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACTG GTGTTATCAA 550
CTTGGAAGGT GATTCTAAGG TCGCGTTGGT TTTCGGTCAA ATGAACGAAC 600
CTCCTGGAGC TAGAGCTAGA GTCGCCTTGA CTGGTTTGAC CATCGCTGAA 650
TACTTCAGAG ATGAAGAAGG TCAAGATGTC TTGTTGTTTA TCGACAACAT 700
TTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA 750
TTCCATCCGC TGTCGGTTAT CAACCAACTT TGGCCACCGA TATGGGTTTG 800
TTGCAAGAAA GAATTACTAC CACCAAGAAG GGTTCCGTCA CTTCTGTCCA 850
AGCCGTTTAC GTGCCAGCTG ATGATTTGAC TGATCCTGCT CCAGCTACCA 900
CTTTCGCGCA TTTGGATGCC ACCACTGTGT TGTCCAGAGG TATCTCTGAA 950
TTGGGTATCT ACCCAGCTGT CGATCCTTTG GATTCCAAAT CTAGATTGTT 1000
GGATGCTGCC GTCGTTGGTC AAGAACATTA CGATGTCGCT ACTCAAGTTC 1050
AACAAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG 1100
GGTATGGATG AATTGTCCGA ACAAGATAAG TTGACCGTCG AAAGAGCTAG 1150
AAAGATTCAA AGATTCTTGT CTCAACCTTT CGCTGTCGCT GAAGTCTTCA 1200
CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CTCTTCTTTC 1250
AAGGCTGTCT TGGACGGTAA GTACGATCAC TTG 1283

2) INFORMATION FOR SEQ ID NO: 475

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida tropicalis*
(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

```
CGACGAAGGT AACTTGCCAG CTATTTTGAA TGCTTTGACT TTGAAGAACG      50
GTGACCAAGA CTTGGTTTTG GAAGTTGCTC AACATTTGGG TGAAAACACC     100
GTCAGGGCTA TTGCTATGGA TGGTACCGAA GGTTTAGTCA GAGGTACTGC     150
TGTCACTGAT ACCGGTGCTC CAATTTCTGT CCCAGTTGGT AGAGGTACCT     200
TGGGTAGAAT TATCAACGTT GTTGGTGAAC CAATTGATGA CAGAGGTCCA     250
ATTGAATGTA AGGAAAGAAA GCCAATTCAC GCTGAACCAC CTTCATTCGT     300
TGAACAATCT ACTGCTGCCG AAATTTTGGA AACCGGTATT AAGGTTGTCG     350
ATTTGTTGGC TCCTTACGCT AGAGGTGGTA AGATTGGTTT GTTCGGTGGT     400
GCTGGTGTCG GTAAAACCGT CTTCATCCAA GAATTGATTA ACAACATTGC     450
CAAAGCTCAT GGTGGTTTCT CTGTCTTTAC CGGTGTCGGT GAAAGAACCA     500
GAGAAGGTAA CGATTTGTAC CGTGAAATGA AAGAAACTGG TGTCATCAAC     550
TTGGAAGGTG ACTCCAAGGT CGCCTTGGTC TTCGGTCAAA TGAACGAACC     600
ACCTGGTGCT AGAGCTAGAG TTGCTTTGAC TGGTTTGACC ATTGCTGAAT     650
ACTTCAGAGA TGAAGAAGGT CAAGATGTCT TGTTGTTCAT TGACAACATT     700
TTCAGATTCA CCCAAGCTGG TTCCGAAGTG TCTGCTTTGT TGGGTCGTAT     750
TCCATCTGCT GTCGGTTATC AACCAACCTT GGCCACTGAT ATGGGTCTTT     800
TGCAAGAACG TATTACCACC ACCAAGAAAG GTTCTGTTAC TTCTGTCCAA     850
GCTGTTTATG TCCCAGCCGA TGATTTAACC GATCCAGCTC CAGCTACCAC     900
CTTCGCTCAC TTGGATGCCA CTACTGTCTT GTCTAGAGGT ATTTCTGAAT     950
TGGGTATTTA CCCAGCTGTC GATCCATTGG ATTCTAAATC CAGATTATTG    1000
GATGCTACTG TTGTTGGTCA AGAACATTAT GATGTTGCCA CTGGTGTTCA    1050
ACAAACTTTA CAAGCTTACA AGTCCTTGCA AGATATCATT GCTATTTTGG    1100
GTATGGATGA ATTGTCCGAA GCCGATAAAT TGACTGTCGA AAGAGCTCGT    1150
AAGATTCAAA GATTCTTGTC CCAACCATTC GCTGTTGCCG AAGTTTTCAC    1200
TGGTATCCCA GGTAGATTGG TTAGATTACA AGATACTGTT AAATCTTTCA    1250
AAGATGTCTT GGAAGGTAAA TACGATCACT TGCCAGAAAA              1290
```

2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1267 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida utilis*
- (B) STRAIN: Csp 388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

```
TTTGAACGCC CTTGAGATCA AGAACCACGA GTCTGGAAGA TTGGTCCTCG      50
AGGTTGCCCA GCACTTGGGT GAGAACACTG TCAGAACTAT TGCCATGGAT     100
GGTACCGAAG GTCTCGTCCG TGGTGAGTCT GTTGTTGACA CCGGTTCTCC     150
AATTACTGTC CCAGTTGGTC GTGAGACCTT GGGTCGTATC ATCAACGTTA     200
TTGGTGAGCC AATTGATGAG CGTGGTCCAA TCAACACCAA GCACAGAAAC     250
CCAATTCACG CTGAGCCACC ATCCTTCGCT GAGCAGTCTA CTGCTGCTGA     300
GGTTTTGGAG ACTGGTATCA AGGTTGTCGA CCTTCTCGCC CCATACGCCA     350
GAGGTGGTAA GATTGGTCTC TTTGGTGGTG CCGGTGTCGG TAAGACCGTT     400
TTCATCCAGG AGTTGATTAA CAACATTGCC AAGGCCCACG GTGGTTTCTC     450
TGTTTTCACC GGTGTCGGTG AGAGAACCAG AGAGGGTAAC GATTTGTACC     500
GTGAGATGAA GGAGACTGGT GTCATCAATC TCGAGGGTGA GTCCAAGGTT     550
GCTCTCGTCT TCGGTCAGAT GAACGAGCCA CCAGGTGCCC GTGCCCGTGT     600
CGCTTTGACC GGTTTGACCA TTGCTGAGTA CTTCAGAGAT GAGGAGGGTC     650
```

AGGATGTCTT GTTGTTTATT GACAACATTT TCAGATTCAC CCAGGCCGGT 700
TCCGAGGTGT CTGCCTTGCT TGGTCGTATT CCATCCGCTG TCGGTTACCA 750
GCCAACTTTG GCCACCGATA TGGGTTTGTT GCAGGAGAGA ATTACCACCA 800
CCCAGAAGGG TTCCGTCACT TCTGTCCAGG CCGTTTACGT CCCAGCTGAT 850
GATTTGACTG ATCCTGCTCC AGCCACCACT TTCGCCCACT TGGACGCCAC 900
CACTGTGTTG TCCCGTGGTA TCTCTGAGTT GGGTATTTAC CCAGCTGTCG 950
ACCCATTGGA CTCCAAGTCC AGATTGTTGG ACGCTGCCGT TGTTGGTGAC 1000
GAGCACTACA ACACCGCCAC CGATGTCCAG CAGACCCTTC AGGCTTACAA 1050
GTCTCTCCAG GATATCATTG CTATTTTGGG TATGGATGAG TTGTCTGAGG 1100
CTGACAAGTT GACTGTCGAG AGAGCCAGAA AGATTCAGCG TTTCCTTTCC 1150
CAGCCATTCG CTGTCGCTGA GGTTTTCACC GGTATCCCAG GTAGATTGGT 1200
TAGACTTCAG GACACCATCA AGTCCTTCAG AGAGGTTTTG GACGGTAAGT 1250
ACGACCACTT GCCAGAG 1267

2) INFORMATION FOR SEQ ID NO: 477

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1296 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida viswanathii*
(B) STRAIN: ATCC 28269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

CCAATTCGAC GAAGGTAGCT TGCCAGCTAT CTTGAACGCC TTGACCTTGA 50
AGAACGGTGA CCAAGACTTG GTCTTGGAAG TTGCCCAACA CTTGGGTGAA 100
AACACTGTCA GAGCTATTGC TATGGATGGT ACCGAAGGTT TGGTCAGAGG 150
TACTGCTGTC ACTGACACCG GTGCTCCAAT CTCCGTCCCA GTCGGTAGAG 200
GTACCTTGGG TAGAATCATC AACGTTGTTG GTGAACCAAT TGACGACAGA 250
GGTCCAATTG AATGTAAGGA AAGAAAGCCA ATTCACGCTG AACCACCTTC 300
TTTCGTTGAA CAATCCACTG CTGCCGAAAT TTTGGAAACC GGTATCAAGG 350
TTGTCGACTT GTTGGCCCCA TACGCCAGAG GTGGTAAGAT TGGTTTGTTC 400
GGTGGTGCCG GTGTCGGTAA GACTGTCTTT ATCCAAGAGT TGATTAACAA 450
CATTGCCAAG GCCCATGGTG GTTTCTCTGT CTTCACTGGT GTCGGTGAAA 500
GAACCAGAGA AGGTAACGAT TTGTACCGTG AAATGAAGGA AACCGGTGTC 550
ATCAACTTGG AAGGTGACTC CAAGGTCGCC TTGGTTTTCG GTCAAATGAA 600
CGAACCACCT GGTGCTAGAG CTAGAGTTGC TTTGACTGGT TTGACCATTG 650
CCGAATACTT CAGAGACGAA GAAGGTCAAG ATGTCTTGTT GTTTATTGAC 700
AACATTTTCA GATTCACCCA AGCCGGTTCC GAAGTGTCTG CTTTGTTGGG 750
TCGTATTCCA TCTGCCGTCG GTTATCAACC AACCTTGGCC ACCGATATGG 800
GTCTTTTGCA AGAACGTATT ACCACCACCA AGAAGGGTTC CGTCACCTCT 850
GTCCAAGCTG TCTATGTCCC AGCCGATGAT TTGACCGATC CTGCTCCAGC 900
CACCACCTTC GCTCACTTGG ATGCCACTAC TGTCTTGTCT AGAGGTATTT 950
CCGAATTGGG TATCTACCCA GCTGTCGATC CATTGGACTC CAAGTCCAGA 1000
TTGTTGGATG CTGCTGTTGT TGGTCAAGAA CATTACGATG TTGCCACTGG 1050
TGTCCAACAA ACCTTGCAAG CTTACAAGTC TTTGCAAGAT ATCATTGCCA 1100
TTTTGGGTAT GGATGAATTG TCTGAATCCG ATAAGTTGAC TGTCGAAAGA 1150
GCTCGTAAGA TCCAAAGATT CTTGTCGCAA CCATTTGCTG TTGCCGAAGT 1200
TTTCACTGGT ATCCCAGGTA GATTAGTTAG ATTGCTGGAA ACCGTCCAAT 1250
CTTTCAAAGA CGTCTTGGCT GGTAAATACG ATCACTTGCC AGAAAA 1296

2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1295 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida zeylanoides*
(B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

TCAATTCGAG CAAGGCAACC TCCCTGCCAT CTTGAACGCT CTCACCTTGA 50
AGAATGGTGA CAACGACTTG GTTTTGGAAG TTGCCCAGCA CTTGGGTGAG 100
AACACCGTCA GAGCCATTGC CATGGATGGT ACCGAGGGTT TGGTTAGAGG 150
TGCGTCCGTC AAGGACACTG GCGCCCCTAT CTCGGTCCCC GTTGGCCGCG 200
GGACTTTGGG TCGTATCATC AACGTCACCG GTGACCCCAT TGACGAGAGA 250
GGTCCCATCG AGCTGACCCA GAGAAACCCT ATCCACGCCG ACCCCCCCTC 300
GTTCGTTGAG CAGTCCACCA ACGCTGAGGT TTTGGAGACT GGTATCAAGG 350
TTGTCGATTT GTTGGCTCCC TACGCCAGAG GTGGTAAGAT TGGTTTGTTC 400
GGTGGTGCCG GTGTCGGTAA GACCGTCTTC ATTCAGGAGT TGATCAACAA 450
CATCGCCAAG GCCCACGGTG GGTTCTCGGT CTTCACTGGT GTCGGTGAGA 500
GAACTAGAGA GGGTAACGAC TTGTACCGTG AGATGAAGGA GACCGGTGTC 550
ATCAACTTGG AGGGTGACTC CAAGGTGGCC TTGGTGTTCG GTCAGATGAA 600
CGAGCCCCCT GGAGCCAGAG CCAGAGTCGC CTTGACCGGG TTGACCATTG 650
CCGAATACTT TAGAGACGAG GAGGGTCAGG ATGTGTTGTT GTTCGTCGAC 700
AACATCTTCA GATTCACCCA AGCTGGTTCG GAGGTGTCGG CCTTGTTGGG 750
TCGTATTCCC TCTGCCGTCG GTTACCAGCC CACCTTGGCA ACTGATATGG 800
GATTGTTGCA GGAGCGTATC ACCACGACCA AGAAGGGTTC CGTCACCTCA 850
GTGCAGGCCG TCTACGTCCC CGCTGATGAC TTGACTGACC CTGCTCCCGC 900
CACCACCTTT GCCCACTTGG ACGCCACCAC CGTGTTGTCC AGAGGTATCT 950
CTGAGTTGGG TATCTACCCC GCCGTCGACC CCTTGGACTC CAAATCGAGA 1000
TTGTTGGACG CTGCCGTGGT CGGTCAGGAG CACTACGATG TTGCCTCGAA 1050
CGTCCAGCAG ACCTTGCAGG CCTACAAGTC CTTGCAGGAT ATCATTGCCA 1100
TTTTGGGTAT GGATGAGTTG TCCGAGGCTG ACAAGTTGAC CGTTGAGAGA 1150
GCCAGAAAGA TCCAGAGATT CTTGTCGCAG CCCTTCGCTG TTGCCGAGGT 1200
TTTCACTGGT ATCAAGGGTA GATTGGTCAG ATTGGAGGAC ACCGTCAGAT 1250
CTTTCAAGGA GGTTTTGGAG GGTAAGTACG ACCACTTGCC CGAGA 1295

2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 534 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Coccidioides immitis*
(B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

```
TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG      50
CTGATATGCT CTAGAACAAC ATTGCTAAGG CTCACGGTGG TTACTCCGTG     100
TTCACTGGTG TCGGTGAGCG TACCCGTGAG GGTAACGATT TGTACCATGA     150
AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC     200
TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCGTGC CCGTGTTGCC     250
CTTACCGGTT TGACCATTGC TGAATACTTC CGTGACGAGG AAGGCCAAGA     300
CGGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA     350
TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTTCACTCAA     400
GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT CGTATTCCTT CCGCTGTCGG     450
TTACCAACCT ACTCTCGCCG TCGACATGGG TGTTATGCAG GAACGTATCA     500
CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA                      534
```

2) INFORMATION FOR SEQ ID NO: 480

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptococcus albidus*
(B) STRAIN: ATCC 66030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

```
CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG     100
TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA     150
CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC     200
GAGGGTGACT CCAAGGTCGC CTTGGTCTTC GGTCAGATGA ACGAGCCCCC     250
TGGAGCCCGA GCCCGAGTCG CCTTGACCGG TTTGACCATT GCCGAATACT     300
TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTCATTGA CAACATTTTC     350
CGATTCACCC AAGCCGGTTC CGAAGTGTCC GCCTTGTTGG GTCGTATCCC     400
CTCCGCCGTC GGTTACCAGC CCACTCTGTC CACCGACATG GGTACCATGC     450
AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC           494
```

2) INFORMATION FOR SEQ ID NO: 481

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

TTCAGGAGCT TATCAACAAC ATCGCCAAGG CCCACGGTGG TTACTCCGTC 50
TTCACTGGTG TCGGTGAGCG AACTCGTGAG GGTAACGATC TGTACCACGA 100
AATGCAGGAG ACTTCCGTCA TTCAGCTTGA TGGCGAGTCC AAGGTCGCCC 150
TGGTCTTCGG TCAGATGAAC GAGCCCCCTG GAGCTCGTGC CCGTGTCGCC 200
CTTACCGGTC TTACTGTAGC TGAATACTTC AGAGATGAGG AGGGTCAGGA 250
CGTGCTGCTC TTCATTGACA ACATTTTCCG ATTCACTCAG GCCGGTTCCG 300
AGGTGTCTGC CCTTCTCGGT CGTATCCCCT CTGCCGTCGG TTACCAGCCC 350
ACCCTCGCCG TCGACATGGG TGGTATGCAA GAGCGTATTA CCACCACCAC 400
CAAGGGTTCC ATTAC 415

2) INFORMATION FOR SEQ ID NO: 482

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1281 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Geotrichum* spp.
(B) STRAIN: Lev-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

AGGACAACCT CCCCGCTATT CTTAACGCTC TTGAGCTTAA GAGAGATAAC 50
GGTGAGAAGC TCGTTCTCGA GGTTGCCCAG CATCTGGGTG AGAACACTGT 100
CCGTACTATT GCTATGGACG GTACTGAGGG TCTCGTCCGT GGTCAGCCCG 150
TTGTTGACAC CGGTGCCCCC ATTACCATTC CCGTTGGTCG TGGTACTCTT 200
GGTAGAATTA TCAACGTCAT TGGTGAGCCC ATCGATGAGC GTGGACCCAT 250
TGAGGCTACC AAGTACCTCC CCATCCACAC CGAGCCCCCC ACCTTCGCTG 300
AGCAGTCTAC CTCCGCTGAG GTTCTTGAGA CTGGTATCAA GGTTGTCGAT 350
CTCCTTGCCC CCTACGCCCG TGGTGGTAAG ATTGGTCTCT TCGGTGGTGC 400
CGGTGTCGGT AAGACCGTTT TCATTCAGGA GCTGATTAAC AACATTGCCA 450
AGGCCCATGG TGGTTTCTCC GTTTTCACCG GTGTCGGTGA GAGAACCCGT 500
GAGGGTAACG ATTTGTACCG TGAGATGAAG GAGACCGGTG TCATCAACCT 550
CGAGGGTGAG TCTAAGGTCG CTCTCGTTTT CGGTCAGATG AACGAGCCCC 600
CTGGAGCCCG TGCCCGTGTT GCTCTTACTG GTCTTACCAT TGCTGAGTAC 650
TTCCGTGATG AGGAGGGTCA GGATGTGTTG CTCTTCGTTG ACAACATTTT 700
CCGTTTCACT CAGGCCGGTT CCGAGGTGTC TGCCCTTTTG GGTCGTATTC 750
CCTCCGCTGT CGGTTACCAG CCCACCCTTG CCACTGATAT GGGTGCCCTG 800
CAAGAGCGTA TTACCACCAC CCAGAAGGGT TCCGTCACTT CCGTCCAGGC 850
CGTCTACGTC CCTGCCGATG ATTTGACCGA TCCTGCCCCT GCTACCACCT 900
TCGCCCATTT GGATGCCACC ACCGTCTTGT CGCGTTCCAT TTCTGAGTTG 950
GGTATCTACC CCGCTGTCGA TCCCCTTGAT TCCAAGTCTC GTCTTTTGGA 1000
TATCACCGTC GTTGGCCAGG AGCACTACGA TGTTGCTACC CAGGTCCAGC 1050
AGACCCTCCA GTCCTACAAG TCTCTTCAGG ATATCATTGC CATTTTGGGT 1100
ATGGATGAGT TGTCTGAGGC TGATAAGCTT ACTGTCGAGC GTGCCCGTAA 1150
GATCCAGAGA TTCCTTTCCC AGCCCTTCAC TGTCGCTGAG GTTTTCACTG 1200
GTATCGAGGG CCGTCTCGTT CCTTTGAAGG ACACTGTTCG CTCTTTCAAG 1250
GAGATCCTTG AGGGCAAGTA CGACCACCTC C 1281

2) INFORMATION FOR SEQ ID NO: 483

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 586 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

ATTCAAGAAT TGATCGTACG TTCCTCCGCC CCACACACGA TCAATGGAGA 50
AAGAAACAAA TTTTTTGGGA GTGGTCATTT TTTCTAATAA TTCGAATAGA 100
ACAACATTGC CAAAGCCCAC GGTGGTTACT CCGTGTTCAC TGGTGTCGGC 150
GAGCGGACCC GTGAAGGAAA TGACTTGTAC CACGAAATGC AGGAAACCCG 200
TGTTATCCAG CTCGATGGAG AGTCCAAGGT CGCCCTCGTT TTCGGTCAGA 250
TGAACGAGCC TCCCGGAGCC CGTGCCCGTG TTGCCCTCAC TGGTCTGACC 300
GTTGCCGAGT ACTTCCGTGA CGAGGAAGGC CAAGACGGTA TGTATAAGTA 350
TACACCGTAG CAAATCAACA CAGAGCTTCA CTCACGCTCG GATTTAGTGC 400
TTCTCTTCAT CGACAACATT TTCCGCTTCA CTCAGGCCGG TTCCGAAGTG 450
TCTGCCCTGC TCGGCCGTAT TCCCTCCGCC GTCGGTTACC AACCCACCCT 500
CGCCGTGGAC ATGGGTGGTA TGCAGGAACG TATCACCACT ACCACCAAGG 550
GCTCCATCAC CTCTGTGCAR GCCGTCTACG TCCCCG 586

2) INFORMATION FOR SEQ ID NO: 484

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Malassezia furfur*
(B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

GCGTGGCCAG AAGGTCATTG ACACTGGTGC TCCCATCACC ATCCCCGTCG 50
GTGGTGCCAC ACTGGGTCGT ATTCTGAACG TCACGGGTGA CCCTATTGAC 100
GAGCGTGGCC CCGTTAAGAC TGACGTTTTC CGCCCCATTC ACCGTGACCC 150
CCCTGCCTTT GTCGAGCAGT CGACTGATGC CGAGATTCTC GAGACTGGTA 200
TCAAAGTCGT TGACCTGATT GCCCCTTACG CCCGTGGTGG TAAGATTGGT 250
CTGTTCGGTG GTGCCGGTGT CGGTAAGACC GTGCTTATCC AGGAGCTCAT 300
CAACAACATC GCCAAGGCCC ACGGTGGTTT CTCCGTGTTC ACTGGTGTCG 350
GTGAGCGTAC TCGTGAGGGT AACGATTTGT ACCACGAGAT GATTGAAACC 400
GGTGTCATTA ACCTCGAGGG TGACTCGAAG GTGGCTCTGG TGTTCGGTCA 450
GATGAACGAG CCCCCGGGTG CCCGTGCGCG TGTCGCTCTT ACTGGTCTGA 500
CTGTGGCCGA GTACTTCCGT GACGACGAGG GCCAGGATGT GCTGCTGTTC 550
ATTGACAACA TTTTCCGTTT CACCCAGGCC GGTTCGGAGA CTTCGGCTCT 600
GCTGGGTCGT ATCCCTTCGT CGGTCGGTTA CCAGCCCACT TTGTCGACCG 650
ATATGGGTGC CATGCAGGAG CGTATCACCA CCACCAAGAA GGGTTCGATT 700
ACGTCGGTGC AGGCCGTCTA CGTGCCCGCC GATGATGTCA CTGACCCTGC 750

CCCTGCCACT ACCTTCGCCC ACCTTGACGC TACCACTGTG CTTGACCGTT 800
CGATCGCTGA GCTGGGTATC TACCCCGCTG TTGACCCGTT GAACTCGAAC 850
TCGCGTATGC TTGACCCCGC TATTGTGGGT CAGGAGCACT ACGACGTGGC 900
CTCTGGCGTG CAGAAGCTGC TCCAGGACTA CAAGTCGCTT CAAGATATCA 950
TTGCCATTCT GGGTATGGAT GAGCTTTCTG AGGAGGACAA GCTCACTGTC 1000
GAGCGTGCCC GTAAGATGCA GCGTTTCATG TCGCAGCCTT TCGCTGTCGC 1050
CCAGGTCTTT ACTGGTATCG AAGGTCGTCT TGTTGCCCTG AAGGACACGA 1100
TCAAGGCCTG CAAGGAGATC CTGTCGGGCA AGCACGACAA CCTCC 1145

2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1261 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Malassezia pachydermatis*
(B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

TCCCGCCATC TTCAACGCCC TGGAGGTCCA GGACATGAAG AACGGTGGCC 50
GCCTTGTTCT GGAGGTTGCC CAGCACCTTG GTGAGAACAC TGTTCGTTGC 100
ATTGCTATGG ACGGTACCGA GGGTCTTGTC CGTGGTCAGA AGGTCCTTGA 150
CACTGGTGCC CCGATCACTA TCCCTGTCGG TAACGGTACC TTGGGCCGYA 200
TCCTGAACGT CACTGGTGAG CCTGTGGATG AGCGTGGTCC GGTTAAGACT 250
GACGTCTACC GTCCAATCCA CCGTGAGCCC CCGGCGTTCG TTGAGCAGTC 300
GACTGATGCT GAGATTCTTG AGACTGGTAT CAAGGTGGTC GACCTGCTCG 350
CCCCATACGC TCGTGGTGGT AAGATTGGTC TWTTCGGTGG TGCYGGTGTY 400
GGTAAGACCG TGCTGATTCA GGAGCTTATC AACAACATTG CCAAGGCCCA 450
CGGTGGTTTC TCGGTGTTCA CTGGTGTCGG TGAGCGTACT CGTGAGGGTA 500
ACGATCTGTA CCATGAAATG ATTGAGACTG GTGTCATCAA CGTTGACGGT 550
GACTCGAAGG TCGCTCTCGT GTTCGGTCAG ATGAACGAGC CCCCGGGTGC 600
CCGTGCCCGT GTCGCCCTGA CYGGTCTGAC CATCGCCGAG TACTTCCGTG 650
ACGACGAGGG TCAGGATGTG CTGCTCTTCA TTGACAACAT TTTCCGTTTC 700
ACTCAGGCTG GTTCGGAGAC TTCGGCTCTG CTGGGTCGTA TCCCGTCGGC 750
TGTCGGTTAC CAGCCKACCC TTGCCACGGA TATGGGTGCC ATGCAGGARC 800
GTATYACCAC CACCAAGAAG GGTTCGATTA CCTCGGTGCA GGCYGTTTAC 850
GTTCCGGCCG ACGATGTGAC TGACCCTGCC CCGGCCACGA CCTTCGCCCA 900
CTTGGACGCC ACCACGGTGT TGGACCGTTC GATTGCYGAG CTGGGTATCT 950
ACCCGGCCGT CGACCCGCTG AACTCGAAGT CGCGTATGCT TGACCCGTCA 1000
ATTGTCGGTG TGGAGCACTA CAACGTTGCT TCGGGTGTCC AGAAGCTTCT 1050
YCAGGACTAC AAGTCGCTCC AAGATATCAT TGCCATTCTG GGTATGGATG 1100
AGTTGTCGGA GGAGGACAAG CTCACTGTCG AGCGTGCCCG TAAGATGCAG 1150
CGTTTCCTGT CGCAGCCTTT CGCTGTGGCC CAGGTCTTCA CTGGTATCGA 1200
GGGTCGTCTT GTGTCGCTCA AGGACACCAT CAACGCCTGC AAGGAGATTC 1250
TGTCCGGTAA G 1261

2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1282 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Metschnikowia pulcherrima*
(B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486

AGGAGGGCAA CTTGCCAGCT ATCTTCAACG CTTTGACGTT GAAGAACGGC 50
GACCAGAAGT TGGTCTTGGA GGTGGCCCAG CACTTGGGTG AGAACACCGT 100
CAGAACCATT GCCATGGACG GTACCGAGGG TTTGGTCAGA GGCGCCTCTG 150
TCACCGACAC YGGTGCCCCT ATCTCCGTGC CTGTCGGCCG TGAGACCTTG 200
GGTCGTATTA TCAATGTTGT TGGTGAGCCA ATCGACGAGA GAGGCCCAAT 250
CAACACCAAG AAGAGAAACC CTATTCACAC CGACCCACCT TCGTTTGTCC 300
AGCAATCCAC TTCCGCCGAG GTCTTGGAGA CTGGTATCAA GGTTGTCGAC 350
TTGTTGGCCC CTTACGCCAG AGGTGGTAAG ATTGGTTTGT TCGGTGGTGC 400
CGGTGTCGGT AAGACCGTGT TCATCCAGGA GTTGATTAAC AACATTGCCA 450
AGGCCCACGG TGGTTTCTCC GTTTTCACCG GTGTCGGTGA GAGAACCAGA 500
GAGGGTAACG ATTTGTACCG TGAAATGCAG GAGACTGGTG TCATCAACTT 550
CGAGGGTGAC TCCAAGGTCG CCTTGGTTTT CGGTCAGATG AACGAGCCTC 600
CAGGAGCTAG AGCYAGAGTT GCCTTGACCG GTTTGACCAT CGCCGAGTAC 650
TTCAGAGACG AGGAGGGTCA GGATGTGTTG TTGTTCGTCG ACAACATTTT 700
CAGATTCACC CAAGCCGGTT CTGAGGTGTC TGCCTTGTTG GGTCGTATTC 750
CATCCGCTGT CGGATACCAG CCAACCTTGG CCACCGATAT GGGTGCCTTG 800
CAGGAGAGAA TTACCACCAC CAAGAAGGGT TCCGTCACCT CCGTCCAGGC 850
CGTCTACGTG CCAGCCGATG ACTTGACTGA CCCTGCGCCA GCCACCACTT 900
TCGCCCACTT GGACGCCACC ACTGTGTTGT CCAGAGGTAT CTCTGAGTTG 950
GGTATCTACC CCGCTGTCGA CCCCTTGGAC TCCAACTCCA GATTGTTGGA 1000
CGCCACCGTT GTTGGCCAGG AGCACTACGA CGTCGCCACC AACGTCCAGC 1050
AAACTTTACA AGCTTACAAG TCCTTGCAGG ATATCATTGC CATTTTGGGT 1100
ATGGATGAGT TGTCCGAGAC CCGACAAGTT GACCCGTCGA GAGAGCCAGA 1150
AAGATCCAGA AGTTCTTGTC CCAGCCATTT GCCGTCGCCG AGGTTTTCAC 1200
CGGTATTGAG GGTAGATTGG TTAGATTGGA GGACACCGTT AGATCCTTTA 1250
AGGAGGTTTT GGAAGGTAAG TACGACCACT TG 1282

2) INFORMATION FOR SEQ ID NO: 487

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487

TGTCTTTATC CAGGAGTTGA TTGTACGTCT TTACCTTTCT GCCTGACTGT 50
TTACGACAAC TAACGAAAGC GTAGAACAAC ATTGCCAAGG CTCACGGTGG 100
TTACTCTGTC TTCACTGGTG TCGGTGAACG TACTCGTGAG GGTAACGATT 150

TGTACCACGA AATGCAGGAA ACTGGTGTCA TTCAGCTCGA GGGTGAATCC 200
AAGGTCGCCC TCGTGTTCGG TCAGATGAAC GAGCCCCCCG GTGCCCGTGC 250
CCGTGTCGCT CTTACTGGTT TGACCATTGC CGAGTACTTC CGTGACGAGG 300
AAGGTCAGGA CGTGCTTCTC TTCATTGACA ACATTTTCCG TTTCACTCAG 350
GCCGGTTCTG AGGTGTCTGC CCTTCTGGGT CGTATCCCCT CTGCCGTCGG 400
TTACCAGCCC ACCCTTGCCG TCGACATGGG TATCATGCAG GAGCGTATTA 450
CCACCACCAC CAAGGGTTCC ATCACCTCCG TC 482

2) INFORMATION FOR SEQ ID NO: 488

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

TCGAACAAGG TAACTTACCA GCTATCTTGA ATGCTTTAGA AATCAAAACC 50
CCAAGTGGTA CTCCATTAGT TTTAGAAGTT GCTCAACATT TAGGTGAAAA 100
CACTGTCAGA ACTATTGCTA TGGATGGTAC TGAAGGTTTA GTTCGTGGTG 150
AACAAGTTAC TGATACTGGT TCTCCAATCA CTGTCCCAGT TGGTCGTGAA 200
ACTTTAGGTC GTATTATCAA CGTTGTTGGT GAACCAATTG ATGAACGTGG 250
TCCAATTAAC ACCAAACAAA GAAACCCAAT TCACGCTGAA CCACCTTCAT 300
TCAGTGAACA ATCAACTGCT GCTGAAGTTT TAGAAACTGG TATCAAAGTT 350
GTYGATTTAT TAGCTCCATA CGCTAGAGGT GGTAAAATTG GTTTATTCGG 400
TGGTGCCGGT GTCGGTAAAA CTGTCTTTAT CCAAGAATTG ATTAACAACA 450
TTGCTAAAGC TCATGGTGGT TTCTCAGTTT TCACCGGTGT TGGTGAAAGA 500
ACCAGAGAAG GTAACGATTT ATACCGTGAA ATGAAAGAAA CTGGTGTTAT 550
TAACTTGGAA GGTGATTCTA AGGTCGCTTT AGTTTTCGGT CAAATGAATG 600
AACCACCAGG TGCTAGAGCT CGTGTTGCTT TAACTGGTTT GACCATTGCT 650
GAATACTTCA GAGATGAAGA AGGTCAAGAT GTCTTGTTAT TCGTTGATAA 700
CATTTTCAGA TTCACCCAAG CCGGTTCAGA AGTTTCTGCC TTATTAGGTC 750
GTATTCCATC TGCTGTCGGT TATCAACCAA CTTTAGCAAC TGATATGGGT 800
TTGTTACAAG AACGTATTAC CACCACACAA AAAGGTTCAG TTACTTCTGT 850
CCAAGCTGTT TATGTCCCAG CTGATGATTT AACAGATCCT GCTCCAGCTA 900
CCACTTTCGC CCATTTGGAT GCTACTACTG TCTTGTCTCG TGGTATTTCA 950
GAATTAGGTA TTTACCCAGC TGTCGATCCA TTAGATTCTA AATCAAGATT 1000
ATTAGATGCT TCAGTTGTTG GTCAAGAACA TTATGATGTT GCTACCAACG 1050
TTCAACAAAC TTTACAAGCT TACAAATCTT TACAAGATAT TATTGCTATT 1100
TTAGGTATGG ATGAATTGTC TGAACAAGAT AAATTGACTG TCGAAAGAGC 1150
AAGAAAAATC CAAAGATTCT TATCTCAACC ATTTGCTGTT GCCGAAGTTT 1200
TCACTGGTAT YCCAGGTAGA TTGGTTAGAT TAAAAGACAC TATCAAATCA 1250
TTCAAAGATG TTTTGGAAGG TAAATATGAT CACTTACCAG 1290

2) INFORMATION FOR SEQ ID NO: 489

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1291 bases
(B) TYPE: Nucleic acid

300

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

```
CCAATTCGAA CAAGGTAACT TACCAGCTAT CTTGAATGCT TTAGAAATCA      50
AAACCCCAAG TGGTACTCCA TTAGTTTTAG AAGTTGCTCA ACATTTAGGT     100
GAAAACACTG TCAGAACTAT TGCTATGGAT GGTACTGAAG GTTTAGTCCG     150
TGGTGAACAA GTTACTGATA CTGGTTCTCC AATCACTGTC CCAGTTGGTC     200
GTGAAACTTT AGGTCGTATT ATCAACGTTG TTGGTGAACC AATTGATGAA     250
CGTGGTCCAA TTAACACCAA ACAAAGAAAC CCAATTCACG CTGAACCACC     300
TTCATTCAGT GAACAATCAA CTGCTGCTGA AGTTTTAGAA ACTGGAATCA     350
AAGTTGTTGA TTTATTAGCT CCATACGCTA GAGGTGGTAA AATTGGTTTA     400
TTCGGTGGTG CCGGTGTCGG TAAAACTGTC TTTATCCAAG AATTGATTAA     450
CAACATTGCT AAAGCTCATG GTGGTTTCTC AGTTTTCACC GGTGTTGGTG     500
AAAGAACCAG AGAAGGTAAC GATTTATACC GTGAAATGAA AGAAACTGGT     550
GTTATTAACT TGGAAGGTGA TTCTAAGGTC GCTTTAGTTT TCGGTCAAAT     600
GAATGAACCA CCAGGTGCTA GAGCTCGTGT TGCTTTAACT GGTTTGACCA     650
TTGCTGAATA CTTCAGAGAT GAAGAAGGTC AAGATGTCTT GTTATTCGTT     700
GATAACATTT TCAGATTCAC CCAAGCCGGT TCAGAAGTTT CTGCCTTATT     750
AGGTCGTATT CCATCTGCTG TCGGTTATCA ACCAACTTTA GCAACTGATA     800
TGGGTTTGTT ACAAGAACGT ATTACCACCA CACAAAAAGG TTCAGTTACT     850
TCTGTCCAAG CTGTTTATGT CCCAGCTGAT GATTTAACAG ATCCTGCTCC     900
AGCTACCACT TTCGCCCATT TGGATGCTAC TACTGTCTTG TCTCGTGGTA     950
TTTCAGAATT AGGTATTTAC CCAGCTGTCG ATCCATTAGA TTCTAAATCA    1000
AGATTATTAG ATGCTTCAGT TGTTGGTCAA GAACATTATG ATGTTGCTAC    1050
CAACGTTCAA CAAACTTTAC AAGCTTACAA ATCTTTACAA GATATTATTG    1100
CTATTTTAGG TATGGATGAA TTGTCTGAAC AAGATAAATT GACTGTCGAA    1150
AGAGCAAGAA AAATCCAAAG ATTCTTATCT CAACCATTTG CTGTTGCCGA    1200
AGTTTTCACT GGTATCCCAG GTAGATTGGT TAGATTAAAA GACACTATCA    1250
AATCATTCAA AGATGTTTTG GAAGGTAAAT ATGATCACTT A            1291
```

2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 508 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Rhodotorula minuta*
(B) STRAIN: ATCC 10658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

```
CGTATTGATT CGTGAGTGGC CGTTCCCTTA CAGCAAGCTT ATAAAGGAGC      50
GAAAAAGATC TGACATTCGG CTTATGTGCT ATACAGAGGA ACTCATCAAC     100
AACGTCGCCA AGGCTCATGG TGGTTACTCT GTCTTCACCG GTGTCGGAGA     150
GCGAACACGT GAAGGTAACG ATCTCTACCA CGAAATGATT GAAACCGGTG     200
```

TCATTCAGCT CAAGAACGAC AAGTCCAAGG CCGCTCTGGT CTTCGGACAG 250
ATGAACGAGC CCCCCGGAGC TCGTGCCCGT GTCGCTCTGA CCGGTCTCAC 300
CATCGCCGAG TACTTCCGTG ACGTCGAAGG ACAGGATGTG CTACTCTTCA 350
TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCAGAGGT ATCTGCCCTG 400
CTCGGACGTA TCCCATCTGC TGTCGGATAC CAGCCCACAC TCTCAACCGA 450
TATGGGTGGT ATGCAAGAGC GAATCACAAC CACCAAGAAG GGTTCGATTA 500
CCTCCGTC 508

2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 686 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Rhodotorula mucilaginosa*
(B) STRAIN: ATCC 66034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

TGTCCTCATT CAGGAGCTCA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
ACTCGGTCTT CACCGGTGTC GGCGAGCGTA CCCGTGAGGG TAACGGTGAG 100
TCTCCCCCTT CAAACTTTTG GCCGGCTAGT TGGCGCAGCG CAAACTGACG 150
CGCGCGCCCT GTCCAGACTT GTACCACGAG ATGATCGAGA CTGGTGTCAT 200
CCAGCTCGAG AACGACAACT CGAAGTGCGC TCTCGTGTTC GGCCAGATGA 250
ACGAGCCCCC TGGTGCCCGT GCCCGTGTCG CTCTCACTGG GTTCGTCCTT 300
TCTCTCTCTC GAGCGTCCTG GCTTGATACG GAACGCTGAC ACGTCACGCA 350
GTCTCACTAT TGCTGAGTAC TTCCGTGACG AGGAGGGCCA GGACGTGCTC 400
CTCTTCATCG ACAACATCTT CCGTTTCACC CAGGGTGAGC CGCCTCCGCG 450
GGCATTCTCC CGTTTCTTTC GCGCTGACGT CTGTCCCGTA TAGCCGGTTC 500
GGAGGTGTCT GCCCTTCTCG GACGTATCCC GTCCGCTGTC GGATACCAGC 550
CGACTCTCTC GACCGACATG GGTCAGATGC AGGAGCGTAT CACGTAAGTT 600
TGGCCGCAGC TCCGTCCGCG GCGCCCTTTG TGTCTGACCG TGTTCCACCG 650
CTCAGCACCA CCAAGAAGGG CTCGATCACC TGTGTC 686

2) INFORMATION FOR SEQ ID NO: 492

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 625 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Sporobolomyces salmonicolor*
(B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

TGTCTTGATT CAGGAGCTCA TCAACAACGT CGCCAAGGCG CACGGTGGTT 50

ACTCCGTTTT CACCGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGGTGAG 100
CACACTTTCG CCGACCTGGC CATTCCGGAA CGTGCGGACT GACGAGGACC 150
ACCTCGAACA GATCTCTACC ACGAGATGAT CGAGACCGGT GTCATTCAGC 200
TCGACAACGA CAAGTCGAAG ACTGCTCTCG TCTTCGGCCA GATGAACGAG 250
CCCCCTGGCG CCCGTGCCCG TGTCGCTCTT ACTGGTCTCA CCATCGCGGA 300
GTACTTCCGT GACGACGAGG GCCAGGACGT GCTTCTCTTC ATCGACAACA 350
TCTTCCGTTT CACCCAGGGT ACGTTCGATC CCGCCCGTCC AACACGAATG 400
TCGTGGTGAC TGACAACCTG TTGCGCGTGC AGCCGGTTCG GAGGTGTCTG 450
CCCTTCTCGG TCGTATCCCG TCCGCTGTCG GATACCAGCC CACTCTCTCG 500
ACCGACATGG GTGGCATGCA GGAGCGTATC ACGTACGCCC TCTTCTGCTT 550
TCTCTCGTTT CGCTCTGCAT CGCTCACGCA TGTTCGCCCG ACAGCACCAC 600
CAAGAAGGGT TCGATCACCT GTGTC 625

2) INFORMATION FOR SEQ ID NO: 493

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1211 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: WSA-148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

TCTCGTCCGT GGTGCTAAGG CCACTGACAC TGGTTCCCCC ATTACCATCC 50
CCGTCGGCCC CGGTACCCTC GGTCGCATCA TGAACGTCAC CGGTGACCCG 100
ATCGACGAGC GCGGTCCCAT CAAGACCGAC AAGTTCCGTC CCATCCACGC 150
TGAGGCTCCC GAGTTCGTTG ACCAGTCGAC CACCGCTGAG GTTCTCGTGA 200
CTGGTATCAA GGTCGTCGAT CTGCTTGCTC CCTACGCCCG TGGTGGTAAG 250
ATTGGTCTGT TTGGCGGTGC CGGTGTTGGC AAGACCGTGT TCATCCAGGA 300
GCTCATCAAC AACATCGCCA AGGCCCACGG TGGTTACTCC GTCTTCACCG 350
GTGTCGGCGA GCGTACCCGT GAGGGTAACG ATCTGTACCA CGAAATGCAG 400
GAGACCTCTG TCATTCAGCT TGACGGTGAC TCCAAGGTCG CCCTGGTGTT 450
CGGTCAGATG AACGAGCCCC CTGGTGCTCG TGCCCGTGTC GCCTTGACCG 500
GTTTGACTGT CGCTGAGTAC TTCCGTGACG AGGAGGGCCA GGATGGTATG 550
TTTTGAATTA TTTCCTTGTC GTACAGTTCC AAATCGAAGA ATTACTAACT 600
TGTCAGTGCT TCTCTTCATC GACAACATTT TCCGCTTCAC CCAGGCCGGT 650
TCTGAGGTGT CTGCCCTTCT GGGTCGTATT CCCTCCGCTG TCGGTTACCA 700
GCCCACGCTC GCCGTGGACA TGGGTCTGAT GCAGGAGCGT ATTACCACCA 750
CCCGCAAGGG CTCAATTACC TCCGTCCAGG CCGTCTACGT GCCCGCTGAC 800
GATCTGACGG ATCCCGCCCC CGCCACCACC TTCGCCCATC TGGACGCCAC 850
CACTGTGCTG TCCCGAGGTA TCTCTGAGCT GGGTATCTAC CCCGCTGTCG 900
ACCCCCTCGA CTCCAAGTCG CGTATGCTGG ACCCCCGTAT TGTCGGTGAC 950
GACCACTACG AGACCGCCAC TCGCGTCCAG CAGATCCTCC AAGAGTACAA 1000
GTCGCTGCAG GACATCATCG CCATTCTGGG TATGGACGAG CTGTCTGAGG 1050
CCGACAAGCT TACAGTCGAG CGTGCTCGTA AGATCCAGCG TTTCCTGAGC 1100
CAGCCGTTCA CGGTCGCGCA GGTCTTCACT GGTATCGAAG GCCAGCTGGT 1150
CGATCTGAAG GACACTATCG CTTCGTTCAA GGCTATCCTG AGCGGTGAGG 1200
GTGACAGCCT T 1211

2) INFORMATION FOR SEQ ID NO: 494

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1133 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stephanoascus ciferrii*
(B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

TCTTGTTAGA GGCACCCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC 50
CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA 100
ATTGATGAGC GTGGACCAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC 150
TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA 200
CCGGTATTAA GGTTGTCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG 250
ATTGGTCTTT TCGGTGGTGC CGGTGTCGGT AAGACTGTGT TCATTCAGGA 300
GCTTATTAAC AACATTGCTA AGGCCCACGG TGGTTACTCT GTCTTCACTG 350
GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG 400
GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTGTT 450
CGGTCAGATG AACGAGCCTC CAGGAGCCCG TGCCCGTGTT GCCTTGACCG 500
GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG 550
TTGTTCATTG ACAACATTTT CCGATTCACC CAGGCCGGTT CTGAGGTCTC 600
TGCCTTGTTG GGTCGTATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG 650
CTACTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAAGGGT 700
TCCGTCACCT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA 750
TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT 800
CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCGA CCCTCTTGGT 850
TCCAAGTCCC GTCTTTTGGA TGCCTCCGTC GTCGGCCAAG AGCACTACGA 900
CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCCTACAAG TCTCTCCAGG 950
ATATCATTGC CATTTTGGGT ATGGACGAAT TGTCTGAGGC TGATAAGCTC 1000
ACTGTCGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTCAC 1050
CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG 1100
ACACCATCCG ATCCTTCAAG GAGATCCTTG ACG 1133

2) INFORMATION FOR SEQ ID NO: 495

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 608 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trichophyton mentagrophytes*
(B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG 50
GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTCG 100

AGTATTAATT GTTTTTATAG AACAACATTG CCAAGGCTCA CGGTGGTTAC 150
TCTGTCTTCA CTGGTGTCGG AGAGCGTACC CGTGAAGGAA ACGATCTCTA 200
CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG 250
TCGCCCTGGT CTTCGGCCAG ATGAACGAGC CCCCAGGTGC CCGTGCCCGT 300
GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG 350
TCAAGACGGT GAGTTTCTTA TGGATAAAAA AAAATTTTTT TTTTTTTTTT 400
TTTTTTTCAA GAAATTCATG TTCTAACAAA GTGTATTCTA GTGCTTCTCT 450
TCATCGACAA CATTTTCCGT TTCACTCAGG CTGGTTCCGA AGTGTCTGCC 500
CTGCTTGGTC GTATCCCATC TGCCGTCGGT TACCAACCCA CTCTTGCCGT 550
CGACATGGGT GGTATGCAGG AACGTATTAC CACCACCAAG AAGGGATCCA 600
TTACCTCC 608

2) INFORMATION FOR SEQ ID NO: 496

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 794 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Wangiella dermatitidis*
(B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

GTTTATTCAA GAACTCATTG TGGGTGGCAT TCTCATAATG TTTCGGCCAC 50
AATTACTGAT TGAAAATAGA ACAACATTGC AAAGGCTCAT GGTGGTTACT 100
CCGTGTTCAC TGGTGTCGGC GAGCGAACTC GTGAGGGTAA CGACTTGTAC 150
CACGAAATGC AGGAGACCTC TGTCATTCAG CTCGATGGCG AGTCCAAGGT 200
CGCGCTGGTG TTTGGTCAAA TGAACGAACC TCCTGGTGCT CGTGCTCGTG 250
TTGCTCTGAC TGGGTAAGTT GTTCCTTCGC TTCTTGCGCG TATCCACATC 300
CCCATCTTGA GAATACGTCT GCCACCATGT CATGTGATGT TGGGCTGGTT 350
CTGGTTTTTG GGAGGCCCTC AAGTTCAATT TTTGGATGAC AGCACCAGCT 400
TTACAAGATT ATGCTAACTT AATGGAGTCT TACGGTGGCT GAGTTCTTCA 450
GGGATGAGGA GGGACAGGAT GGTAAGTTTG ATAACAATCT CGTCGGTGTC 500
AATATCGACG GCGTACTCTT CGCATCAAAA AACCAAAGAG GTGGTTTGGT 550
GTGAGAAGTG CGCCGGAAAT AATGGCAACC ACGTGACAAT GACCACGTGT 600
GGGGCTCCCG TGCTAACACG TGACAGTCTT GCTCTTCATC GACAACATTT 650
TCCGATTCAC TCAASCCGGT TCTGARGTGT CTGCCTTGCT TGGTCGTATT 700
CCATCTGCCG TCGGTTACCA ACCCACACTC GCCGTCGACA TGGGTCTCAT 750
GCAGGAACGT ATCACCACCA CCCGGAAGGG ATCCATCACA TCTG 794

2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1148 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

```
TCTTGTCCGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC      50
CCGTCGGCCG AGGTACCCTT GGTCGAATCA TCAACGTCTG TGGTGAGCCC     100
ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC     150
TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA     200
CCGGTATTAA GGTCGTCGAC CTCCTCGCCC CTTACGCCCG AGGTGGTAAG     250
ATTGGTCTCT TCGGTGGTGC CGGTGTCGGT AAGACTGTCT TCATCCAGGA     300
GCTGATTAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG     350
GTGTCGGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG     400
GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT     450
CGGTCAGATG AACGAGCCTC CCGGAGCCCG TGCCCGAGTC GCCCTTACTG     500
GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG     550
CTCTTCGTTG ACAACATTTT CCGATTCACC CAGGCCGGTT CCGAGGTGTC     600
CGCTCTGCTT GGTCGAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG     650
CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT     700
TCCGTCACTT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA     750
TCCTGCTCCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCCTGT     800
CCCGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCGA TCCCCTTGAT     850
TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAAGG AGCACTACGA     900
TGTTGCTTCC AACGTCCAGC AGACCCTCCA GGCTTACAAG TCTCTCCAGG     950
ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG    1000
ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCCTGTCTC AGCCCTTCAC    1050
CGTCGCCGAG GTTTTCACCG GTATTGAGGG ACGACTTGTC TCTCTCAAGG    1100
ACACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC      1148
```

2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 966 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

```
GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT      50
CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTCG CGAATAGGCC     100
CCAGACTCGT GAGCATTTGC TGCTCGCCCG CCAGGTTGGT GTCCAGAAGA     150
TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG     200
GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCGA     250
GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGCTCTCTGT GCTCTCGAAG     300
GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT     350
GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTTCTT     400
GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT     450
CTGGTCGTGT CGAGCGTGGT ATCTTGAAGA AGGACTCTGA GGTTGAGATT     500
GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC     550
CTTCAAGAAG AGCTGTGATG AATCGCGTGC TGGTGACAAC TCTGGTCTCC     600
TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCATTGCT     650
```

GTTCCCGGCA GCACCAAGGC TCACGACAAG TTCCTCGTCT CCATGTACGT 700
CCTGACCGAG GCGGAGGGTG GTCGTCGTAC TGGCTTCGGT GCCAACTACC 750
GTCCCCAAGT CTTCATCCGT ACTGCAGGTA AGTTCCCGCA CACCGTGTCC 800
AGATCTTCCG AGAGATTAGC GATATATGCT AATGATTCAT CAGACGAGGC 850
TGCTGACCTC AGCTTCCCTG ACGGCGACCA ATCTCGCAGA GTTATGCCTG 900
GTGACAACGT CGAGATGATC CTGAAGACCC ACCACCCTGT TGCTGCTGAG 950
GCTGGTCAAC GCTTCA 966

2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Blastoschizomyces capitatus*
(B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

TGGTGCTATT ATTGTTGTTG CTGCTTCTGA TGGTCAAATG CCCCAAACCC 50
GTGAGCACTT GCTTCTTGCT CGTCAAGTTG GTGTTAAGCA CATTGTTGTT 100
TTCGTTAACA AGATTGATAC TATTGATGAT CCTGAAATGT TGGAACTTGT 150
CGAAATGGAA ATGAGAGAAC TTCTTTCTTC TTACGGTTTT GATGGCGATA 200
ACACCCCTGT CATTATGGGT TCTGCTCTCT GTGCTCTTGA AGGTCGTGAA 250
CCAGAAATTG GTGAACAAAG AATCAACCAA CTCCTTGATG CTATCGATGA 300
ATACATTCCT ACCCCAGTTC GTGATATGGA CCAACCTTTC TTGATGCCAC 350
TTGAAGGTGT TTTCTCTATT CCAGGTCGTG GTACTGTTGC CACTGGACGT 400
GTCTATCGTG GTACTTTGAA GAGAGGTGAA GAAGTTGAAG TTGTTGGCTA 450
CAATGATGCT CCAATCAAGA CCACCGTTAC TGGTATTGAA ATGTTCAAGA 500
AGGAACTTGA TCAAGCTCAA GCTGGTGACA ACGCTGGTAT TCTTTTGAGA 550
GGTGTTAAGC GTGAAGACCT TAAGCGTGGT ATGGTTGTTG CTAAACCAGG 600
TACCGTTAAG CCACACACCA AGTTCCTTGC CTCCATCTAT GTTTTGACTA 650
AGGAAGAAGG TGGCAGACAC TCTGGCTTTG GTCTTAACTA CAGACCTCAA 700
CTTTTCCTTG GTTCTGCTGA TGTTACCACT GTCTTGACCT TCCCAGAGGG 750
TGTTGACCAA AGCACTCAAG TCATGCCAGG TGACAACACT GAAATGGTTT 800
GCGAACTTGT TCACCCAGTT GCTGTCGAAC AAGGCCAACG TTTCAA 846

2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida rugosa*
(B) STRAIN: ATCC 96275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

```
GGTGCCATTA TTGTTGTTGC TGCCTCTGAT GGACAGATGC CCCAGACCCG      50
TGAGCATCTT TTGCTTGCCC GCCAAGTCGG TATGCAAAAG GTCGTTGTGT     100
TTGTTAACAA GATTGATACC ATTGATGACC CTGAAATGCT TGATCTTGTC     150
GAGATGGAGA TGCGTGAACT GTTGAATGAA TATGACTTCG ATGGAGATAA     200
CTCTCCTGTC ATTATGGGCT CTGCTCTTGC TGCTCTTGAG GACAAGAACC     250
CCGAGATTGG TAAGGACCGT ATCATGCAGC TCTTGGACGC TGTTGATGAA     300
TGGATCCCTA CCCCCGAGCG TGACCTTGAC AAGCCTTTCA TGATGCCTAT     350
TGAGGCCTCT TTCTCCATTT CTGGTCGTGG TACTGTTGCC ACTGGCCGTG     400
TCGAGCGTGG TATTCTCAAG AAGGGTGAGG AAGTCGAGAT CGTTGGTTTC     450
AACAAGCAGC CCCTGAAATC TGTTGTTACT GGTATTGAAA TGTTCAAGAA     500
GGAACTTGAT CAGGCCCAGG GCGGTGATAA TGCTGGTATC TTGCTTCGTG     550
GTATTCGTCG TGAGGACTTG CAGCGTGGTA TGGTTTTGGC CAAGCCTGGA     600
ACTGTTAAGG CTCACACCAA GTTCCTTTCC TCCATCTACG TTCTCTCCAA     650
GGAAGAGGGC GGCCGTCACT CTCCTTTCGG TATGAACTAT CGTCCCCAGA     700
TGTTCGTTTC TGCAGCTGAT GTCACCGTTA CTCTTACTTT CCCTGAGGGT     750
GTTGAACAGC ACACTCAGGT CTTCCCTGGT GAGAACACCG AGATGGTTGG     800
CGAGCTCGTT CACCCTACTG CTATTGAGGT TGGTCAACGC TTCAAC         846
```

2) INFORMATION FOR SEQ ID NO: 501

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 944 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Coccidioides immitis*
- (B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

```
AGTTGTCGTC GTTGCTGCTT CAGACGGTCA AATGTATGCA ACCGAGAGCA      50
CTCCCGGATC TTGGTTTAAA TGGCACTAAT ATAAGACAGG CCTCAAACTC     100
GAGAGCATTT ACTTCTCGCC CGTCAGATCG GTATCCAAAA AATCGTCGTC     150
TTCGTGAACA AGGTTGATGC CATCGAGGAC AAAGAGATGT TGGAGCTTGT     200
TGAATTGGAG ATGCGTGAAC TCCTAACCAG CTACGGTTTC GAGGGTGAAG     250
AAACTCCCAT CATTTTTGGC TCTGCTCTCT GTGCCCTCGA AGGAAGACAA     300
CCCGAGATCG GTGTTACCAA GATTGATGAG CTCTTGCAGG CCGTCGACAC     350
CTGGATTCCC ACTCCTCAGC GTGAGACTGA CAAGCCCTTC TTGATGTCCA     400
TTGAGGAAGT GTTCTCTATT TCCGGACGAG GAACCGTTGT CTCCGGCCGT     450
GTGGAGCGTG GTATCCTCAA GAAGGACTCC GAAGTTGAAA TTGTCGGCGG     500
TTCGCCCGAG CCAATCAAAA CCAAGGTTAC CGATATCGAA ACCTTTAAGA     550
AGTCTTGCGA CGAGTCTCGC GCTGGTGATA ACTCCGGCTT GCTCCTACGA     600
GGCGTTAAGC GTGAAGATAT TAGCCGTGGC ATGGTCGTCG CTGTACCAGG     650
AAGTGTCAAG GCCCATACTG AATTCTTAGT TTCGCTTTAC GTCCTCACCG     700
AAGCTGAGGG TGGGCGCAAA TCTGGATTCA GCAGCAAGTA CCGCCCACAG     750
ATGTTCATTC GCACTGCCGG TATGTAATAC TGTGATAATT TCGTTGACAT     800
GGTACTGATT GAATTCTATA GACGAAGCGG CTCAGCTCAG CTGGCCCGGA     850
GAAGATCAAG ACAAGATGGC TATGCCAGGA GACAATATCG AAATGATTTG     900
CACCACCTTG CACCCAGTTG CCGCCGAGGC TGGCCAGCGA TTCA           944
```

2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 849 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

GCTATCATCG TCGTTGCTGC CTCCGATGGA CAGATGCCCC AGACCCGTGA 50
ACACTTGCTC CTCGCTCGTC AGGTCGGTGT CCAGCGAATT GTCGTCTTCG 100
TCAACAAGGT CGATGCCATT GATGACCCCG AGATGCTTGA GCTCGTCGAG 150
ATGGAGATGC GCGAGCTTCT TAACACCTAC GGCTTCGAAG GCGACGACAC 200
TCCCGTCATC ATGGGCTCTG CTCTTATGTC TCTCCAGAAC CAGCGCCCCG 250
AGATTGGCAC CGAGAAGATC GATGAGCTCC TTGCTGCCGT CGACGAGTGG 300
ATCCCAACCC CCGAGCGTGA CCTTGACAAG CCCTTCCTTA TGTCCGTCGA 350
GGATGTCTTC TCCATTGCCG GCCGTGGTAC CGTCGTGTCT GGCCGTGTGG 400
AGCGTGGTAT TCTGAAGCGT GATCAGGAGA TCGAGCTTGT CGGAAAGGGG 450
CAGGAGGTTA TCAAGACCAA GGTTACCGAC ATTGAGACCT TCAAGAAGTC 500
TTGTGAGCAG TCCCAGGCTG GTGACAACTC TGGTCTCCTC ATCCGAGGTG 550
TTCGCCGTGA GGATGTCCGC CGTGGTATGG TTGTCTGCGC TCCTGGCACC 600
GTCAAGTCTC ATACCCAGTT TCTCGCTTCC CTCTACGTCC TCACCAAGGA 650
GGAGGGTGGC CGACACACCG GTTTCCAGGA GCACTACCGA CCCCAGCTCT 700
ATCTCCGAAC TGCAGATGAG TCCATTGACC TGACTTTCCC CGAGGGTACT 750
GAGGATGCCT CCAGTAAGAT GGTCATGCCT GGTGACAACA CCGAGATGGT 800
TGTCACCATG GGTCACCCCA ATGCCATCGA GGTTGGTCAG CGATTCAAC 849

2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1064 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

TGGTGCTATT GTCGTTGTTG CTGCTGCTGA CGGCCAAATG TAAGACGCCG 50
CGAGGGACTG CTGAGGGTTT TATGCTTTTT AGGCCCCCTT GTTTCTGAGA 100
GCATGATGAT ACTAATATTC GGAAACGTAT CTATTAGGCC TCAAACACGT 150
GAGCATTTGC TCCTTGCCCG ACAGGTCGGT GTCCAAAAGA TCGTCGTTTT 200
CGTGAACAAA GTCGACGCCC TTGAGGACAA GGAGATGTTG GAGCTTGTCG 250
AGTTAGAAAT GAGAGAGCTC TTAAACACCT ACGGCTTCGA GGGTGAAGAG 300
ACACCCATCA TCTTTGGTTC TGCCCTTTGC GCCATGGAAG GCCGTGAGCC 350
TGAGTTGGGA GAAAAGAAAA TTGATGAATT GCTGGAGGCT GTTGATACTT 400

```
GGATCCCCAC ACCACAACGT GATACCGAAA AACCTTTCTT GATGTCCGTT      450
GAGGAAGTAT TCTCTATCTC CGGCCGTGGA ACCGTTGCCT CCGGTCGTGT      500
TGAGCGCGGT GTCCTCAAGA AGGATTCAGA AGTCGAGCTA ATTGGGGGCG      550
GCTCCACCCC CATCAGGACG AAGGTAACTG ATATCGAAAC TTTCAAGAAA      600
TCCTGTGACG AGTCTAGAGC TGGGGACAAC TCCGGTCTTT TATTGCGTGG      650
TATCAAGCGT GAAGATATCC GCCGTGGTAT GGTAGTTGCC GTTCCTGGCA      700
GCGTCAAGGC CCACGACAAG TTCTTGGTGT CGATGTATGT CCTGACCGAA      750
GCTGAGGGTG GTCGCCGAAC CGGATTCGGC CAGAACTATC GTCCTCAAAT      800
GTTCATCCGC ACAGCTGGTA TGTCAAAATG GGACCCCTTT TCATAATCCT      850
TTCTTTTTTT CCTTTTCCTC TCTATCTCTC TTTCTGTTTC CTTTCAACTC      900
GCCTGATTCA CGAAATTAAC TAACCCGTTT GATTATAGAC GAAGCCGCCC      950
ATCTCAGCTT CCCTAGTGGA GCAGATGAAA GCAAACTCGT TATGCCTGGT     1000
GACAACGTCG AGATGATCCT CCAGACACAC CGCCCCGTGG CTGCTGAGGC     1050
CGGCCAGCGA TTCA                                           1064
```

2) INFORMATION FOR SEQ ID NO: 504

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Paracoccidioides brasiliensis*
- (B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

```
TGGTGCTATC GTCGTTGTTG CTGCCTCTGA CGGCCAAATG TAGGGATTTT       50
GCAAGACTGG TGAAAAAATC TAAAGAAAAT AGAAAAGATT GTGCTGATGT      100
TTGGTATCAG GCCCCAAACA CGCGAGCATC TGCTTCTTGC CAGACAAGTC      150
GGTGTTCAGA AAATCGTTGT TTTCGTCAAC AAGGTCGATG CTGTAGAGGA      200
TAAGGAGATG TTGGAGCTTG TCGAATTGGA GATGAGAGAG CTCTTGACCA      250
CCTATGGGTT CGAGGGTGAG AAGACACCTA TCATCTTTGG TTCTGCGCTC      300
TGTGCTATGG AGGGCCGTCA GCCCGAGTTG GGAGAGCAGA AAATTGATGA      350
ATTACTCGAG GCTGTGGATA CTTGGATCCC TACGCCACAG CGTGATACTG      400
ACAAGCCCTT CCTGATGTCC ATTGAGGAGG TGTTCTCTAT CTCTGGACGA      450
GGAACCGTTG CCTCCGGCCG CGTTGAGCGT GGTATCCTCA AGAAGGACTC      500
CGAAGTTGAA ATTATTGGCG GCGGTGTTCC CACAATCCTG ACCAAGGTGA      550
CTGATATCGA AACCTTCAAG AAGTCTTGCG ACGAGTCCAG AGCCGGGGAC      600
AACTCCGGCC TCTTGTTGCG CGGTGTCAAG CGTGAGGATA TCCGCCGTGG      650
TATGGTCGTT GCAGTTCCCG GAAGCGTCAA AGCACATGAC AGATTCTTGG      700
TGTCGATGTA CGTTCTGACC GAGGCTGAGG GTGGTCGCCG CACTGGCTTC      750
GGTCAGAACT ATCGTCCTCA AATGTTCATC CGCACAGCTG GTACGTTCAT      800
TCTTTCACTA TATTCCTATA TGCATAGCCC GATCCTCCCA TTAACTAATT      850
GACACAGACG AGGCTGCTGA ACTCAGCTGG CCTGATGGAG ACGACGAAGC      900
CAAAATGGTC ATGCCCGGTG ACAATGTTGA AATGGTCCTG AAGTCACACC      950
GCCCGGGGCC GCTGAGGCTG GACAGCGATT CA                        982
```

2) INFORMATION FOR SEQ ID NO: 505

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 931 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

```
CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG      50
AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG     100
CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT     150
CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT     200
TGGAAATGCG TGAACTCTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC     250
CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA     300
GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA     350
TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG     400
GAAGTTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA     450
GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA     500
AGAACCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT     550
TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT     600
CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA     650
CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT     700
GAAGGTGGTC GTCGTACTGG ATTCGGCGCC AACTACCGTC CTCAAGCTTT     750
CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT     800
GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT     850
CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC     900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G                         931
```

2) INFORMATION FOR SEQ ID NO: 506

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

```
TGGTGCTATT ATTGTTGTTG CTGCTTCTGA TGGTCAAATG CCTCAAACCA      50
GAGAACATTT RTTATTGGCT AGACAAGTTG GTGTTCAACA CATTGTTGTC     100
TTTGTTAACA AAGTTGATAC TATTGATGAC CCAGAAATGT TGGAATTAGT     150
TGAAATGGAA ATGAGAGAAT TGTTAAGTAC TTATGGTTTT GATGGTGATA     200
ACGTCCCAGT TGTTATGGGT TCTGCTTTAT GTGCCTTGGA AGGTCGTGAA     250
GAAGAAATTG GTGTCAAAGC TATTGATAAA TTATTAGCTG CTGTTGATGA     300
ATATATCCCA ACCCCACAAA GAGATTTAGA AAAACCATTC TTGATGGGTG     350
TTGAAGATGT CTTYTCAATC TCAGGTAGAG GTACCGTTGT TACTGGTCGT     400
GTTGAACGTG GTAACTTGAA GAAAGGTGAT GAAGTTGAAA TTGTTGGTTT     450
AAACAAAACT CCATTGAAAA CTACTGTYAC NGGTATTGAA ATGTTCAAAA     500
```

AAGAATTGGA CCAAGCTATG GCTGGTGATA ACTGTGGTAT CTTATTACGT 550
GGTATCAAAA GAGATGACAT YAAAAGAGGT ATGGTTATTG CTAAAACCGG 600
TACCATCTCW GCTCACACTA AATTCTTAGC CTCAATGTAT ATTTTGACTA 650
AAGAAGAAGG TGGTCGTCAC TCAGGTTTTG GTGAACATTA CAGACCTCAA 700
TTATTCATCA GAACTGGTGA TGTTACCGTT GTTTTAACCT TYCCAGAAGG 750
TGGTGATTCA TCTCAACAAA TCTTACCAGG TGACAATGTC GAAATGGTTT 800
GTGAATTGGT TCACCCAACT GCTTTAGAAG CTGGTCAAAG ATTCAA 846

2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 964 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trichophyton mentagrophytes*
(B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

GGAGCTGTTG TCGTTGTCGC AGCTTCTGAC GGTCAAATGT AATTGAATGC 50
CCGCCCAGAC GGATGAAAGG ATTTGACGTT TCTAACATCA GTCTAGGCCT 100
CAGACCAGAG AACATTTGCT CCTTGCCCGC CAGGTCGGTG TCCAGAAGCT 150
GGTCGTTTTC GTTAACAAGG TCGATGCCGT TGAGGACCCA GAGATGTTGG 200
AGCTTGTCGA ACTTGAAATG CGTGAACTCC TCAGCCACTA CAGTTTTGAG 250
GGTGAGGAGA CCCCCATCAT TTTTGGCTCT GCTCTCTGTG CCCTCGAGTC 300
CCGTCGACCT GAGCTTGGTG TCGAGAAGAT TGACGAGCTA TTGAACGCCG 350
TCGACACCTG GATCCCCACC CCCGAGCGCG CCACTGATAA GCCTTTCCTC 400
ATGTCCATTG AGGAAGTGTT CTCTATCTCT GGTCGTGGTA CCGTCGTCTC 450
CGGTCGTGTT GAGCGTGGTA TCCTCAAGAA GGATTCCGAC GTCGAAATTG 500
TTGGTGGCTC TACCACCCCT ATCAAGACCA AGGTCACAGA TATCGAAACC 550
TTCAAGAAGT CCTGCGATGA ATCTCGAGCT GGTGACAACT CTGGTCTCCT 600
TCTCCGAGGT ATCAAGCGTG AGGACTTGAA GCGTGGAATG GTTGTTGCTG 650
CCCCCGGATC CACCAAGGCT CACACCGACT TCATGGTCTC CCTCTACGTC 700
CTGACTGAGG CTGAGGGTGG TCGTTCCAAC GGCTTCACCC ACAAGTACCG 750
CCCTCAAATG TTCATCCGTA CTGCTGGTAT GTAACCAAAG TTTCCGCTAT 800
TTACTAAGTA GATCATTGCT AACTTGTATT CCCTTCCGTA GACGAAGCCG 850
CATCTTTCAG CTGGCCTGGA GAAGACCAAG ACAAGAAGGC TATGCCTGGT 900
GACAACGTCG AGATGATTTG CAAAACCCTC CACCCCATTG CTGCCGAGGC 950
TGGCCAACGA TTCA 964

2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 844 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

```
GGTGCTATCA TTGTCGTTGC TGCTGGAGAC GGTTCCAAGC CCCAGACCCG      50
AGAGCATCTG CTGCTTGCTC GACAGGTCGG TGTCCAGAAC CTGGTTGTGT     100
TTGTTAACAA GGTTGATCAG ATTGATGATA AGGAGATTCT TGAGCTCGTT     150
GACATGGAGA TGCGAGATCT GCTGACCCAG TACGGTTTTG ATGGTGACAA     200
CACCCCCGTT GTCATGGGCT CTGCTCTGTG CGCTCTTGAG GGCAAGCAGA     250
AGGATATTGG AGAGGACGCC ATCATGGCCC TTATGGATGC CGTTGATGAG     300
CACATCCCTA CCCCTAACCG TGACCTTGAG AAGCCCTTCC TGATGCCCGT     350
TGAGGACGTT TTCTCCATCT CTGGCCGAGG AACTGTTGTT ACTGGCCGAG     400
TCGAGCGAGG AAACCTGAAG AAGGGTGAGG AAATCGAGAT TGTTGGCTAC     450
AACAACAAGC CCATCAAGGC TGTTGTTACC GGTATTGAGA TGTTCAAGAA     500
GGAGCTCGAG TCCGCCATGG CCGGTGACAA CGCCGGTATC CTGCTCCGAG     550
GTATCAAGCG AGACGAGATC AAGCGAGGTA TGGTCATGTG CAAGCCTGGC     600
ACCGTCAACG CCCACACCAA GTTCCTTGCT TCTCTTTACA TCATCCCCAC     650
CGAGGAGGGT GGTCGAACCA GCTCTTTCGG CGCCAACTAC CGACCCCAGA     700
TGTTCATCCG AACTTCTTCC GTCACCGCCA CTCTCACCTT CCCCGAGGGT     750
ACCGACGAGT CCCAGACCGT CAACCCCGGT GACAACACTG AGATGGTTCT     800
CGAGCTTGTT CACCCTACCG CCATTGAGGT CAACCAGCGA TTCA           844
```

2) INFORMATION FOR SEQ ID NO: 509

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1067 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Babesia bigemina*
(B) STRAIN: Suarez-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

```
CTTGGACAAG CTGAAGAGCG AGCGTGAGCG TGGTATCACC ATTGACATTA      50
CCCTGTGGAA GTTCGAAACT GGCAAGTACT ACTACACCGT CATTGACGCC     100
CCCGGTCACC GTGACTTCAT TAAGAACATG ATTACGGGTA CCTCCCAGGC     150
CGATGTTGCT ATGCTTGTCG TGCCCGCCGA GGCTGGTGGT TTCGAAGCTG     200
CCTTCTCTAA GGAAGGTCAG ACCCGTGAGC ACGCTCTTTT GGCCTTCACC     250
CTTGGTGTCA AGCAGATCAT TTGCGCCATC AACAAGATGG ACAAGTGCGA     300
CTACAAGGAG GACCGTTACA GCGAAATCCA GAAGGAAGTT CAGGGTTACC     350
TGAAGAAGGT CGGTTACAAC ATCGAGAAGG TGCCTTTCGT CGCCATCTCC     400
GGTTTCATGG GTGACAACAT GGTTGAGCGC TCCACCAACA TGCCGTGGTA     450
CAAGGGCAAG ACCTTGGTCG AGGCCCTCGA CATGATGGAG CCCCCGAAGA     500
GGCCCGTCGA CAAGCCCCTG CGTCTTCCCC TCCAGGGTGT GTACAAGATC     550
GGTGGTATCG GTACCGTCCC TGTCGGTCGT GTGGAGACTG GTCAGCTCAA     600
GGCCGGTATG GTCCTCACCT TCGCCCCCAA CCCGATCACT ACTGAGTGCA     650
AATCCGTCGA AATGCACCAC GAAGTTATCG ATGTTGCCAG CCCTGGTGAC     700
AACGTTGGTT TCAACGTGAA GAACGTGTCC ACCTCTGACA TCCGCACTGG     750
TCACGTCGCT TCTGACTCCA AGAACGACCC CGCCAAGGCC GCCGTGTCCT     800
TCACCGCCCA GGTCATCATC TTGAACCACC CTGGTACCAT CAAGGCCGGT     850
TACTCCCCTG TGGTTGACTG CCACACTGCC CACATCTCGT GCAAATTCGA     900
CGAGATCACC AGCCGTATGG ACAAGCGTAC CGGTAAGGCC CTTGAGGAGA     950
```

ACCCCAAGAC CATCAAGAAC GGCGACGCCG CTATGGTCGT CCTGAAGCCG 1000
TGCAAGCCCA TGGTCGTCGA GGCCTTCACT GAATACGCTC CCCTTGGTCG 1050
TTTCGCCGTG CGTGACG 1067

2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Babesia bovis*
(B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA ACGTGGTATT ACTATTGATA TTACCTTATG GAAGTTCGAG 50
ACCACCAAGT ACTACTACAC CGTCATTGAT GCCCCTGGTC ACCGTGACTT 100
CATCAAGAAC ATGATTACGG GTACTTCTCA AGCCGATGTT GCTATGCTTG 150
TTGTACCAGC TGAGGCTGGT GGTTTCGAGG CCGCTTTCTC CAAGGAAGGA 200
CAGACCCGTG AGCACGCTCT TTTGGCTTTC ACCCTTGGTG TCAAACAGAT 250
CATCTGTGCC ATTAACAAGA TGGACAAGTG CGACTACAAG GAGGACCGTT 300
ACAGTGAAAT CCAGAAGGAA GTCCAGGGTT ACCTCAAGAA GGTCGGTTAC 350
AATATTGAGA AGGTGCCCTT CGTTGCCATC TCCGGTTTCA TGGGAGACAA 400
CATGGTTGAG CGTTCCACCA ACATGCCCTG GTATAAGGGA AAGACATTGG 450
TCGAGGCCCT TGATCAGATG GAACCCCCAA AGAGGCCCGT TGACAAGCCA 500
CTTCGTCTTC CCCTCCAGGG TGTCTACAAG ATCGGTGGTA TCGGTACCGT 550
CCCCGTCGGT CGTGTTGAAA CTGGTATGTT GAAGGCTGGT ATGATTCTAA 600
CCTTTGCTCC TAACCCAATC ACCACTGAAT GCAAATCCGT TGAAATGCAC 650
CACGAAACCG TTGAGGTTGC TTACCCCGGT GACAACGTCG GTTTCAACGT 700
AAAGAACGTT TCTACTTCTG ACATTCGCAG TGGTCACGTT GCCTCTGATT 750
CTAAGAACGA CCCTGCCAAG GCTGCTGTTT CCTTCACTGC CCAGGTCATT 800
GTGCTCAACC ACCCTGGTAC CATTAAGGCC GGTTACTGCC CCGTCGTCGA 850
TTGCCACACC GCTCACATTT CATGTAAATT CGAAGAGATC ACCAGCCGTA 900
TGGACAAGCG TACCGGTAAA TCTCTTGAGG AAAACCCCAA GACCATCAAG 950
AACGGTGACG CTGCCATGGT TGTGCTCAAG CCAATGAAGC CCATGGTTGT 1000
CGAATCCTTC ACTGAGTATG CTCCTCTTGG TCGTTTCGCT GTTCGTGAC 1049

2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1070 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Crithidia fasciculata*
(B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

```
TGGACAAGCT GAAGGCGGAG CGCGAGCGCG GTATCACGAT CGATATTGCC      50
CTGTGGAAGT TCGAGTCGCC CAAGTCCGTG TTCACGATCA TCGATGCCCC     100
CGGCCACCGC GACTTCATCA AGAACATGAT CACCGGCACC TCCCAGGCCG     150
ATGCCGCCAT TCTGATGATT GACTCGACCC AGGGTGGCTT CGAGGCTGGC     200
ATCTCCAAGG ACGGCCAGAC CCGCGAGCAC GCCCTGCTTG CCTTCACGCT     250
GGGCGTGAAG CAGATGGTTG TGTGCTGCAA CAAGATGGAC GACAAGACGG     300
TGCAGTACGC CCAGGCCCGC TACGAGGAGA TCAGCAAGGA GGTCGGCGCG     350
TACCTGAAGC GCGTGGGCTA CAACCCGGAG AAGGTGCGCT TCATCCCGAT     400
CTCGGGCTGG CAGGGCGACA ACATGATCGA GAAGTCCGAC AACATGTCGT     450
GGTACAAGGG TCCCACGCTG CTGGAGGCGC TCGACCTGCT GGAGGCCCCC     500
GTGCGTCCGG TGGACAAGCC GCTGCGCCTG CCCCTGCAGG ACGTGTACAA     550
GATCGGCGGT ATCGGCACTG TGCCCGTGGG CCGTGTGGAG ACCGGCGTGA     600
TGAAGCCGGG CGACGTTGTG GTGTTCGCGC CTGCCAACGT GACGACCGAG     650
GTGAAGTCGA TCGAGATGCA CCACGAGCAG CTGGCTGAGG CCGTGCCCGG     700
CGACAACGTG GGCTTCAACG TGAAGAACGT GTCCGTGAAG GATATCCGCC     750
GTGGTAACGT GTGCGGCAAC ACGAAGAGCG ACCCCCCGAA GGAGGCGGCC     800
GACTTCACTG CCCAGGTGAT CGTGCTGAAC CACCCCGGCC AGATCAGCAA     850
CGGCTACGCG CCGGTGCTGG ACTGCCACAC GAGCCACATC GCGTGCAAGT     900
TCGCGGACAT CGAGTCCAAG ATCGACCGCC GCTCTGGCAA GGAGCTGGAG     950
AAGAGCCCGA AGGCCATCAA GTCCGGCGAT GCGGCCATCG TGAAGATGAT    1000
CCCGCAGAAG CCGATGTGCG TGGAGGTGTT CAACGACTAC CCGCCGCTGG    1050
GCCGCTTCGC TGTCCGCGAT                                    1070
```

2) INFORMATION FOR SEQ ID NO: 512

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Entamoeba histolytica*
- (B) STRAIN: HM1-IMMS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

```
GCTGAAAGAG AAAGAGGAAT TACTATTGAT ATTTCATTAT GGAAATTCGA      50
AACATCTAAA TACTACTTCA CTATTATTGA TGCCCCAGGT CAYAGAGATT     100
TCATTAAGAA CATGATTACT GGAACTTCAC AAGCTGATGT TGCCATCCTT     150
ATTGTTGCTG CTGGTACTGG WGAATTTGAA GCTGGTATTT CAAAGAATGG     200
ACAAACCAGA GAACAYATTC TTCTTTCATA CACTCTTGGA GTTAAACAAA     250
TGATTGTTGG WGTTAACAAG ATGGATGCTA TTCAATATAA ACAAGAAAGA     300
TATGAAGAAA TTAAGAAAGA AATTAGTGCA TTCCTTAAGA AGACWGGATA     350
TAATCCAGAC AAGATTCCAT TTGTCCCAAT TTCAGGATTC CAAGGAGATA     400
ATATGATTGA ACCATCAACC AACATGCCAT GGTACAAAGG ACCAACATTA     450
ATTGGAGCAC TTGATTCAGT CACACCACCA GAAAGACCAG TTGATAAACC     500
ACTTAGACTT CCACTTCAAG ATGTTTAYAA GATTTCAGGT ATTGGAACTG     550
TACCATGTGG AAGAGTTGAA ACTGGAGTTC TTAGACCAGG AACTATTGTT     600
CAATTTGCAC CATCAGGAGT TTCATCTGAA TGTAAATCAG TTGAAATGCA     650
TCACACAGCA CTTGCTCAAG CTATTCCAGG TGATAATGTT GGATTCAATG     700
TTAGAAAYTT AACAGTTAAA GATATTAAGA GAGGAAATGT AGCATCAGAT     750
GCTAAGAATC AACCAGCTGT TGGATGTGAA GATTTCACTG CTCAAGTCAT     800
TGTCATGAAC CATCCAGGAC AAATTAGAAA GGGATATACA CCAGTTCTTG     850
```

```
ATTGCCATAC ATCACACATT GCATGTAAAT TCGAAGAATT ATTAAGCAAG      900
ATTGATAGAA GAACAGGTAA ATCCATGGAA GGAGGAGAAC CAGAATATAT      950
TAAGAATGGA GATTCAGCAC TTGTTAAGAT TGTTCCAACT AAACCACTTT     1000
GTGTTGAAGA ATTTGCTAAA TTCCCACCAT TGGGAAGATT TGCTGTTAGA     1050
GA                                                        1052
```

2) INFORMATION FOR SEQ ID NO: 513

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1082 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Giardia lamblia*
(B) STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

```
GACGAGCGCG AGCGCGGGAT CACGATCAAC ATCGCGCTCT GGAAGTTCGA       50
GACGAAGAAG TACATCGTCA CGATCATCGA CGCCCCGGGC CACCGCGACT      100
TCATCAAGAA CATGATCACG GGGACGTCCC AGGCCGACGT CGCGATCCTC      150
GTCGTCGCGG CGGGCCAGGG CGAGTTCGAG GCCGGGATCT CGAAGGACGG      200
CCAGACGCGC GAGCACGCGA CCCTTGCGAA CACGCTCGGG ATCAAGACGA      250
TGATCATCTG CGTCAACAAG ATGGACGACG GCCAGGTCAA GTACTCGAAG      300
GAGCGCTACG ACGAGATCAA GGGCGAGATG ATGAAGCAGC TCAAGAACAT      350
CGGCTGGAAG AAGGCCGAGG AGTTCGACTA CATCCCGACG TCCGGCTGGA      400
CCGGGGACAA CATCATGGAG AAGTCCGACA AGATGCCCTG GTACGAGGGC      450
CCGTGCCTGA TCGACGCGAT CGACGGGCTC AAGGCCCCGA AGCGCCCGAC      500
CGACAAGCCC CTCCGCCTCC CGATCCAGGA CGTCTACAAG ATCTCGGGCG      550
TCGGGACCGT CCCCGCGGGC CGCGTCGAGA CGGGCGAGCT CGCGCCCGGG      600
ATGAAGGTCG TCTTCGCCCC GACGTCCCAG GTCTCGGAGG TCAAGTCCGT      650
CGAGATGCAC CACGAGGAGC TCAAGAAGGC CGGGCCCGGG GACAACGTCG      700
GCTTCAACGT CCGCGGGCTC GCCGTCAAGG ACCTCAAGAA GGGCTACGTC      750
GTCGGGGACG TGACGAACGA CCCGCCCGTC GGCTGCAAGA GCTTCACCGC      800
CCAGGTCATC GTCATGAACC ACCCGAAGAA GATCCAGCCC GGCTACACGC      850
CCGTCATCGA CTGCCACACC GCGCACATCG CGTGCCAGTT CCAGCTCTTC      900
CTCCAGAAGC TCGACAAGCG CACGCTCAAG CCCGAGATGG AGAACCCGCC      950
CGACGCAGGC CGCGGCGATT GCATCATCGT CAAGATGGTC CCCCAGAAGC     1000
CCCTGTGCTG CGAGACGTTC AACGACTACG CGCCCCTCGG CCGCTTCGCC     1050
GTCCGCGACA TGCGCCAAAC CGTTGCCGTC GG                        1082
```

2) INFORMATION FOR SEQ ID NO: 514

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
(B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

```
ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG CGGCATCACG      50
ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCCG TGTTCACGAT     100
CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG ATCACGGGCA     150
CGTCGCAGGC GGACGCCGCC ATCCTGATGA TCGACTCGAC GCATGGTGGC     200
TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACCCGCGAGC ACGCGCTGCT     250
TGCCTTCACT CTTGGCGTGA AGCAGATGGT GGTGTGCTGC AACAAGATGG     300
ACGACAAGAC GGTGACGTAC GCGCAGTCGC GCTACGATGA GATCAGCAAG     350
GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG AGAAGGTGCG     400
CTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC GAGAAGTCGG     450
ACAACATGCC GTGGTACAAG GGTCCCACGC TGCTGGACGC GCTCGACATG     500
CTGGAGCCGC CGGTGCGCCC GGTGGACAAG CCGCTGCGCC TGCCCCTGCA     550
GGACGTGTAC AAGATCGGCG GTATCGGGAC GGTGCCCGTG GGGCGCGTGG     600
AGACCGGCAT CATGAAGCCG GGCGACGTGG TGACGTTCGC GCCCGCCAAC     650
GTGACGACTG AGGTGAAGTC GATCGAGATG CACCACGAGC AGCTGGCGGA     700
GGCGCAGCCC GGCGACAACG TCGGCTTCAA CGTGAAGAAC GTGTCGGTGA     750
AGGACATCCG CCGTGGTAAC GTGTGCGGCA ACTCGAAGAA CGACCCGCCG     800
AAGGAGGCGG CCGACTTCAC GGCGCAGGTG ATCGTGCTGA ACCACCCCGG     850
CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC ACGAGCCACA     900
TTGCGTGCCG CTTCGCGGAA ATCGAGTCCA AGATCGACCG CCGCTCCGGC     950
AAGGAGCTGG AGAAGAACCC CAAGGCGATC AAGTCTGGCG ATGCCGCGAT    1000
CGTGAAGATG GTGCCGCAGA AGCCGATGTG CGTGGAGGTG TTCAACGACT    1050
ACGCGCCGCT GGGCCGCTTT GCCGTGCGCG ACATGCGCCA AACCGTTG      1098
```

2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1104 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania aethiopica*
(B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

```
TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA     100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC     150
ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG     200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC     250
TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG     300
GACGACAAGA CGGTGACGTA CGCGCAGTCG CGCTACGAGG AGATCAGCAA     350
GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC     400
GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG     450
GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT     500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC     550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCGT GGGCCGCGTG     600
GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA     650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG     700
```

```
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
CGTC                                                      1104
```

2) INFORMATION FOR SEQ ID NO: 516

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1106 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

```
TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC       50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA      100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
TTGCCTTCAC KCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
GACGACAAGA CGGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG      450
GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC      550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCGT GGGGCGCGTG      600
GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA      650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
CGTCGG                                                    1106
```

2) INFORMATION FOR SEQ ID NO: 517

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1099 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania donovani*
(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

```
TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA     100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC     150
ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG     200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC     250
TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG     300
GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA     350
GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC     400
GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTCG     450
GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT     500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC     550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG     600
GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA     650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG     700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG     750
AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC     800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG     850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC     900
ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG     950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA    1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC    1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG     1099
```

2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania infantum*
(B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

```
TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA     100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC     150
ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG     200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC     250
TTGCCTTCAC GCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG     300
GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA     350
GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC     400
GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTCG     450
```

GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 50
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG 600
GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA 650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG 750
AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTT 1098

2) INFORMATION FOR SEQ ID NO: 519

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1071 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

CTCGACAAGC TGAAGGCGGA GCGCGAGCGC GGCATCACGA TCGACATTGC 50
GCTGTGGAAG TTCGAGTCGC CCAAGTCTGT GTTCACGATC ATCGATGCGC 100
CCGGCCACCG CGACTTCATC AAGAACATGA TCACCGGCAC GTCGCAGGCC 150
GACGCCGCCA TCCTGATGAT CGACTCGACC CAGGGCGGCT TCGAGGCTGG 200
CATCTCGAAG GACGGCCAGA CCCGCGAGCA CGCGCTGCTC GCCTTCACGC 250
TTGGTGTGAA GCAGATGGTG GTGTGCTGCA ACAAGATGGA CGACAAGACG 300
GTGCAGTACT CGCAGGCGCG CTACGAGGAG ATCAGCAAGG AGGTGGGCGC 350
GTACCTGAAG CGCGTCGGCT ACAACCCGGA GAAGGTGCGC TTCATCCCGA 400
TCTCGGGCTG GCAGGGCGAC AACATGATCG ACAAGTCGGA CAGCATGCCG 450
TGGTACAAGG GGCCCACGCT GCTGGACGCG CTCGACATGC TGGAGGCGCC 500
GGTGCGCCCG GTGGACAAGC CGCTGCGCCT GCCCCTGCAG GACGTGTACA 550
AGATCGGCGG TATCGGGACG GTGCCCGTGG GCCGCGTGGA GACCGGCATC 600
ATGAAGCCTG GCGACGTGGT GACGTTTGCG CCCGCCAACG TGACGACGGA 650
GGTGAAGTCG ATCGAGATGC ACCACGAGCA GCTGGCGGAG GCGGTGCCCG 700
GCGACAACGT CGGCTTCAAC GTGAAGAACG TGTCGGTGAA GGACATCCGC 750
CGTGGTAACG TGTGCGGCAA CTCGAAGAAC GACCCGCCGA AGGAGGCGGC 800
CGACTTCACG GCGCAGGTGA TCGTGCTGAA CCACCCTGGC CAGATCAGCA 850
ACGGCTACGC GCCGGTGCTG GACTGCCACA CGAGCCACAT CGCGTGCCGC 900
TTCGCGGATA TCGAGTCCAA GATCGACCGC CGCTCTGGCA AGGAGCTGGA 950
GAAGAACCCC AAGGCGATCA AGTCCGGCGA TGCGGCCATC GTGAAGATGG 1000
TGCCGCAGAA GCCGATGTGC GTGGAGGTGT TCAACGACTA CCCGCCGCTG 1050
GGGCGCTTCG CTGTGCGCGA C 1071

2) INFORMATION FOR SEQ ID NO: 520

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1071 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania gerbilli*
(B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

```
CTCGACAAGC TGAAGGCGGA GCGCGAGCGC GGCATCACGA TCGACATTGC        50
GCTGTGGAAG TTCGAGTCGC CCAAGTCCGT GTTCACGATC ATCGATGCGC       100
CCGGCCACCG CGACTTCATC AAGAACATGA TCACGGGCAC GTCGCAGGCG       150
GACGCCGCCA TCCTGATGAT CGACTCGACG CATGGTGGCT TCGAGGCTGG       200
CATCTCGAAG GACGGCCAGA CCCGCGAGCA CGCGCTGCTT GCCTTCACTC       250
TTGGCGTGAA GCAGATGGTG GTGTGCTGCA ACAAGATGGA CGACAAGACG       300
GTGACGTACG CGCAGTCGCG CTACGATGAG ATCAGCAAGG AGGTGGGCGC       350
GTACCTGAAG CGCGTGGGCT ACAACCCGGA GAAGGTGCGC TTCATCCCGA       400
TCTCGGGCTG GCAGGGCGAC AACATGATCG AGAAGTCGGA CAACATGCCG       450
TGGTACAAGG GTCCCACGCT GCTGGACGCG CTCGACATGC TGGAGCCGCC       500
GGTGCGCCCG GTGGACAAGC CGCTGCGCCT GCCCCTGCAG GACGTGTACA       550
AGATCGGCGG TATCGGGACG GTGCCCGTGG GCCGCGTGGA GACCGGCATC       600
ATGAAGCCGG GCGACGTGGT GACGTTCGCG CCCGCCAACG TGACGACTGA       650
GGTGAAGTCG ATCGAGATGC ACCACGAGCA GCTGGCGGAG GCGCAGCCCG       700
GCGACAACGT CGGCTTCAAC GTGAAGAACG TGTCGGTGAA GGACATCCGC       750
CGTGGTAACG TGTGCGGCAA CTCGAAGAAC GACCCGCCGA AGGAGGCGGC       800
CGACTTCACG GCGCAGGTGA TCGTGCTGAA CCACCCCGGC CAGATCAGCA       850
ACGGCTATGC GCCGGTGCTG GACTGCCACA CGAGCCACAT TGCGTGCCGC       900
TTCGCGGAAA TCGAGTCCAA GATCGACCGC CGCTCCGGCA AGGAGCTGGA       950
GAAGAACCCC AAGGCGATCA AGTCTGGCGA TGCCGCGATC GTGAAGATGG      1000
TGCCGCAGAA GCCGATGTGC GTGGAGGTGT TCAACGACTA CGCGCCGCTG      1050
GGCCGCTTTG CCGTGCGCGA C                                     1071
```

2) INFORMATION FOR SEQ ID NO: 521

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1114 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania hertigi*
(B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

```
TCGTTCAAGT ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG        50
CGGTATCACG ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCGG       100
TGTTCACGAT CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG       150
ATCACCGGCA CGTCGCAGGC GGATGCTGCC ATTCTGATGA TCGATTCGAC       200
GCAGGGTGGC TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACGCGCGAGC       250
ACGCGCTGCT GGCCTTCACG CTGGGCGTGA AGCAGATGGT TGTGTGCTGC       300
```

```
AACAAGATGG ACGACAAGAC GGTGCAGTAC GCGCAGGCGC GCTACGAGGA      350
GATCAGCAAG GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG      400
AGAAGGTGCG CTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC      450
GAGAAGTCCG ACAACATGTC GTGGTACAAG GGTCCCACGC TGCTGGAGGC      500
GCTGGACATG CTGGAGGCGC CGGTGCGCCC GGTGGACAAG CCGCTGCGCC      550
TGCCCCTGCA GGACGTGTAC AAGATCGGCG GCATTGGCAC GGTGCCGGTG      600
GGCCGTGTGG AGACCGGCAT CATGAAGCCC GGCGACGTGG TGACGTTCGC      650
GCCCGCCAAC GTGACGACGG AGGTGAAGTC GATCGAGATG CACCACGAGC      700
AGCTGCAGGA GGCTGTGCCC GGCGACAACG TCGGCTTCAA CGTGAAGAAC      750
GTGTCGGTGA AGGACATCCG CCGTGGTAAC GTGTGTGGCA ACTCGAAGAA      800
CGACCCGCCG AAGGAGGCGG CTGACTTCAC GGCGCAGGTG ATCGTGCTGA      850
ACCACCCCGG CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC      900
ACCAGCCACA TCGCGTGCCG CTTCGCGGAC ATCGAGTCGA AGATCGACCG      950
CCGCTCCGGC AAGGAGCTGG AGAAGAACCC CAAGTCCATC AAGTCCGGCG     1000
ACGCCGCCAT CGTGAAGATG GTGCCGCAGA AGCCGATGTG CGTGGAGGTG     1050
TTCAACGACT ACCCGCCGCT GGGCCGCTTT GCGGTGCGCG ACATGCGCCA     1100
AACCGTTGCC GTCG                                           1114
```

2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1106 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania major*
- (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

```
TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC       50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTCACGA      100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
ACGTCGCAGG CGGACGCCGC CATTCTGATG ATCGACTCGA CGCATGGCGG      200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
GACGACAAGA CGGTGACGTA CGCGCAGTCR CGCTACGATG AGATCAGCAA      350
GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG      450
GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC      550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCGT GGGCCGCGTG      600
GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA      650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAT GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
CGTCGG                                                    1106
```

2) INFORMATION FOR SEQ ID NO: 523

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1105 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania amazonensis*
(B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCGAAGTCC GTGTTCACGA 100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
ACGTCGCAGG CGGACGCGGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
GACGACAAGA CGGTGATGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
GGAGGTGAGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
GCTTCATCCC GATCTCGGGG TGGCAGGGCG ACAACATGAT CGACAAGTCG 450
GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCGT GGGCCGCGTG 600
GAGACCGGGA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA 650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG 750
AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
ATCGCGTGCC GCTTCGCGGA GATCGAGTCC AAGATCGACC GCCGCTCCGG 950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GACGCCGCGA 1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
CGTCG 1105

2) INFORMATION FOR SEQ ID NO: 524

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania mexicana*
(B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCGAAGTCC GTGTTCACGA 100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
ACGTCGCAGG CGGACGCGGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
GACGACAAGA CGGTGATGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
GGAGGTGAGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
GCTTCATCCC GATCTCGGGG TGGCAGGGCG ACAACATGAT CGACAAGTCG 450
GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCGT GGGCCGCGTG 600
GAGACCGGGA TCATGAAGCC GGGCGACGTG GTGACGTTCG CGCCCGCCAA 650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG 750
AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
ATCGCGTGCC GCTTCGCGGA GATCGAGTCC AAGATCGACC GCCGCTCCGG 950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GACGCCGCGA 1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTT 1098

2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1081 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania tarentolae*
(B) STRAIN: II WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

GCTGAAGGCG GAGCGCGAGC GCGGCATCAC GATCGACATT GCGCTGTGGA 50
AGTTCGAGTC GCCCAAGTCG GTGTTCACGA TCATCGATGC GCCCGGCCAC 100
CGCGACTTCA TCAAGAACAT GATCACGGGC ACGTCGCAGG CGGACGCGGC 150
CATCCTGATG ATCGACTCGA CGCACGGTGG GTTCGAGGCT GGCATCTCGA 200
AGGACGGGCA GACGCGCGAG CACGCGCTGC TTGCCTTCAC TCTTGGCGTG 250
AAGCAGATGG TTGTGTGCTG CAACAAGATG GACGACAAGA CGGTGATGTA 300
CGCGCAGTCG CGCTACGATG AGATCAGCAA GGAGGTGGGC GCGTACCTGA 350
AGCGCGTGGG CTACAACCCG GAGAAGGTGC GCTTCATCCC GATCTCGGGC 400
TGGCAGGGCG ACAACATGAT CGAGAAGTCG GACAACATGC CGTGGTACAA 450
GGGTCCCACG CTGCTGGACG CGCTCGACAT GCTGGAGGCG CCGGTGCGCC 500
CGGTGGACAA GCCGCTGCGC CTGCCCCTGC AGGACGTGTA CAAGATCGGC 550
GGCATCGGCA CGGTGCCCGT GGGCCGCGTG GAGACCGGCA TCATGAAGCC 600
GGGCGACGTG GTGACGTTCG CGCCCGCGAA CGTGACGACG GAGGTGAAGT 650
CGATCGAGAT GCACCACGAG CAGCTGGCGG AGGCGCAGCC CGGCGACAAC 700
GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG AAGGACATCC GCCGTGGGAA 750
CGTGTGCGGT AACTCGAAGA ACGACCCGCC GAAGGAGGCC GCCGACTTCA 800
CGGCGCAGGT GATCGTGCTG AACCACCCCG GCCAGATCAG CAACGGCTAC 850
GCGCCGGTGC TGGACTGCCA CACGAGCCAC ATCGCGTGCC GGTTCGCGGA 900
CATCGAGTCC AAGATTGACC GCCGCTCCGG CAAGGAGCTG GAGAAGAACC 950

```
CCAAGGCGAT CAAGTCCGGC GATGCCGCGA TCGTGAAGAT GGTGCCGCAG     1000
AAGCCGATGT GCGTGGAGAT GTTCAACGAC TACGCGCCGC TTGGCCGCTT     1050
TGCTGTGCGC GACATGCGCC AAACCGTTGC C                         1081
```

2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1102 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 50129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

```
AAATACGCGT GGGTGCTCGA CAAGCTGAAG GCGGAGCGCG AGCGCGGCAT       50
CACGATCGAC ATTGCGCTGT GGAAGTTCGA GTCGCCCAAG TCCGTGTTCA      100
CGATCATCGA TGCGCCCGGC CACCGCGACT TCATCAAGAA CATGATCACG      150
GGCACGTCGC AGGCGGACGC CGCCATCCTG ATGATCGACT CGACGCATGG      200
TGGCTTCGAG GCTGGCATCT CGAAGGACGG CCAGACCCGC GAGCACGCGC      250
TGCTTGCCTT CACKCTTGGC GTGAAGCAGA TGGTGGTGTG CTGCAACAAG      300
ATGGACGACA AGACGGTGAC GTACGCGCAG TCGCGCTACG ATGAGATCAG      350
CAAGGAGGTG GGCGCGTACC TGAAGCGCGT GGGCTACAAC CCGGAGAAGG      400
TGCGCTTCAT CCCGATCTCG GGCTGGCAGG GCGACAACAT GATCGAGAAG      450
TCGGACAACA TGCCGTGGTA CAAGGGTCCC ACGCTGCTGG ACGCGCTCGA      500
CATGCTGGAG CCGCCGGTGC GCCCGGTGGA CAAGCCGCTG CGCCTGCCCC      550
TGCAGGACGT GTACAAGATC GGCGGTATCG GGACGGTGCC CGTGGGGCGC      600
GTGGAGACCG GCATCATGAA GCCGGGCGAC GTGGTGACGT TCGCGCCCGC      650
CAACGTGACG ACTGAGGTGA AGTCGATCGA GATGCACCAC GAGCAGCTGG      700
CGGAGGCGCA GCCCGGCGAC AACGTCGGCT TCAACGTGAA GAACGTGTCG      750
GTGAAGGACA TCCGCCGTGG TAACGTGTGC GGCAACTCGA AGAACGACCC      800
GCCGAAGGAG GCGGCCGACT TCACGGCGCA GGTGATCGTG CTGAACCACC      850
CCGGCCAGAT CAGCAACGGC TACGCGCCGG TGCTGGACTG CCACACGAGC      900
CACATTGCGT GCCGCTTCGC GGAAATCGAG TCCAAGATCG ACCGCCGCTC      950
CGGCAAGGAG CTGGAGAAGA ACCCCAAGGC GATCAAGTCT GGCGATGCCG     1000
CGATCGTGAA GATGGTGCCG CAGAAGCCGA TGTGCGTGGA GGTGTTCAAC     1050
GACTACGCGC CGCTGGGCCG CTTTGCCGTG CGCGACATGC GCCAAACCGT     1100
TG                                                        1102
```

2) INFORMATION FOR SEQ ID NO: 527

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1105 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Neospora caninum*

(B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

```
GGACRAACTT AAAGCTGAAC GTGAGCGTGG TATCACCATT GATATCTCCC      50
TGTGGAAATT TGAGACCAGC AAGTACTATG TTACCATCAT TGATGCCCCA     100
GGACACAGAG ACTTCATCAA AAACATGATT ACAGGCACAT CCCAGGCTGA     150
CTGTGCTGTC CTGATTGTTG CTGCTGGTGT TGGTGAATTT GAAGCCGGTA     200
TCTCCAAGAA CGGGCAGACC CGTGAGCATG CCCTTNTGGC TTACACCCTG     250
GGTGTGAAAC AACTAATTGT TGGCGTTAAC AAAAKGGATT CCACTGAGCC     300
ACCCTATAGC CARAAGAGAT ACGARGAAAT TGTTAAGGAA GTCAGCMCCT     350
AYNTTAAAAA AATTGGYTAC AACCCCGACA CAGTANCATT TGKGCCAATT     400
TNTGGCTGGA ATGGTGACAA CATGCTGGAN CCAAGTGCTA ATATGCCATG     450
GTTCAAGGGA TGGAAAGTCM CCCGTAAGGA CGGCAATGCC AGKGGAACCM     500
CCCTGCTTGA AGCTYTGGAT TGCATTYTGC CACCAAYTTG CCCAACTGAC     550
AAACCCTTGC GTTTGCCTYT CCAGGATGTC TATAAAATTG GKGGTATTGG     600
TACTGTCCCT GTGGGTCGTG TGGAGACTGG TGTTCTCAAA CCTGGCATGG     650
TGGTCACCTT TGCTCCAGTC AATGTAACAA CTGAAGTGAA GTCTGTAGAA     700
ATGCACCATG AAGCATTGAG TGAAGCCCTT CCTGGGGACA ATGTGGGCTT     750
CAATGTCAAG AACGTGTCTG TCAAAGATGT CCGTCGTGGC AATGTGGCTG     800
GTGACAGCAA AAATGATCCA CCCATGGAAG CTGCTGGCTT CACAGCTCAG     850
GTGATTATTT TGAACCATCC AGGCCAAATC AGTGCTGGAT ATGCACCTGT     900
GCTGGATTGT CACACAGCTC ACATTGCTTG CAAGTTTGCT GAGCTGAAGG     950
AGAAGATTGA TCGTCGTTCT GGGAAAAAGC TGGAAGATGG CCCTAAATTC    1000
TTGAAATCTG GTGACGCTGC CATCGTTGAT ATGGTTCCTG GCAAGCCCAT    1050
GTGTGTCGAG AGCTTCTCTG ATTATCCTCC CCTGGGCCGT TTTGCTGTGC    1100
GTGAC                                                    1105
```

2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 935 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trichomonas vaginalis*
(B) STRAIN: ATCC 30001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

```
GCACATCCCA GGCTGATGCT GCTATCCTTG TCATCGACTC CACACTCGGT      50
GGYTTCGAAG CCGGTATCGC TGAACAAGGC CAGACACGTG AACACGCTCT     100
TCTTGCCTTC ACACTCGGCA TCAAGCAGGT CATTGTCGCC GTCAACAAGA     150
TGGATGACAA GACAGTCAAC TACAACAAGG CYCGTTTCGA CGAAATCACA     200
GCCGAAATGA CACGCATCCT TACAGGCATC GGCTACAAGC CAGAAATGTT     250
CCGCTTCGTC CCAATCTCCG GCTGGGCTGG CGACAACATG ACAGAGAAGT     300
CTCCAAACAT GCCATGGTAC AATGGCCCAT ACCTTCTTGA AGCCCTCGAT     350
TCCCTTCAGC CACCAAAGCG CCCATTCGAC AAGCCACTCC GTCTTCCACT     400
CCAGGATGTC TACAAGATCA ACGGTATCGG TACAGTTCCA GTCGGCCGTG     450
TCGAATCCGG CACAATGAAG CCAGGCATGA TCGTTAACTT CGCCCCATCC     500
ACAGTTACAG CTGAAGTTAA GTCCATCGAA ATGCACCACG AATCCCTTCC     550
AGAGGCTCTT CCAGGTGACA ACATCGGCTT CAACGTCAAG AACGTTTCCA     600
CAGCTGATGT CAAGCGTGGC TACGTCGTTG GTGATACAAA GCGTGACCCA     650
CCAGTCGAAT GCGCTTCCTT CACAGCTCAR ATGATCATCT CCAACCACCC     700
```

AGGCAAGATC CACGCCGGCT ACCAGCCAGT TTTCGACTGC CACACAAGCTC 750
ACATCGCCTG CAAGTTCGAC AAGCTCATCC AGCGTATCGA TCGTCGCCAC 800
GGCAAGAAGG CTACAGAGAA CCCAGAATAC ATTCAGAAGG ATGATGCCGC 850
TATCGTCGAG GTTGTCCCAT CCAAGCCACT CGTCGTCGAG TCCTTCCAGG 900
AGTACCCACC ACTCGGCCGT TTCGCCATCC GTGAT 935

2) INFORMATION FOR SEQ ID NO: 529

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1065 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
(B) STRAIN: EATRO795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

AAGCTGAAGG CTGAGCGCGA ACGTGGTATC ACGATCGACA TTGCACTGTG 50
GAAATTCGAG TCACCCAAGT CTGTCTTCAC TATTATTGAT GCTCCTGGGC 100
ACCGTGACTT CATCAAGAAC ATGATCACCG GCACATCGCA AGCCGACGCA 150
GCCATCCTCA TCATTGCCTC TGCGCAGGGT GAGTTCGAGG CTGGTATCTC 200
CAAGGATGGA CAGACCCGCG AGCACGCGTT GCTGGCCTTC ACTTTGGGTG 250
TGAAGCAGAT GGTTGTGTGC TGCAACAAGA TGGACGACAA GACTGTGAAC 300
TACGGACAGG AGCGGTATGA CGAGATTGTG AAGGAGGTGT CTGCTTACAT 350
CAAGAAGGTT GGGTACAACG TGGAGAAGGT GCGCTTCGTC CCCATCTCCG 400
GATGGCAGGG CGACAACATG ATTGAGAAAT CCGAGAAGAT GCCATGGTAC 450
AAGGGTCCAA CGCTCCTGGA GGCACTAGAC ATGCTGGAGC CACCAGTGCG 500
TCCGAGCGAC AAGCCCCTGC GTCTGCCACT GCAGGACGTG TACAAGATCG 550
GTGGTATTGG CACCGTGCCC GTTGGTCGTG TGGAGACCGG CGTGATGAAG 600
CCTGGTGATG TGGTGACGTT TGCCCCCGCC AACGTGACGA CCGAGGTGAA 650
ATCGATCGAG ATGCACCACG AGCAGCTCGC TGAGGCGACC CCCGGTGACA 700
ACGTCGGCTT TAACGTGAAG AACGTTTCTG TAAAGGACAT CCGCCGTGGC 750
AACGTCTGCG GTAACACCAA GAACGACCCC CCAAAGGAGG CCGCCGACTT 800
CACGGCACAG GTGATCATCC TGAACCACCC CGGACAGATT GGAAACGGTT 850
ATGCGCCCGT GCTGGACTGC CACACATCGC ACATTGCCTG CAAGTTCGCG 900
GAGATCGAGT CGAAGATCGA CCGTCGCTCT GGCAAGGAGC TGGAGAAGGC 950
TCCCAAGTCG ATCAAGTCTG GCGACGCCGC GATCGTGCGC ATGGTGCCGC 1000
AGAAGCCTAT GTGCGTGGAG GTCTTCAACG ACTACGCGCC ACTCGGCCGC 1050
TTTGCCGTGC GTGAC 1065

2) INFORMATION FOR SEQ ID NO: 530

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1297 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Crithidia fasciculata*
(B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

```
TTCGCGGAGG GCGTGCCGCC GGTGCTGACG GCGCTGGACG TGACGGAGGA      50
CCTCGGCCGC GACGAGCCGC TGACGCTGGA GATTGTGCAG CACTTGGACG     100
CGAACACCGG CCGCTGCATT GCCATGCAGA CGACGGATCT GCTGAAGCTG     150
AAGTCGAAGG TTGTGTCGAC GGGCGGCAAC ATCTCCGTGC CGGTTGGCCG     200
CGAGACGCTG GGCCGCATCT TCAACGTGCT CGGCGACGCG ATCGACCAGC     250
GCGGTGTGGT GGGCGAGAAG ATGCGCATGC CGATCCACGC CGAGGCGCCG     300
AAGCTGGCGG ACCAGGCCGC GGAGGACGCG ATTCTGACGA CCGGCATCAA     350
GGTGATCGAC CTGATTCTGC CGTACTGCAA GGGTGGCAAG ATCGGGCTGT     400
TCGGCGGTGC TGGTGTGGGC AAGACTGTGA TCATCATGGA GCTGATCAAC     450
AACGTGGCCA AGGGCCACGG TGGTTTCTCC GTGTTCGCCG GCGTTGGCGA     500
GCGCACCCGC GAGGGCACGG ATCTGTACCT GGAGATGATG CAGTCGAAGG     550
TCATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTGGTGTA CGGCCAGATG     600
AACGAGCCCC CGGGTGCGCG TGCGCGTGTT GCGCAGTCTG CGCTGACGAT     650
GGCGGAGTAC TTCCGTGACG TGGAGGGCCA GAACGTGCTG CTGTTCATCG     700
ACAACATCTT CCGCTTCACC CAGGCCAACT CCGAGGTGTC CGCCCTGCTG     750
GGCCGCATTC CCGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT     800
TGGTATGCTG CAGGAGCGCA TTACGTCGAC GACGAAGGGC TCGATTACGT     850
CTGTGCAGGC CGTGTACGTG CCGGCCGATG ATATCACGGA TCCGGCGCCG     900
GCGACGACCT TCTCGCACCT GGATGCGACG ACGGTGCTGG ACCGCGCGGT     950
TGCCGAGTCT GGCATCTACC CCGCCGTGAA CCCGCTGGAG TGCGCGTCGC    1000
GTATCATGGA CCCCGATGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG    1050
GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC    1100
CGTGCTGGGT ATCGACGAGC TGAGCGAGGA GGACAAGCTT GTGGTGGACC    1150
GCGCTCGCAA GGTGACGCGC TTCCTGTCGC AGCCGTTCCA GGTGGCCGAG    1200
GTGTTCACCG GCATGACGGG CCACTACGTG CAGCTGGAGG ACACAGTGGA    1250
GTCGTTCTCT GGCCTGCTGA TGGGCTCGTA CGACCAGATC CCGGAGA       1297
```

2) INFORMATION FOR SEQ ID NO: 531

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1298 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania tropica*
(B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

```
CTTCTCGGAG GGCGTGCCGC CCGTGCTGAC GGCGCTGGAT GTGACGGAGG      50
ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC     100
GCGAACACGG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT     150
GAAGTCGAAG GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC     200
GTGAGACGCT GGGCCGCATC TTCAAYGTTC TGGGCGACGC GATCGACCAG     250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC     300
GAAGCTGGCG GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA     350
AGGTGATCGA CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG     400
TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA     450
CAACGTCGCG AAGGGCCACG GCGGTTTCTC CGTGTTTGCC GGCGTTGGCG     500
```

AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
GTGATTGACC TGAAGGGCGA GTCGAAGTGY GTGCTTGTGT ATGGGCAGAT 600
GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA 650
TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG 850
TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
CGTATCATGG ACCCTGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
CGGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTTGTGGAC 1150
CGCGCGCGCA AGGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA 1200
GGTGTTCACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298

2) INFORMATION FOR SEQ ID NO: 532

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1297 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania aethiopica*
(B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

TTCTCGGAGG GCGTGCCGCC CGTGCTGACG GCGCTGGATG TGACGGAGGA 50
CCTTGGCCGC GATGAGCCGC TGACGCTGGA GATCGTGCAG CACTTGGACG 100
CGAACACCGG CCGCTGCATT GCGATGCAGA CGACGGACCT GCTGAAGCTG 150
AAGTCGAAGG TTGTGTCGAC CGGCGGCAAC ATCTCTGTGC CGGTGGGCCG 200
TGAGACGCTG GGCCGCATCT TCAACGTTCT GGGCGACGCG ATCGACCAGC 250
GCGGCCCCGT GGGCGAGAAG ATGCGCATGG CGATCCACGC CGAGGCCCCA 300
AAGCTGGCGG ATCAGGCCGC GGAGGACACG ATCCTGACGA CCGGCATCAA 350
GGTGATCGAC CTGATTCTGC CCTACTGCAA GGGTGGCAAG ATCGGCCTGT 400
TCGGCGGTGC CGGTGTGGGC AAGACTGTGA TCATCATGGA GCTGATCAAC 450
AACGTCGCGA AGGGCCACGG TGGTTTCTCC GTGTTTGCCG GCGTTGGCGA 500
GCGCACGCGC GAGGGCACGG ACCTGTACCT GGAGATGATG CAGTCGAAGG 550
TGATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTTGTGTA CGGGCAGATG 600
AACGAGCCCC CGGGTGCGCG CGCGCGCGTT GCGCAGTCTG CGCTGACGAT 650
GGCGGAGTAC TTCCGCGACG TGGAGGGCCA GAACGTGCTG CTGTTCATCG 700
ACAACATCTT CCGCTTCACG CAGGCGAACT CCGAGGTGTC TGCGCTGCTG 750
GGCCGCATTC CAGCCGCCGT GGGCTACCAG CCGACGCTTG CGGAGGATCT 800
TGGTATGCTG CAGGAGCGCA TCACGTCGAC AACGAAGGGG TCGATCACGT 850
CCGTGCAGGC CGTGTACGTG CCAGCGGATG ATATCACGGA TCCCGCGCCC 900
GCGACGACGT TCTCGCACCT GGACGCGACG ACTGTGCTGG ACCGCGCGGT 950
GGCGGAGTCG GGCATCTACC CTGCCGTGAA CCCGCTGGAG TGCGCGTCGC 1000
GTATCATGGA CCCCGACGTG ATCGATGTGG ACCACTACAA CGTTGCGCAG 1050
GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC 1100
GGTGCTTGGC ATCGACGAGC TGAGCGAGGA AGACAAGGTT GTTGTGGACC 1150
GCGCGCGCAA GGTGACCCGG TTCCTGTCGC AGCCGTTCCA GGTTGCGGAG 1200
GTGTTCACGG GCATGACGGG CCACTACGTG CAGCTGGTCG ACACGGTGGA 1250

GTCGTTCTCT GGCCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA 1297

2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1298 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania donovani*
(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

CTTCTCGGAG GGCGTGCCGC CCGTACTGAC GGCGCTGGAT GTGACGGAGG 50
ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT 100
GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
GTGAGACGCT GGGCCGCATC TTCAACGTTC TGGGCGACGC GATCGACCAG 250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
GAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG 400
TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGCGTTGGCG 500
AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG 550
GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA 650
TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC 800
TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG 850
TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACGG ATCCCGCGCC 900
CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150
CGCGCGCGCA AGGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA 1200
GGTGTTCACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250
AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298

2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1298 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*
(B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

```
CTTCTCGGAG GGCGTGCCGC CCGTACTGAC GGCGCTGGAT GTGACGGAGG      50
ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT     100
GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT     150
GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC     200
GTGAGACGCT GGGCCGCATC TTCAACGTTC TGGGCGACGC GATCGACCAG     250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC     300
AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA     350
AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG     400
TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA     450
CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGCGTTGGCG     500
AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG     550
GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT     600
GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA     650
TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC     700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT     750
GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC     800
TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG     850
TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC     900
CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG     950
TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG    1000
CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA    1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG    1100
CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC    1150
CGCGCGCGCA AGGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA    1200
GGTGTTCACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG    1250
AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA      1298
```

2) INFORMATION FOR SEQ ID NO: 535

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1301 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania gerbilli*
(B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

```
GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG     100
GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA     150
GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG     200
GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TGCGATCGAC     250
CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC     300
CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA     350
TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY     400
CTGTTCGGCG GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT     450
CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG     500
```

```
GCGAGCGCAC GCGCGAGGGC ACGGACCTGT ACCTGGAGAT GATGCAGTCG      550
AAGGTGATTG ACCTGAAGGG CGAGTCGAAG TGCGTGCTTG TGTACGGGCA      600
GATGAACGAG CCCCCGGGTG CGCGCGCGCG CGTTGCGCAG TCTGCGCTGA      650
CGATGGCGGA GTACTTCCGC GACGTGGAGG GCCAGAACGT GCTGCTGTTC      700
ATCGACAACA TCTTCCGCTT CACGCAGGCG AACTCCGAGG TGTCCGCGCT      750
GCTGGGCCGC ATTCCGGCCG CCGTGGGCTA CCAGCCGACG CTTGCGGAGG      800
ATCTTGGTAT GCTGCAGGAG CGCATCACGT CGACAACGAA GGGGTCGATC      850
ACGTCCGTGC AGGCCGTGTA CGTGCCAGCG GATGATATCA CGGATCCCGC      900
GCCCGCGACG ACGTTCTCGC ACCTTGACGC GACGACTGTG CTGGACCGCG      950
CGGTGGCGGA GTCGGGCATC TACCCTGCCG TGAACCCGCT GGAGTGCGCG     1000
TCGCGTATCA TGGACCCCGA TGTGATCGAT GTGGACCACT ACAACGTTGC     1050
GCAGGATATC GTGCAGATGC TGACCAAGTA CAAGGAGCTG CAGGACATCA     1100
TTGCGGTGCT TGGCATCGAC GAGCTGAGCG AGGAAGACAA GGTTGTGGTG     1150
GACCGCGCGC GCAAGGTGAC CCGGTTCCTG TCGCAGCCGT TCCAGGTTGC     1200
GGAGGTGTTC ACGGGCATGA CGGGCCACTA CGTGCAGCTG GTCGACACGG     1250
TGGAGTCGTT CTCTGGCTTG CTGATGGGGT CGTACGACCA GATCCCGGAG     1300
A                                                         1301
```

2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1298 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania hertigi*
- (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

```
CTTCGCGGAG GGCGTGCCGC CGGTGCTGAC GTCGCTGGAT GTGACGGAGA       50
ACCTCGGCCG CGATGAGCCG CTGACGCTGG AGATTGTGCA GCACTTGGAC      100
GCGAACACCG GTCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT      150
GAAGTCGAAG GTCGTGTCGA CCGGTGGCAA CATCTCTGTG CCTGTTGGCC      200
GCGAGACGCT GGGTCGCATC TTCAACGTGC TTGGCGATGC GATTGACCAG      250
CGCGGCCCTG TGGGTGAGAA GATGCGCATG GCGATCCACG CCGAGGCGCC      300
GAAGCTGGCG GATCAGGCGG CAGAGGACAC GATCCTGACG ACCGGCATCA      350
AGGTGATCGA TCTTATTCTG CCGTACTGCA AGGGTGGTAA GATCGGTCTG      400
TTCGGTGGTG CCGGTGTAGG CAAGACTGTG ATTATTATGG AGCTGATCAA      450
TAACGTGGCG AAGGGCCACG GTGGGTTTTC CGTGTTTGCT GGCGTGGGCG      500
AGCGCACGCG CGAGGGCACT GACCTGTACC TGGAGATGAT GCAGTCGAAG      550
GTGATTGACC TGAAGGGCGA ATCAAAGTGC GTGCTTGTGT ACGGACAGAT      600
GAACGAGCCC CCGGGTGCGC GTGCGCGCGT TGCGCAGTCT GCGCTGACGA      650
TGGCCGAGTA CTTCCGCGAT GTGGAGGGCC AGAACGTGCT GCTGTTCATT      700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT      750
GGGTCGCATT CCTGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC      800
TGGGCATGCT GCAGGAGCGC ATTACGTCGA CGACGAAGGG CTCGATTACG      850
TCTGTGCAGG CCGTGTACGT GCCTGCGGAT GATATCACGG ACCCGGCGCC      900
CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGTGCGG      950
TGGCAGAGTC GGGCATTTAC CCTGCGGTGA ACCCGCTGGA GTGCGCGTCG     1000
CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA     1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG     1100
CCGTGCTTGG TATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC     1150
CGCGCGCGCA AGGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA     1200
```

GGTGTTCACT GGCATGACGG GTCACTACGT TCAGCTGGAG GACACGGTGG 1250
AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA 1298

2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1297 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania major*
(B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

CTTCTCGGAG GGCGTGCCGC CCGTGCTGAC GGCGCTGGAT GTGACGGAGG 50
ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
GTGAGACGCT GGGCCGCATC TTCAACGTTC TGGGCGATGC GATCGACCAG 250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
CAATGTCGCG AAGGGCCACG GTGGTTTCTC CGTGTTTGCC GGCGTTGGCG 500
AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA 650
TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT 750
GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG 850
TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG 950
TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTG 1100
CGGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150
CGCGCGCGCA AGGTGACCCG GTTCCTGTCG CAGCCGTTCC AGGTTGCGGA 1200
GGTGTTCACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAG 1297

2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1297 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania amazonensis*
(B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

```
TTCTCGGAGG GCGTGCCGCC CGTGCTGACG GCGCTGGATG TGACGGAGGA       50
CCTTGGCCGC GATGAGCCGC TGACGCTGGA GATCGTGCAG CACCTGGACG      100
CGAACACCGG CCGCTGCATT GCGATGCAGA CGACGGACCT GTTGAAGCTG      150
AAGTCGAAGG TTGTGTCGAC CGGCGGCAAC ATCTCTGTGC CGGTGGGCCG      200
TGAGACGCTG GGCCGCATCT TCAACGTGCT GGGCGACGCG ATCGACCAGC      250
GCGGCCCCGT GGGTGAGAAG ATGCGCATGG CGATCCACGC CGAGGCCCCG      300
AAGCTGGCGG ATCAGGCCGC GGAGGACACG ATCCTGACGA CCGGCATCAA      350
GGTGATCGAC CTGATTCTGC CCTACTGCAA GGGTGGCAAG ATCGGCCTGT      400
TTGGTGGCGC CGGTGTGGGC AAGACCGTGA TCATCATGGA GTTGATTAAC      450
AACGTCGCGA AGGGCCACGG TGGTTTCTCG GTGTTTGCCG GCGTTGGCGA      500
GCGCACGCGC GAGGGCACGG ACCTGTACCT GGAGATGATG CAGTCGAAGG      550
TGATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTTGTGTA CGGGCAGATG      600
AACGAGCCCC CGGGTGCGCG CGCGCGCGTT GCGCAGTCTG CGCTGACGAT      650
GGCGGAGTAC TTCCGAGACG TGGAGGGCCA GAATGTGCTG CTGTTCATCG      700
ACAACATCTT CCGCTTCACG CAGGCGAACT CCGAGGTGTC TGCGCTGCTG      750
GGCCGCATTC CGGCCGCCGT GGGCTACCAG CCGACGCTTG CGGAGGATCT      800
TGGTATGCTG CAGGAGCGCA TCACGTCGAC GACGAAGGGG TCGATCACGT      850
CCGTGCAGGC CGTGTACGTG CCTGCGGATG ATATCACGGA TCCGGCGCCC      900
GCGACGACGT TCTCGCACCT GGACGCGACG ACTGTGCTGG ACCGCGCGGT      950
GGCGGAGTCG GGGATCTACC CTGCCGTGAA CCCGCTGGAG TGCGCGTCGC     1000
GTATCATGGA CCCCGATGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG     1050
GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC     1100
GGTGCTTGGT ATCGACGAGC TGAGCGAGGA GGACAAGGTC GTGGTGGACC     1150
GCGCGCGCAA GGTGACCCGG TTCCTGTCGC AGCCGTTCCA GGTTGCGGAG     1200
GTGTTCACGG GCATGACGGG CCACTACGTG CAGCTGGCCG ACACGGTGGA     1250
GTCGTTCTCT GGGCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA        1297
```

2) INFORMATION FOR SEQ ID NO: 539

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG 27

2) INFORMATION FOR SEQ ID NO: 540

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG 23

2) INFORMATION FOR SEQ ID NO: 541

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

GTKGAAATGT TCCGCAAGCT GCT 23

2) INFORMATION FOR SEQ ID NO: 542

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

CGGAARTAGA ACTGSGGACG GTAG 24

2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

ATCTTAGTAG TTTCTGCTGC TGA 23

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTMC CAT 23

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG 26

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

CCRCGICCGG TRATGGTGAA GAT 23

2) INFORMATION FOR SEQ ID NO: 547

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

GTACAGTTGC TTCAGGACGT ATC 23

2) INFORMATION FOR SEQ ID NO: 548

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548

ACGTTCGATT TCATCACGTT G 21

2) INFORMATION FOR SEQ ID NO: 549

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549

GAACGTGATA CTGACAAACC TTTA 24

2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550

GAAGAAGAAC ACCAACGTTG 20

2) INFORMATION FOR SEQ ID NO: 551

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551

GAAGAAAAAA TCTTCGAACT GGCTA 25

2) INFORMATION FOR SEQ ID NO: 552

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

TACACGGCCG GTGACTACG 19

2) INFORMATION FOR SEQ ID NO: 553

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA 25

2) INFORMATION FOR SEQ ID NO: 554

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

GTTCCTTACA TCGTTGTTTT TCTC 24

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

TCTCGAACTT TCTCTATGTA TGCA 24

2) INFORMATION FOR SEQ ID NO: 556

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

CGGCGCNATC YTSGTTGTTG C 21

2) INFORMATION FOR SEQ ID NO: 557

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

CCMAGGCATR ACCATCTCGG TG 22

2) INFORMATION FOR SEQ ID NO: 558

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

TCITTYAART AYGCITGGGT 20

2) INFORMATION FOR SEQ ID NO: 559

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

CCGACRGCRA YIGTYTGICK CAT 23

2) INFORMATION FOR SEQ ID NO: 560

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

GAYTTCATYA ARAAYATGAT YAC 23

2) INFORMATION FOR SEQ ID NO: 561

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

ACIGTICGGC CRCCCTCACG GAT 23

2) INFORMATION FOR SEQ ID NO: 562

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

CARATGRAYG ARCCICCIGG IGYIMGIATG 30

2) INFORMATION FOR SEQ ID NO: 563

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT 26

2) INFORMATION FOR SEQ ID NO: 564

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA 29

2) INFORMATION FOR SEQ ID NO: 565

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

GGYTGRTAIC CIACIGCIGA IGGDAT 26

2) INFORMATION FOR SEQ ID NO: 566

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

TTYGGIGGIG CIGGIGTIGG IAARAC 26

2) INFORMATION FOR SEQ ID NO: 567

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCYTG 26

2) INFORMATION FOR SEQ ID NO: 568

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

RTIATIGGIG CIGTIRTIGA YGT 23

2) INFORMATION FOR SEQ ID NO: 569

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

RTIRTIGGIS CIGTIRTIGA TAT 23

2) INFORMATION FOR SEQ ID NO: 570

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

RTIRYIGGIC CIGTIRTIGA YGT 23

2) INFORMATION FOR SEQ ID NO: 571

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

RTIRTIGGIC CIGTIRTIGA TGT 23

2) INFORMATION FOR SEQ ID NO: 572

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

RTIRTIGGIS CIGTIRTIGA 20

2) INFORMATION FOR SEQ ID NO: 573

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

CCICCIACCA TRTARAAIGC 20

2) INFORMATION FOR SEQ ID NO: 574

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

ATIGCIATGG AYGGIACIGA RGG 23

2) INFORMATION FOR SEQ ID NO: 575

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

TIACCATTTC AGTACCTTCT GGTAA 25

2) INFORMATION FOR SEQ ID NO: 576

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

AACTTCRTCA AGAAGGTYGG TTACAA 26

2) INFORMATION FOR SEQ ID NO: 577

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

CATGATTGAA CCATCCACCA 20

2) INFORMATION FOR SEQ ID NO: 578

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA 20

2) INFORMATION FOR SEQ ID NO: 579

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

GAAGGCCGTG CTGGTGAGAA 20

2) INFORMATION FOR SEQ ID NO: 580

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

GCTAAACCAG CTACAATCAC TCCAC 25

2) INFORMATION FOR SEQ ID NO: 581

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

ACATCGGTGC ATTATTACGT GG 22

2) INFORMATION FOR SEQ ID NO: 582

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT 28

2) INFORMATION FOR SEQ ID NO: 583

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG 35

2) INFORMATION FOR SEQ ID NO: 584

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA 20

2) INFORMATION FOR SEQ ID NO: 585

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

ACCACATACT GAATTCAAAG 20

2) INFORMATION FOR SEQ ID NO: 586

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

CAGAAGTATA CGTATTATCA 20

2) INFORMATION FOR SEQ ID NO: 587

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

CGTATTATCA AAAGACGAAG 20

2) INFORMATION FOR SEQ ID NO: 588

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

TCTTCTCAAA CTATCGTCCA 20

2) INFORMATION FOR SEQ ID NO: 589

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

GCACGAAACT TCTAAAACAA 20

2) INFORMATION FOR SEQ ID NO: 590

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

TATACGTATT ATCTAAAGAT 20

2) INFORMATION FOR SEQ ID NO: 591

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

TCCTGGTTCT ATTACACCAC 20

2) INFORMATION FOR SEQ ID NO: 592

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

CAAAGCTGAA GTATACGTAT 20

2) INFORMATION FOR SEQ ID NO: 593

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

TTCACTAACT ATCGCCCACA 20

2) INFORMATION FOR SEQ ID NO: 594

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

ATTGGTATCC ATGACACTTC 20

2) INFORMATION FOR SEQ ID NO: 595

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

TTAAAGCAGA CGTATACGTT 20

2) INFORMATION FOR SEQ ID NO: 596

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

GAAATTATTG GTATCAAAGA 20

2) INFORMATION FOR SEQ ID NO: 597

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAAACTTC 20

2) INFORMATION FOR SEQ ID NO: 598

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT 20

2) INFORMATION FOR SEQ ID NO: 599

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA 20

2) INFORMATION FOR SEQ ID NO: 600

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

ATGCAAGAAG AATCAAGCAA 20

2) INFORMATION FOR SEQ ID NO: 601

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

GTTTCACGTG ATGATGTACA 20

2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

AAGTTGAAGT TGTTGGTATT 20

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

GGTATTAAAG ACGAAACATC 20

2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

GGTGATGAAG TAGAAATCGT 20

2) INFORMATION FOR SEQ ID NO:605

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

GAAATGTTCC GTAAATTATT 20

2) INFORMATION FOR SEQ ID NO:606

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

ATTAGACTAC GCTGAAGCTG 20

2) INFORMATION FOR SEQ ID NO: 607

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACAC 50
GTGAACATAT CTTATTATCA CGTAACGTTG GTGTACCATA CATCGTTGTA 100
TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGACT TATTATCAGA ATACGATTTC CCAGGCGATG 200
ATGTTCCAGT TATCGCAGGT TCTGCTTTGA AAGCTTTAGA AGGCGACGAG 250
TCTTATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT 300
CCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG 350
ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG ACGTGTTGAA 400
CGTGGTGAAG TTCGCGTTGG TGACGAAGTT GAAATCGTTG GTATTAAAGA 450
CGAAACATCT AAAACAACTG TTACAGGTGT TGAAATGTTC CGTAAATTAT 500
TAGACTACGC TGAAGCAGGC GACAACTTCG GTGCTTTATT ACGTGGTGTA 550
GCACGTGAAG ATATCGAACG TGGACAAGTA TTAGCTAAAC CAGCTACAAT 600
CACTCCACAC ACAAAATTCA AAGCTGAAGT ATACGTATTA TCAAAAGAAG 650
AAGGCGGACG TCACACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC 700
TTCCGTACAA CAGACGTTAC TGGTGTTGTA GAATTGCCAG AAGGTACTGA 750
AATGGTAATG CCTGGTGATA ACGTTGCTAT GGACGTTGAA TTAATTCACC 800
CAATCGCTAT CGAAGACGGA A 821

2) INFORMATION FOR SEQ ID NO: 608

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

CGGAGCTATC TTGGTAGTTT CTGCTGCTGA CGGCCCAATG CCTCAAACTC 50
GTGAACACAT CCTATTGTCT CGTCAAGTTG GTGTTCCTTA CATCGTTGTA 100
TTCTTGAACA AAGTAGACAT GGTTGATGAC GAAGAATTAC TAGAATTAGT 150
TGAAATGGAA GTTCGTGACC TATTAACAGA ATACRAATTC CCTGGTGRCG 200
ATGTTCCTGT AGTTGCTGGA TCAGCTTTGA AAGCTCTAGA AGGCGACGCT 250
TCATACGAAG AAAAAATTCT TGAATTAATG GCTGCAGTTG ACGAATACAT 300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG 350
ACGTGTTCTC AATTACTGGA CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAGTTGTTG GTATTGCTGA 450
AGAAACTTCA AAAACAACAG TTACTGGTGT TGAAATGTTC CGTAAATTGT 500
TAGACYACGC TGAAGCTGGA GACRACATTG GTGCTTTACT ACGTGGTGTT 550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT 600
CACACCTCRT ACAAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC 700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA 750
A 751

2) INFORMATION FOR SEQ ID NO: 609

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

```
CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACTC      50
GTGAACACAT CTTGTTATCA CGTAACGTTG GCGWACCATA CATCGTTGTT     100
TTCTTGAACA AAATGGATAT GGTTGAYGAC GAAGAATTGC TAGAATTAGT     150
TGAAATGGAA GTTCGTGACC TATTGTCTGA ATATGACTTC CCAGGCGACG     200
ATGTTCCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA AGGAGATCCT     250
TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCAGTTG ACGAATACGT     300
TCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG     350
ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA     400
CGTGGACAAG TTCGCGTTGG TGATGAAGTA GAAATCGTTG GTATTGCTGA     450
CGAAACTGCT AAAACAACTG TAACAGGTGT TGAAATGTTC CGTAAATTGT     500
TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGGGTT     550
GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACRAT     600
CACACCTCAT ACAAAATTCA AAGCTGAAGT TTATGTTTTG ACAAAAGAAG     650
AAGGTGGRCG TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC     700
TTCCGTACAA CTGACGTAAC TGGTGTTGTT GAATTACCAG AAGGAACTGA     750
A                                                         751
```

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 891 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Haemophilus influenzae* Rd
(B) STRAIN: KW20
(C) ACCESSION NUMBER: extracted from U32739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

```
AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC      50
AGCAACAGAT GGTCCTATGC CACAAACTCG TGAACACATC TTATTAGGTC     100
GCCAAGTAGG TGTTCCATAC ATCATCGTAT TCTTAAACAA ATGCGACATG     150
GTAGATGACG AAGAGTTATT AGAATTAGTC GAAATGGAAG TTCGTGAACT     200
TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC GTACGTGGTT     250
CAGCATTACA AGCGTTAAAC GGCGTAGCAG AATGGGAAGA AAAAATCCTT     300
GAGTTAGCAA ACCACTTAGA TACTTACATC CCAGAACCAG AACGTGCGAT     350
TGACCAACCG TTCCTTCTTC CAATCGAAGA TGTGTTCTCA ATCTCAGGTC     400
GTGGTACTGT AGTAACAGGT CGTGTAGAAC GAGGTATTAT CCGTACAGGT     450
GATGAAGTAG AAATCGTCGG TATCAAAGAT ACAGCGAAAA CTACTGTAAC     500
GGGTGTTGAA ATGTTCCGTA AATTACTTGA CGAAGGTCGT GCAGGTGAAA     550
ACATCGGTGC ATTATTACGT GGTACCAAAC GTGAAGAAAT CGAACGTGGT     600
CAAGTATTAG CGAAACCAGG TTCAATCACA CCACACACTG ACTTCGAATC     650
```

AGAAGTGTAC GTATTATCAA AAGATGAAGG TGGTCGTCAT ACTCCATTCT 700
TCAAAGGTTA CCGTCCACAA TTCTATTTCC GTACAACAGA CGTGACTGGT 750
ACAATCGAAT TACCAGAAGG CGTGGAAATG GTAATGCCAG GCGATAACAT 800
CAAGATGACA GTAAGCTTAA TCCACCCAAT TGCGATGGAT CAAGGTTTAC 850
GTTTCGCAAT CCGTGAAGGT GGCCGTACAG TAGGTGCAGG C 891

2) INFORMATION FOR SEQ ID NO: 611

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

CGGCGGTATC TTAGTTGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 200
ATGTACCTGT AATCGCTGGT TCTGCATTAA AAGCATTAGA AGGCGATGCT 250
GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCAGTTG ATGATTACAT 300
TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATGCACGA 450
AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTTGCA 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCTATTAC 600
ACCACACACA AAATTCAAAG CTGAAGTATA CGTATTATCT AAAGATGAAG 650
GTGGACGTCA CACTCCATTC TTCACTAACT ATCGCCCACA ATTCTATTTC 700
CGTACTACTG ACGTAACTGG TGTTGTAAAC TTACCAGAAG GTACAGAAAT 750
GGTTATGCCT GGCGACAACG TTGAAATGAC AGTTGAATTA ATCGCTCCAA 800
TCGCTATCGA AGACGGAA 818

2) INFORMATION FOR SEQ ID NO: 612

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Parathyphi A
(B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT 150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
CACGCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC 300
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC 400
GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
GTACTACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCAATGGAC GACGGTCTGC GTTTC 825

2) INFORMATION FOR SEQ ID NO: 613

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 778 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia ficaria*
(B) STRAIN: ATCC 33105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCAATGC CTCAGACCCG 50
TGAGCACATC CTGCTGGGTC GYCAGGTTGG CGTTCCTTTC ATCATCGTRT 100
TCATGAACAA ATGCGACATG GTTGATGATG AAGAGCTGCT GGAACTGGTA 150
GAAATGGAAG TTCGCGAACT GCTGTCCGCT TACGACTTCC CTGGCGATGA 200
CCTGCCGGTG ATTCGCGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCCG 250
AGTGGGAAGC TAAAATCATC GAGCTGGCTG AMCMSCTGGA TACTTACATC 300
CCAGAACCAG AGCGCGCTAT CGACAAGCCG TTCCTGCTGC CAATCGAAGA 350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT GGTTACCGGT CGTGTTGAGC 400
GCGGTATCAT CAAAGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAC 450
ACCGTCAAGT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAGC 550
GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCCATCAAG 600
CCGCACACCC AGTTCGATTC AGAAGTGTAC ATCCTGAGCA AAGAAGAAGG 650
TGGTCGTCAC ACKCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700
GTACTACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTTGAGATG 750
GTAATGCCTG GCGACAACGT GAACATGA 778

2) INFORMATION FOR SEQ ID NO: 614

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 653 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus malodoratus*
(B) STRAIN: ATCC 43197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

GTGCGATCTT AGTAGTATCA GCTACTGATG GTCCAATGCC TCAAACTCGT 50
GAACACATTT TGTTATCACG TCAAGTTGGT GTTAAGCACT TGATCGTTTT 100
CTTGAACAAA GTAGATTTAG TTGATGACGA AGAATTGATC GACTTAGTTG 150
AAATGGAAGT ACGTGAATTA CTTTCTGAAT ATGGTTTCCC AGGTGATGAT 200
ATTCCAGTGC TTAAAGGTTC TGCTTTGAAA GCATTAGAAG GCGATCCAGA 250
ACAAGAACAA GTTATTCTTG ATTTGATGGA TACCGTTGAT GAATATATCC 300
CAACACCTGA ACGTGACAAT GACAAACCGT TCTTGTTACC AGTTGAGGAT 350
GTTTTCTCGA TCACAGGACG TGGTACTGTA GCTTCTGGTC GTATCGACCG 400
TGGCGAAGTT AAAGTCGGCG ATGAAATTGA AATCATCGGG ATCAAACCTG 450
AAGTTCAAAA AGCAATCGTT ACTGGACTTG AAATGTTCCG TAAAACATTG 500
GATTATGGTG AAGCTGGCGA TAACGTTGGG GTTCTATTAC GTGGGATTAC 550
ACGTGATGAA ATCGAACGTG GCCAAGTATT AGCTAAACCA GGTTCAATCA 600
CACCACATAC TAAGTTCAAA GCCGAAGTAT ATGTGTTGAC GAAAGAAGAA 650
GGT 653

2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus durans*
(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

CCATTCTAGT TGTATCTGCA ACAGATGGAC CAATGCCACA AACACGTGAA 50
CATATTTTAT TGTCACGTCA AGTAGGTGTT AAATATTTGA TCGTCTTCTT 100
GAACAAAATC GACTTAGTAG ATGATGAAGA ATTGATTGAT CTTGTCGAAA 150
TGGAAGTTCG TGAATTATTA AGCGAATATG GTTTCCCAGG TGACGATACA 200
CCAGTCATCA AAGGTTCAGC ATTAAAAGCT TTACAAGGAG ATCCTGATGC 250
AGAAGCAGCT ATCATGGAAT TGATGGATAC TGTTGATGAA TATATCCCAA 300
CACCAGAACG TGATACAGAC AAACCATTAT TGTTACCAGT GGAAGATGTC 350
TTCTCAATCA CAGGTCGTGG GACTGTTGCT TCAGGTCGTA TCGATCGTGG 400
TGCAGTTCGT GTAGGTGATG AAATCGAAAT CGTCGGTATC AAACCTGAAA 450
CACAAAAAGC TGTTGTAACT GGGGTCGAAA TGTTCCGCAA GACATTAGAC 500
TATGGTGAAG CAGGAGATAA CGTTGGGGTA TTGTTACGTG GTATCCAACG 550
TGAAGATATC GAACGTGGAC AAGTAATCGC AAAACCAGGT TCAATCACAC 600
CACATACAAA ATTCAAAGCA GAAGTGTACG TATTGACAAA AGAAGAAGGT 650
GGACGTCATA CACCATTCTT CAATAACTAT CGTCCACAAT TCTACTTCCG 700
TACAACTGAC GTAACTGGAA CAATCGTTTT ACCTGGAGGC ACTGAAATGG 750

TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCCAGTT 800
GCCATCGAAA ACGGAACAAC TTTCTCTAT 829

2) INFORMATION FOR SEQ ID NO: 616

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 669 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

GGTGCAATTT TAGTAGTATC TGCTACTGAT GGCCCAATGC CACAAACACG 50
TGAACATATC TTGTTATCAC GTCAAGTAGG GGTTAAACAC TTAATCGTCT 100
TCTTGAACAA AGTTGATTTA GTTGATGATG AAGAATTGAT CGATTTAGTT 150
GAAATGGAAG TTCGGGAATT GCTTTCTGAA TATGGTTTCC CAGGCGATGA 200
TATTCCAGTA CTTAAAGGTT CTGCTTTGAA AGCTTTAGAA GGCGATCCTG 250
AACAAGAACA AGTAATCCTT GACTTGATGG ATACGGTTGA TGAATACATC 300
CCAACGCCTG AACGTGATAC TGACAAACCA TTCTTGTTAC CAGTCGAAGA 350
TGTCTTCTCA ATCACAGGAC GTGGTACGGT TGCATCTGGT CGTATCGATC 400
GTGGGGAAGT TAAAGTCGGT GATGAAGTTG AAATCATCGG GATCAAACCT 450
GAAGTGCAAA AAGCTGTCGT AACTGGACTA GAAATGTTCC GTAAGACATT 500
GGATTACGGT GAAGCTGGCG ATAACGTTGG GGTTCTATTA CGTGGGATTA 550
CTCGTGATGA AATCGAACGT GGACAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CGAAATTCAG TGCAGAAGTT TATGTATTGA CGAAAGAAGA 650
AGGTGGCCGT CATACGCCA 669

2) INFORMATION FOR SEQ ID NO: 617

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus dispar*
(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

CGGGGCAATT TTAGTTGTAT CTGCAACTGA TGGCCCAATG CCACAAACAC 50
GTGAACACAT TTTGTTAGCT CGTCAAGTAG GGGTTAAATA TTTAATCGTC 100
TTCTTGAACA AAACAGATTT AGTTGATGAT GAAGAATTAT TGGAACTAGT 150
TGAAATGGAA GTTCGTGAAT TATTAAATGA ATACAATTTC CCTGGCGATG 200
ATATTCCTGT TATTCGCGGA TCTGCTTTAA AAGCATTAGA AGGCGATCCA 250
GAACAAGAAG AAGTAATTAT GAACTTGATG GATACTGTGG ATGAATATAT 300

```
CCCAACTCCA GAACGTGACA ATGATAAACC ATTCTTGTTA CCAGTGGAAG      350
ATGTCTTCAC AATTACTGGT CGTGGTACTG TTGCTTCAGG TCGTATCGAC      400
CGTGGTAAAG TCAACGTTGG TGATGAAATT GAAATTATCG GAATTAAACC      450
AGAAACACAA AAAGCTGTTG TAACCGGTTT GGAAATGTTC CGTAAAACTT      500
TGGATTATGG TGAAGCTGGT GATAACGTTG GGGTCTTATT ACGTGGGATT      550
ACTCGTGATG AAGTAGAACG TGGTCAAGTA TTAGCAAAAC CAGGTTCCAT      600
TACACCGCAT ACCAAATTTA AAGGTGAAGT TTATATCTTA ACAAAAGAAG      650
AAGGTGGACG TCATACTCCT TTCTTTAATA ACTATCGTCC TCAATTTTAT      700
TTCCGTACAA CTGATGTGAC TGGTAACATC GCATTACCTG AAGGAACTGA      750
AATGGTAATG CCTGGTGATA ATGTAACAAT TGAAGTTGAA TTGATTCATC      800
CAATCGCCGT TGAAAAAGGG ACTACTTTCT CAATT                     835
```

2) INFORMATION FOR SEQ ID NO: 618

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

```
GGTGCAATCC TAGTAGTATC AGCTACTGAT GGTCCAATGC CGCAAACACG       50
TGAACATATT TTGCTATCAC GGCAAGTGGG TGTTAAACAC TTAATCGTAT      100
TTTTAAACAA AGTTGATTTA GTCGATGATG AAGAATTGAT CGATCTAGTT      150
GAAATGGAAG TCCGTGAATT ACTTTCTGAA TATGGTTTCC CAGGTGACGA      200
TATTCCAGTT CTCAAAGGTT CAGCTTTGAA AGCATTAGAA GGCGATCCTG      250
AACAAGAACA AGTAATCCTT GATTTAATGG ATACAGTTGA CGAATATATC      300
CCAACTCCAG AACGTGACAC TGACAAGCCA TTCTTGTTAC CAGTCGAAGA      350
TGTATTTTCT ATCACTGGTC GTGGGACTGT AGCGTCTGGA CGGATTGATC      400
GTGGTGAAGT TAAAGTCGGC GATGAAGTTG AAATCATCGG GATCAAACCT      450
GAAATTCAAA AAGCAGTCGT AACTGGACTT GAAATGTTCC GTAAAACTTT      500
AGATTATGGT GAAGCTGGCG ATAACGTTGG GGTTCTATTA CGTGGGATTA      550
CACGTGATGA AATCGAACGT GGTCAAGTCT TAGCTAAACC AGGTTCAATC      600
ACACCACATA CAAAATTCAG TGCAGAAGTT TACGTATTGA CGAAAGAAGA      650
AGGTGGACGT CATACACCAT CTT                                  673
```

2) INFORMATION FOR SEQ ID NO: 619

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1713 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: K00428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

```
TTTCATATTT TTAAGGATTT TGTTTTAGCA CCCATCCGAC CTCAGTCAAT      50
ATATCCTTTC GCGACCAGGC TTTCCTCCCT TTTGCTGCTA ACTGGTTACA     100
GATTTTCCTA TTTTTGGTCA TTTTTATCTT TGAAACTGAT TAAGCTGAAA     150
AAATTTGAGC TTCTTTGTTG TAAACTATTT TGTGCTTTCA GTTTTATTCT     200
AGCTCGACAA AGGTAACAGA CAAAAATGTC AGCTTTATTA CCAAGATTAC     250
TCACAAGAAC AGCTTTTAAA GCTTCTGGGA AACTTCTGAG GCTCTCTTCA     300
GTAATTTCTA GGACCTTTTC TCAAACTACT ACTTCCTATG CAGCTGCTTT     350
TGATCGTTCC AAACCGCATG TAAATATAGG TACGATCGGC CATGTTGATC     400
ATGGGAAGAC AACTTTAACC GCAGCCATTA CGAAAACGTT AGCCGCAAAA     450
GGTGGTGCCA ACTTCTTGGA CTATGCTGCC ATCGATAAGG CTCCGGAAGA     500
AAGAGCTCGT GGTATTACAA TTTCTACTGC ACACGTGGAA TACGAAACGG     550
CCAAGAGACA TTATTCTCAC GTCGACTGTC CAGGCCACGC TGATTACATC     600
AAGAATATGA TTACCGGTGC TGCTCAAATG GATGGTGCTA TCATTGTTGT     650
AGCTGCTACC GATGGACAAA TGCCCCAAAC TAGAGAACAT TTACTTTTGG     700
CCAGACAAGT TGGTGTCCAA CATATTGTCG TTTTTGTTAA CAAGGTTGAT     750
ACCATTGATG ATCCAGAAAT GTTAGAGTTA GTCGAAATGG AAATGAGAGA     800
ACTTTTAAAC GAATATGGGT TTGACGGTGA TAATGCTCCA ATTATCATGG     850
GTTCTGCCCT TTGCGCTTTG GAAGGTCGCC AACCTGAAAT TGGGGAGCAG     900
GCCATCATGA AACTTTTGGA TGCAGTGGAT GAGTATATTC CTACACCTGA     950
AAGAGATTTG AACAAGCCTT TCTTGATGCC CGTTGAAGAT ATCTTCTCTA    1000
TCTCCGGTAG AGGTACTGTG GTCACTGGTC GTGTGGAAAG GGGTAATTTA    1050
AAGAAAGGTG AGGAATTGGA AATTGTTGGT CACAACTCCA CCCCATTGAA    1100
AACAACAGTT ACTGGTATTG AAATGTTTAG AAAGGAATTG GACTCTGCTA    1150
TGGCAGGTGA CAATGCCGGT GTTTTACTTA GAGGTATCAG GAGAGATCAA    1200
TTGAAGAGAG GTATGGTCTT AGCTAAGCCA GGTACCGTTA AAGCCCATAC    1250
AAAGATTCTA GCCTCTTTGT ACATTTTATC CAAAGAGGAA GGTGGTAGAC    1300
ATTCTGGGTT TGGTGAAAAC TACAGACCAC AAATGTTTAT AAGAACAGCT    1350
GATGTTACAG TTGTGATGAG ATTTCCTAAG GAGGTTGAAG ATCATTCTAT    1400
GCAAGTTATG CCAGGTGACA ATGTTGAAAT GGAATGTGAT TTGATCCATC    1450
CTACCCCATT AGAAGTTGGT CAACGTTTCA ATATCAGAGA GGGTGGAAGA    1500
ACTGTTGGTA CCGGTCTAAT CACACGTATT ATTGAATAGA CTTATTGATG    1550
CAACTGGAGT ATATTTCTAT ATATTCTGTT CATTTCCCCT CTCATAATAT    1600
ATACTTGTTT CGTTAAAATT TTATACGTGT AAATAAAGTG CCATAAATTT    1650
TTCAGCTTTA CTTTTGGTAG AGTCCTGCTA GCACTAGATT TTACAATTTC    1700
ATGTGCACAC ACC                                           1713
```

2) INFORMATION FOR SEQ ID NO: 620

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

```
ATTGGTGCAT TGCTACGT                                      18
```

2) INFORMATION FOR SEQ ID NO: 621

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

TGGTGCAATC TTAGTTGTTT CTGCAACTGA CGGTCCGATG CCTCAAACAC 50
GTGAACACAT TTTATTGTCA CGCCAAGTTG GTGTAAAATA CCTGATTGTT 100
TTCTTGAACA AAGTTGATTT AGTCGATGAT GAAGAATTGA TCGATTTGGT 150
AGAAATGGAA GTTCGCGAGT TATTGAGCGA ATATGGTTTC CCAGGCGATG 200
ACACTCCTGT GATCAAAGGT TCCGCATTAA AAGCATTGCA AGGCGATCCA 250
GATGCTGAAG CTGCTATTAT GGAATTGATG GATACAGTAG ATGAATATAT 300
CCCAACACCA GAACGTGATA CAGATAAACC ATTACTATTG CCAGTGGAAG 350
ACGTCTTCTC AATTACAGGT CGAGGAACTG TTGCCTCAGG TCGTATTGAT 400
CGTGGTGCTG TTCGTGTCGG TGATGAGGTA GAGATCGTAG GGATCAAACC 450
TGAAACACAA AAAGCAGTTG TAACAGGTGT AGAAATGTTC CGTAAAACGT 500
TAGATTACGG GGAAGCTGGG GATAACGTAG GCGTGTTGTT ACGGGGGATC 550
CAACGTGACG ATATCGAACG TGGACAAGTA CTTGCTAAAC CAGGTTCCAT 600
TACTCCACAT ACAAAATTCA AAGCAGAAGT GTACGTGTTG ACAAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCAACA ACTATCGTCC ACAGTTCTAC 700
TTCCGCACAA CTGATGTTAC AGGAACAATC ACATTGCCAG AAGATACAGA 750
A 751

2) INFORMATION FOR SEQ ID NO: 622

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Saccharomyces cerevisiae*
(B) STRAIN: ATCC 13264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

GTCAAATGGG ACGAATCCAG ATTCCAAGAA ATTGTCAAGG AAACCTCCAA 50
CTTTATCAAG AAGGTTGGTT ACAACCCAAA GACTGTTCCA TTCGTCCCAA 100
TCTCTGGTTG GAACGGTGAC AACATGATTG AAGCTACCAC CAACGCTCCA 150
TGGTACAAGG GTTGGGAAAA GGAAACCAAG GCCGGTGTCG TCAAGGGTAA 200
GACTTTGTTG GAAGCCATTG ACGCCATTGA ACAACCATCT AGACCAACTG 250
ACAAGCCATT GAGATTGCCA TTGCAAGATG TTTACAAGAT TGGTGGTATT 300
GGTACTGTGC CAGTCGGTAG AGTTGAAACC GGTGTCATCA AGCCAGGTAT 350
GGTTGTTACT TTCGCCCCAG CTGGTGTTAC CACTGAAGTC AAGTCCGTTG 400
AAATGCATCA CGAACAATTG GAACAAGGTG TTCCAGGTGA CAACGTTGGT 450
TTCAACGTCA AGAACGTTTC CGTTAAGGAA ATCAGAAGAG GTAACGTCTG 500
TGGTGACGCT AAGAACGATC CACCAAAGGG TTGCGCTTCT TTCAACGCTA 550
CCGTCATTGT TTTGAACCAT CCAGGTCAAA TCTCTGCTGG TTACTCTCCA 600

GTTTTGGATT GTCACACTGC TCACATTGCT TGTAGATTCG ACGAATTGTT 650
GGAAAAGAAC GACAGAAGAT CTGGTAAGAA GTTGGAAGAC CATCCAAAGT 700
TCTTGAAGTC CGGTGACGCT GCTTTGGTCA AGTTCGTTCC ATCTAAGCCA 750

2) INFORMATION FOR SEQ ID NO:623

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptococcus neoformans*
(B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC TTAAGGCCGA GCGAGAGCGA GGTATCACCA TCGACATTGC 50
TCTTTGGAAG TTCGAGACCC CCAGGTACCA GGTCACCGTC ATTGACGCCC 100
CCGGTCACCG AGACTTCATC AAGAACATGA TCACCGGTAC CTCCCAGGCT 150
GACTGTGCCA TCCTCATCAT TGCCACCGGT ATCGGTGAGT TCGAGGCCGG 200
TATCTCCAAG GACGGTCAGA CCCGAGAGCA CGCCCTCCTC GCCTTCACCC 250
TCGGTGTCAG GCAGCTCATT GTTGCTTGCA ACAAGATGGA CACCTGCAAG 300
TGGTCCGAGG ACCGATTCAA CGAAATCGTC AAGGAGACCA ACGGTTTCAT 350
CAAGAAGGTT GGTTACAACC CCAAGGCTGT CCCCTTCGTC CCCATCTCTG 400
GTTGGCACGG TGACAACATG TTGGAGGAGA CCACCAAGTC AGTGAATCCG 450
CTTCTACGTG ATGAGATGTT TTTCTGACTT TCCGTGCAGC ATGCCCTGGT 500
ACAAGGGATG GACCAAGGAG ACCAAGTCTG GTGTTTCCAA GGGTAAGACC 550
CTCCTCGAGG CCATCGACGC CATCGAGCCC CCTACCCGAC CCACCGACAA 600
GCCCCTCCGT CTCCCTCTCC AGGACGTCTA CAAGATCGGT GGTATCGGCA 650
CAGTCCCTGT CGGCCGAGTC GAGACCGGTG TCATCAAGGC CGGTATGTTG 700
TCTCATCTCT CTTGTCTCGT AACATGCGTC TCGTAACATG CGCTTACTTC 750
ATTTTCAGGT ATGGTCGTCA AGTTCGCCCC CACCAACGTC ACCACTGAAG 800
TCAAGTCCGT TGAGATGCAC CACGAGCAGA TCCCCGAGGG TCTTCCCGGA 850
GACAACGTTG GTTTCAACGT CAAGAACGTT TCCATCAAGG ACATCCGACG 900
AGGTAACGTC TGTGGTGACT CCAAGAACGA CCCCCCTATG GAGGCTGCTT 950
CTTTCAACGC CCAGGTTATC GTCCTTAACC ACCCTGGTCA GATCGGTGCC 1000
GGTTACACCC CCGTTCTCGA CTGTCACACT GCCCGTAAGC CTGACCCAAT 1050
ACCTCCAACA TACCTTTGAA GCTGACCCTT TCTAGACATT GCCTGCAAGT 1100
TTGCTGAGTT GATCGAGAAG ATTGACCGAC GAACCGGTAA GGTCATGGAG 1150
GCCGCCCCCA AGTTCGTCAA GTCTGGTGAC GCCGCCATTG TCAAGCTTGT 1200
TGCCCAGAAG CCCCTCTGTG TTGAGACCTA CGCCGACTAC CCCCCTCTTG 1250
GTCGATTCGC CGTCCGAGA 1269

2) INFORMATION FOR SEQ ID NO: 624

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 36801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

TCTGTCAAAT GGGACAAAAA CAGATTTGAA GAAATCATCA AGGAAACCTC 50
CAACTTCGTC AAGAAGGTTG GTTACAACCC AAAGACTGTT CCATTCGTTC 100
CAATCTCTGG TTGGAATGGT GACAACATGA TTGAACCATC CACCAACTGT 150
CCATGGTACA AGGGTTGGGA AAAGGAAACC AAATCCGGTA AAGTTACTGG 200
TAAGACCTTG TTAGAAGCTA TTGACGCTAT TGAACCACCA ACCAGACCAA 250
CCGACAAACC ATTGAGATTG CCATTGCAAG ATGTTTACAA GATCGGTGGT 300
ATTGGTACTG TGCCAGTCGG TAGAGTTGAA ACTGGTATCA TCAAAGCCGG 350
TATGGTTGTT ACTTTCGCCC CAGCTGGTGT TACCACTGAA GTCAAATCCG 400
TTGAAATGCA TCACGAACAA TTGGCTGAAG GTGTTCCAGG TGACAATGTT 450
GGTTTCAACG TTAAGAACGT TTCCGTTAAA GAAATTAGAA GAGGTAACGT 500
TTGTGGTGAC TCCAAGAACG ATCCACCAAA GGGTTGTGAC TCTTTCAATG 550
CCCAAGTCAT TGTTTTGAAC CATCCAGGTC AAATCTCTGC TGGTTACTCT 600
CCAGTCTTGG ATTGTCACCC TGCCCACATT GCTTGTAAAT TCGACACTTT 650
GGTTGAAAAG ATTGACAGAA GAACTGGTAA GAAATTGGAA GAAAATCCAA 700
AATTCGTCAA ATCCGGTGAT GCTGCTATCG TCAAGATGGT CCCAACCAAA 750
CCA 753

2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

CGTTGAAGAC ACGACCCAAA GTATCC 26

2) INFORMATION FOR SEQ ID NO: 626

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

TACCACCTTT TAAGTAAGGT GCTAAT 26

2) INFORMATION FOR SEQ ID NO: 627

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627

ATTGTCTATA AAAATGGCGA TAAGTC 26

2) INFORMATION FOR SEQ ID NO: 628

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628

AAAATGGCGA TAAGTCACAA AAAGTA 26

2) INFORMATION FOR SEQ ID NO: 629

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629

AAGTTCCATC TCAACAAGGT CAATA 25

2) INFORMATION FOR SEQ ID NO: 630

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630

CGGAGCTATC CTAGTCGTTT CA 22

2) INFORMATION FOR SEQ ID NO: 631

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631

CAGACCAACY GAIAARCCAT TRAGAT 26

2) INFORMATION FOR SEQ ID NO: 632

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632

CCCTTTGGTG GRTCSTKCTT GGA 23

2) INFORMATION FOR SEQ ID NO: 633

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633

CAGACCAACY GAIAARCCIT TRAGAT 26

2) INFORMATION FOR SEQ ID NO: 634

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRRCIATTGC YATGGA 26

2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

AAACCRGTIA RRGCRACTCT IGCTCT 26

2) INFORMATION FOR SEQ ID NO: 636

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

ACTGGYGTTG AIATGTTCCG YAA 23

2) INFORMATION FOR SEQ ID NO: 637

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

ACGTCAGTIG TACGGAARTA GAA 23

2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT 26

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTTCWACAC CWGTIACA 28

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA 23

2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

TGATAACCWA CIGCIGAIGG CATACG 26

2) INFORMATION FOR SEQ ID NO: 642

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642

GGCGTIGGIG ARCGIACICG TGA 23

2)INFORMATION FOR SEQ ID NO: 643

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643

ACTGGIGTIG ARATGTTCCG YAA 23

2)INFORMATION FOR SEQ ID NO: 644

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644

ACGTCIGTIG TICKGAARTA GAA 23

2)INFORMATION FOR SEQ ID NO: 645

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645

ACGTCIGTIG TICKGAARTA RAA 23

2) INFORMATION FOR SEQ ID NO: 646

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646

ATCGACAAGC CITTCYTIAT GSC 23

2) INFORMATION FOR SEQ ID NO: 647

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647

ACGTCCGTSG TRCGGAAGTA GAACTG 26

2) INFORMATION FOR SEQ ID NO: 648

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648

ACGTCSGTSG TRCGGAAGTA GAACTG 26

2) INFORMATION FOR SEQ ID NO: 649

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC 26

2) INFORMATION FOR SEQ ID NO: 650

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

TTACGGAACA TYTCAACACC IGT 23

2) INFORMATION FOR SEQ ID NO: 651

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

TGACGACCAC CITCYTCYTT YTTCA 25

2) INFORMATION FOR SEQ ID NO: 652

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

CCWAYAGTIY KICCICCYTC YCTIATA 27

2) INFORMATION FOR SEQ ID NO: 653

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT 20

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG 20

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA 20

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

AATTAATGGC TGCAGTTGAY GA 22

2) INFORMATION FOR SEQ ID NO: 657

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA 22

2) INFORMATION FOR SEQ ID NO: 658

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT 23

2) INFORMATION FOR SEQ ID NO: 659

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

GCTTTTTGIG TTTCWGGTTT RAT 23

2) INFORMATION FOR SEQ ID NO: 660

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

GTAGAATTGA GGACGGTAGT TAG 23

2) INFORMATION FOR SEQ ID NO: 661

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661

GTAGAAYTGT GGWCGATART TRT 23

2) INFORMATION FOR SEQ ID NO: 662

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC 50
GTGAGCACGT TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT 100
GCTCTGAACA AGTGCGACAT GGTTGATGAT GAGGAAATCA TCGAGCTCGT 150
CGAGATGGAG ATCCRTGAGC TGCTCGCTGA GCAGGATTAC GACGAAGAGG 200
CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG CGACGAGAAG 250
TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC 300
AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA 350
TCTTCACCAT CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT 400
GGCTCCCTGA AGGTCAACGA GGACGTCGAG ATCATCGGTA TCCGCGAGAA 450
KGCTACCACC ACCACCGTTA CCGGTATCGA GATGTTCCGT AAGCTTCTCG 500
ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG TGGCGTTAAG 550
CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC 600
CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG 650
GTGGCCGCCA CACCCCATTC TTCGACAACT ACCGCCCACA GTTCTACTTC 700
CGCACCACCG ACGTTACCGG TGTTGTGAAG CTTCCTGAGG GCACCGAGAT 750
GGTCATGCCT GGCGACAACG TCGACATGTC CGTCACCCTG ATCCAGCCTG 800
TCGCTATGGA TGAGGGCCTG CGCTTCGCTA TC 832

2) INFORMATION FOR SEQ ID NO: 663

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1192 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida catenulata*
(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA 50
CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA 100
CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT 150
ACCTTGGGCC GGATCATCAA CGTTGTCGGT GAGCCCATCG ACGAGCGTGG 200
TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT 250
TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT 300
GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG 350
TGGTGCCGGT GTCGGTAAGA CCGTGTTCAT CCAGGAGTTG ATTAACAACA 400
TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CGGTGAGCGT 450
ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT 500
CAACTTGGAG GGCGACTCCA AGGTGGCCTT GGTGTTCGGT CAGATGAACG 550
AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC 600
GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA 650
CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC 700
GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT 750
TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT 800
GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCCGCCA 850
CCACTTTCGC TCACTTGGAC GCCACCACCG TGTTGTCGCG TGGTATCTCC 900
GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGACTCCA AGTCGAGATT 950
GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG 1000
TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT 1050
TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC 1100
CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTCGCTGTC GCCGAGGTTT 1150
TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG 1192

2) INFORMATION FOR SEQ ID NO: 664

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

AAYATGATIA CIGGIGCIGC ICARATGGA 29

2) INFORMATION FOR SEQ ID NO: 665

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1377 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

ATGGGTAAAG AGAAGTCTCA CATTAACGTT GTCGTTATCG GTCATGTCGA 50
TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA 100
TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT 150
AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG 200
AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA 250
AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG 300
AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC 350
TGGTGGTGTC GGTGAATTCG AAGCCGGTAT CTCTAAGGAT GGTCAAACCA 400
GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT 450
GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA 500
AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA 550
AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT 600
GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTTGGGAAA AGGAAACCAA 650
GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG 700
AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT 750
GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC 800
CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTTGCCCCA GCTGGTGTTA 850
CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT 900
GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA 950
AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG 1000
GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA 1050
ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC 1100
TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA 1150
AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC 1200
AAGTTCGTTC CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC 1250
ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCG 1300
GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG 1350
GCTGCTCAAA AGGCTGCTAA GAAATAA 1377

2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1536 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from M12082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

ATGGTTTTGC CAAGACTATA TACTGCTACA TCCCGTGCTG CTTTTAAAGC 50
AGCCAAACAA TCCGCTCCGC TTCTATCCAC TTCGTGGAAA AGATGTATGG 100
CCTCAGCTGC TCAATCTACT CCAATCACCG GTAAAGTTAC CGCTGTCATT 150
GGTGCCATTG TTGACGTTCA TTTTGAACAA TCAGAGTTGC CCGCTATTTT 200

GAACGCTTTA GAAATTAAAA CACCTCAAGG TAAGTTGGTT TTGGAAGTTG 250
CTCAACATTT GGGTGAAAAC ACTGTCAGAA CCATTGCTAT GGATGGTACC 300
GAAGGTTTGG TCCGTGGTGA AAAGGTTCTT GACACTGGTG GCCCTATCTC 350
CGTCCCAGTT GGGAGAGAAA CTTTAGGGAG AATCATCAAC GTTATCGGTG 400
AACCTATTGA TGAAAGAGGT CCAATTAAGT CCAAACTAAG AAAGCCAATT 450
CACGCAGACC CTCCTAGTTT TGCAGAACAA TCTACTTCGG CTGAAATTTT 500
GGAAACAGGT ATCAAAGTCG TCGATCTATT AGCTCCTTAT GCCAGAGGTG 550
GTAAGATTGG TCTTTTCGGT GGTGCAGGTG TCGGTAAGAC TGTGTTCATT 600
CAAGAATTGA TTAACAATAT CGCCAAGGCC CATGGTGGTT TTTCCGTTTT 650
CGCCGGTGTT GGTGAAAGGA CCAGAGAGGG TAATGACTTG TACCGTGAAA 700
TGAAGGAAAC TGGAGTCATT AACTTGGAAG GTGAATCCAA GGTCGCCTTA 750
GTTTTCGGTC AAATGAACGA ACCTCCAGGA GCCAGAGCCA GAGTCGCTTT 800
AACTGGTTTG ACGATCGCTG AATATTTCAG AGATGAAGAA GGTCAAGACG 850
TCTTGTTGTT TATCGACAAT ATCTTTAGAT TTACTCAAGC TGGTTCAGAA 900
GTCTCTGCCC TTTTGGGTCG TATTCCATCT GCCGTCGGTT ATCAACCAAC 950
TTTGGCCACT GATATGGGTC TCTTACAAGA AAGAATTACC ACCACAAAGA 1000
AGGGTTCTGT CACTTCTGTG CAAGCCGTTT ATGTTCCAGC CGATGATTTA 1050
ACAGATCCGT CTCCGTCCAC ATCTTTTGCC CATTTGGACG CATCATCCGT 1100
CTTGTCAAGA GGTATTTCAG AATTAGGTAT TTACCCTGCA GTGGATCCAT 1150
TGGATTCTAA ATCAAGGTTA TTGGATGCCG CCGTTGTCGG TCAAGAACAT 1200
TATGACGTCG CCTCCAAGGT TCAAGAAACT TTACAGACCT ATAAATCTTT 1250
ACAAGATATC ATTGCTATTT TGGGTATGGA TGAATTGTCC GAACAAGATA 1300
AACTAACTGT CGAAAGGGCA AGAAAGATTC AAAGATTCTT ATCTCAACCA 1350
TTTGCTGTCG CCGAAGTCTT TACTGGTATC CCAGGTAAAT TAGTGAGATT 1400
AAAGGACACC GTTGCCTCGT TCAAAGCCGT TTTGGAAGGT AAATACGATA 1450
ATATACCAGA ACATGCTTTC TATATGGTTG GTGGTATTGA AGATGTTGTT 1500
CGTAAAGCTG AAAAGTTAGC CCGTGAAGCC AACTAG 1536

2) INFORMATION FOR SEQ ID NO: 667

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1293 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trypanosoma cruzi*
(B) STRAIN: Y

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

CGGAAGGCGT GCCGCCGGTG TTAACTGCTT TGGATGTGGT GGAAAAACTT 50
GGCCGTGACG AGCCCTTGAC ACTTGAAATT GTACAGCACT TGGACGCCCA 100
CACCGGCCGT TGCATTGCGA TGCAGACGAC AGATCTGCTT AAGCTGAAAT 150
CGAAGGTAGT CTCGAGTGGC GGGAACATTT CTGTGCCTGT GGGTCGGGAG 200
ACACTTGGCA GAATCTTCAA TGTGCTGGGC GATGCCATTG ACCAGCGCGG 250
CCATGTTGGA GAGAAGCAAC GCATGCCTAT TCACGCTGTG GCACCAAAGT 300
TGGCGGATCA GGCGGCAGAG GACACCATTC TCACAACGGG TATCAAGGTG 350
ATTGATCTGA TTTTGCCCTA CTGCAAGGGT GGGAAGATTG GTCTTTTTGG 400
TGGTGCTGGC GTGGGCAAGA CGGTTATTAT CATGGAACTT ATTAACAACG 450
TTGCCAAGGG CCATGGTGGG TTCTCCGTCT TTGCGGGTGT TGGTGAACGC 500
ACGCGTGAGG GGACGGATCT TTACCTGGAG ATGATGCAAT CCAAAGTTAT 550
TGACCTGAAG GGTGACTCGA AGTGTGTGTT GGTGTATGGT CAGATGAACG 600
AGCCTCCGGG TGCCCGTGCT CGTGTGGCGC AGTCTGCCTT GACAATGGCC 650
GAGTACTTCC GTGATGTGGA AGGGCAAGAC GTGTTGCTTT TTATCGACAA 700

```
CATTTTCCGC TTTACGCAGG CAAACTCTGA GGTGTCAGCG CTGTTGGGTC      750
GTATTCCCGC TGCCGTCGGC TACCAGCCTA CCCTTGCTGA GGATCTTGGG      800
CAGTTGCAGG AGCGCATTAC GTCCACGACA AAAGGTTCCA TTACCTCTGT      850
GCAGGCTGTG TACGTGCCAG CCGATGATAT TACCGACCCT GCGCCAGCAA      900
CGACCTTTTC CCACCTCGAT GCCACGACGG TGCTGGACCG TGCCGTTGCC      950
GAATCCGGCA TTTACCCCGC TGTCAACCCA CTGGAGTGTG CCTCGCGTAT     1000
CATGGACCCG GATGTAATCA GCGTTGACCA CTACAACGTG GCGCAGGATG     1050
TGGTGCAGAT GCTTACCAAG TACAAGGAGC TGCAGGATAT CATTGCGGTG     1100
CTTGGCATTG ATGAGCTCAG TGAGGAGGAT AAACTTATCG TGGACCGTGC     1150
GCGTAAGGTG ACAAAGTTTC TCTCCCAGCC TTTCCAGGTG GCGGAGGTGT     1200
TTACTGGCAT GACAGGCCAC TACGTGCAGC TGGAGGAGAC CATTGAGTCT     1250
TTTTCCGGCC TGTTGATGGG CACATATGAT CAGGTGCCGG AGA            1293
```

2) INFORMATION FOR SEQ ID NO: 668

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1191 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Corynebacterium glutamicum*
(C) ACCESSION NUMBER: X77034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

```
GTGGCAAAGG CGAAGTTCGA GCGTACCAAG CCCCACGTAA ACATCGGCAC       50
CATCGGTCAC GTTGACCACG GTAAGACCAC CACCACCGCG GCTATCACCA      100
AGGTTCTGGC TGACACTTAC CCTGAGCTCA ACGAGGCTTT CGCCTTCGAC      150
TCCATCGATA AGGCTCCTGA GGAGAAGGAG CGTGGCATCA CGATCAACAT      200
CTCCCACGTT GAGTACCAGA CTGAAAAGCG CCACTACGCA CACGTTGACG      250
CTCCAGGCCA CGCCGACTAC ATCAAGAACA TGATTACCGG CGCTGCTCAG      300
ATGGACGGCG CAATCCTCGT TGTTGCTGCT ACCGACGGCC CAATGCCTCA      350
GACCCGTGAG CACGTTCTTC TTGCTCGCCA GGTTGGCGTT CCTTACATCC      400
TCGTTGCTCT TAACAAGTGC GACATGGTTG AGGATGAGGA AATCATCGAG      450
CTCGTCGAGA TGGAAGTTCG TGAACTTCTT GCTGAGCAGG ACTACGACGA      500
AGAGGCTCCA ATTGTTCACA TCTCCGCTCT GAAGGCTCTT GAGGGCGACG      550
AGAAGTGGGG CAAGCAGATC CTTGAGCTCA TGCAGGCTTG CGATGACAAC      600
ATCCCTGACC CAGTTCGTGA GACCGACAAG CCATTCCTCA TGCCTATCGA      650
GGACATCTTC ACCATCACCG GTCGTGGCAC CGTTGTTACC GGTCGTGTTG      700
AGCGCGGTAC CCTGAACGTG AACGATGATG TTGACATCAT CGGCATCAAG      750
GAGAAGTCCA CCTCCACCAC CGTTACCGGT ATCGAGATGT TCCGTAAGCT      800
TCTTGACTCC GCTGAGGCTG GCGACAACTG TGGTCTGCTT CTCCGTGGTA      850
TCAAGCGCGA AGATGTTGAG CGTGGCCAGG TTATCGTTAA GCCAGGCGCT      900
TACACCCCTC ACACCGAGTT CGAGGGCTCT GTCTACGTTC TGTCCAAGGA      950
TGAAGGTGGC CGCCACACCC CATTCTTCGA CAACTACCGT CCTCAGTTCT     1000
ACTTCCGCAC CACCGACGTT ACCGGTGTTG TGAAGCTTCC AGAGGGCACC     1050
GAGATGGTCA TGCCTGGCGA CAACGTCGAC ATGTCCGTCA CCCTGATCCA     1100
GCCTGTCGCT ATGGACGAGG GCCTGCGTTT CGCTATCCGC GAAGGCTCCC     1150
GCACCGTTGG CGCTGGTCGT GTCACCAAGA TCATCAAGTA A              1191
```

2) INFORMATION FOR SEQ ID NO: 669

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: extracted from V00267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

```
ATGGCTACTG GAAAGATTGT CCAGGTAATC GGCGCCGTAG TTGACGTCGA      50
ATTCCCTCAG GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA     100
ATGGTAATGA GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT     150
ATCGTACGTA CCATCGCAAT GGGTTCCTCC GACGGTCTGC GTCGCGGTCT     200
GGATGTAAAA GACCTCGAAC ACCCGATTGA AGTCCCGGTA GGTAAAGCGA     250
CTCTGGGCCG TATCATGAAC GTACTGGGTG AACCGGTCGA CATGAAAGGC     300
GAGATCGGTG AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA     350
CGAAGAGCTG TCAAACTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA     400
TCGACCTGAT GTGTCCGTTC GCTAAGGGCG GTAAAGTTGG TCTGTTCGGT     450
GGTGCGGGTG TAGGTAAAAC CGTAAACATG ATGGAGCTCA TTCGTAACAT     500
CGCGATCGAG CACTCCGGTT ACTCTGTGTT TGCGGGCGTA GGTGAACGTA     550
CTCGTGAGGG TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC     600
GACAAAGTAT CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAAACCG     650
TCTGCGCGTT GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG     700
AAGGTCGTGA CGTTCTGCTG TTCGTTGACA ACATCTATCG TTACACCCTG     750
GCCGGTACGG AAGTATCCGC ACTGCTGGGC CGTATGCCTT CAGCGGTAGG     800
TTATCAGCCG ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAACGTATCA     850
CCTCCACCAA AACTGGTTCT ATCACCTCCG TACAGGCAGT ATACGTACCT     900
GCGGATGACT TGACTGACCC GTCTCCGGCA ACCACCTTTG CGCACCTTGA     950
CGCAACCGTG GTACTGAGCC GTCAGATCGC GTCTCTGGGT ATCTACCCGG    1000
CCGTTGACCC GCTGGACTCC ACCAGCCGTC AGCTGGACCC GCTGGTGGTT    1050
GGTCAGGAAC ACTACGACAC CGCGCGTGGC GTTCAGTCCA TCCTGCAACG    1100
TTATCAGGAA CTGAAAGACA TCATCGCCAT CCTGGGTATG GATGAACTGT    1150
CTGAAGAAGA CAAACTGGTG GTAGCGCGTG CTCGTAAGAT CCAGCGCTTC    1200
CTGTCCCAGC CGTTCTTCGT GGCAGAAGTA TTCACCGGTT CTCCGGGTAA    1250
ATACGTCTCC CTGAAAGACA CCATCCGTGG CTTTAAAGGC ATCATGGAAG    1300
GCGAATACGA TCACCTGCCG GAGCAGGCGT TCTACATGGT CGGTTCCATC    1350
GAAGAAGCTG TGGAAAAAGC CAAAAAACTT TAA                      1383
```

2) INFORMATION FOR SEQ ID NO: 670

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1410 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
(B) STRAIN: NCTC 11638
(C) ACCESSION NUMBER: extracted from AF004014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

```
ATGAAAGCGA TGGAAGGTAA AATCATTCAG GTTTTAGGCC CGGTGGTAGA      50
TGTGGAGTTT GAATCCTATC TGCCGGCGAT TTTTGAAGCA CTAGACATTA     100
ATTTTGAAGT TAATGGCGTT CAAAAATCTT TAGTTTTAGA GGTGGCAGCC     150
CATTTGGGTG GTAATCGGGT GCGAGCGATT GCTATGGATA TGACAGAAGG     200
CTTAGTGCGT AACCAAGCCG TCAAAGCTCG TGGCAAAATG ATTGAAGTGC     250
CTGTGGGCGA AGAAGTGTTA GGGCGTATTT TTAATGTTGT GGGCGAGAGC     300
ATTGATAATT TAGAGCCGCT TAAGCCGTCC TTAACTTGGC CCATTCACAG     350
AAAAGCCCCT AGTTTTGAGC AGCAAAGCAC TAAAACAGAA ATGTTTGAAA     400
CCGGTATTAA AGTCATTGAC TTGCTCGCGC CTTATTCTAA GGGCGGTAAA     450
GTAGGCTTGT TTGGTGGGGC TGGCGTAGGC AAAACGGTGA TCATTATGGA     500
GCTTATCCAC AATGTGGCTT ATAAGCATAA CGGGTATTCG GTGTTTGCAG     550
GTGTGGGGGA GCGCACCAGA GAAGGGAACG ATCTGTATTT TGAGATGAAA     600
GAAGGGGGCG TTTTAGACAA AGTTGCGTTG TGCTATGGGC AAATGAATGA     650
GCCACCAGGT GCAAGGAATC GCATCGCATT CACCGGCTTG ACGATGGCGG     700
AGTATTTCCG TGATGAAAAG GGCTTAGATG TGTTGATGTT TATTGATAAC     750
ATCTTTAGAT ACGCTCAAAG CGGTGCGGAA ATGAGCGCGC TATTAGGCCG     800
TATCCCTTCA GCGGTGGGGT ATCAGCCCAC GCTAGCCGGG GAAATGGGGA     850
AACTTCAAGA GCGTATCGCT TCCACTAAAA ATGGCTCTAT CACTTCGGTT     900
CAAGCGGTGT ATGTGCCAGC AGACGACTTG ACTGACCCAG CCCCTGCTTC     950
GGTGTTTGCG CATTTAGATG CGACTACGGT GTTGAATAGA AAGATCGCTG    1000
AAAAAGGGAT TTATCCGGCG GTGGATCCTT TGGATTCCAC TTCAAGGATT    1050
TTAAGCCCTC AAATGATTGG CGAGAAGCAC TATGAAATCG CCACCGGTAT    1100
CCAGCAAGTT TTGCAAAAAT ACAAGGATTT GCAAGATATT ATTGCGATTT    1150
TGGGATTGGA CGAATTGAGC GAAGAGGATA AAAAAACGGT TGAAAGGGCC    1200
AGAAAAATTG AGAAGTTTTT ATCCCAGCCG TTTTTTGTGG CTGAAGTGTT    1250
TACAGGAAGT CCCGGTAAGT ATGTGACTCT CCAAGAGACT TTAGAGGGCT    1300
TTGGAGGGAT TTTAGAGGGC AAATACGATC ACATTCCTGA AAACGCGTTT    1350
TACATGGTGG GCAGCATTCA AGAGGTTTTA GAAAAAGCTA AAAACATGAA    1400
AAATTCCTAA                                                1410
```

2) INFORMATION FOR SEQ ID NO: 671

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1401 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium acetobutylicum*
- (B) STRAIN: DSM 792
- (C) ACCESSION NUMBER: extracted from AF101055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

```
ATGCCAGAAC ATGTAGGTAA AATTGTTCAG GTAATAGGAC CTGTTGTGGA      50
TATTAAATTT GATGCAGAGA ACCTTCCTGA CATCTATAAT TCCATAGAAA     100
TAGATATGGG AGATAATAAA AAACTCATTG CTGAAGTTGA ACAACATGTA     150
GGAGATGACA TAGTAAGAAC AATAGCAATG GAAGGTACTG ACGGATTAAA     200
AAGAGGAATG GAAGCAGTTA ACACTGGTAA ACCAATATCT GTACCAGTTG     250
GAGAAAATGT TTTAGGACGT CTTTTTAATG TTTTAGGTCA GACAATAGAT     300
GAAGCAGGAG ACATGAATGC TGATAAGTAT TATCCAATTC ATAGACCAGC     350
TCCAACCTTT GAAGAACAAT CAGTTCAACC AGAAATGTTT GAAACAGGTA     400
TTAAGGTTAT AGATTTACTT GCTCCATATC AAAAGGGTGG AAAAATCGGT     450
```

```
TTGTTCGGTG GTGCCGGTGT TGGTAAAACA GTTCTTATTC AGCAACTTAT      500
AAATAATATA GCAAAAGAAC ACGGTGGATT ATCAGTATTC ACAGGTGTTG      550
GAGAAAGAAC AAGAGAAGGT AATGACCTTT ATTATGAAAT GAAAGATTCA      600
GGAGTTATAA ATAAAACAGC TCTAGTATTT GGTCAGATGA ATGAACCACC      650
TGGCGCTAGA ATGAGAGTTG CTTTAACAGG ACTTACAATG GCTGAATATT      700
TTAGAGACAA AGGTCAAGAT GTGCTTCTAT TTATAGATAA TATATTCAGA      750
TTTACACAAG CTGGTTCAGA GGTTTCAGCT TTACTTGGTA GAATACCTAG      800
TGCCGTTGGT TATCAGCCAA CACTTGCAAA TGAAATGGGT GCTCTTCAAG      850
AGAGAATAAC ATCAACAAAA CAGGGTTCAA TCACATCCGT TCAGGCTGTA      900
TATGTTCCTG CTGATGACCT TACAGACCCA GCTCCAGCAA CAACATTTAC      950
GCATCTTGAT GCAACAACAG TTCTTTCAAG AGAAATATCA AACTTAGGAA     1000
TATATCCTGC AGTTAGTCCT CTTGAATCAA CTTCAAGAAT ACTTGATCCA     1050
AGAATTGTTG GAGAAGAGCA TTATGAAGTT GCTAACAAGG TTAAACATAT     1100
ACTTGAAAGA TATCAAGAAC TTCAAGATAT CATAGCTATA CTTGGTGTTG     1150
ATGAACTTTC AGATGAGGAT AGATTGTTAG TTGGAAGAGC AAGAAGAGTA     1200
CAGAGATTCT TATCTCAAGC TTTTAGTGTT GCTGAACAAT TTACAGGAAT     1250
GAAAGGTCAG TTTGTACCTG TAAAAGATAC TATAAGAAGT TTTAAAGAAA     1300
TATTAGATGG TAAGTGTGAT GATCTTCCAG AAGCTGCATT TTTATTTGCA     1350
GGAACAATAG AAGATGTAAA AGAAAAAGCT AAAAAAATGA TGGAAAGCTA     1400
A                                                         1401
```

2) INFORMATION FOR SEQ ID NO: 672

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1509 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cytophaga lytica*
- (B) STRAIN: DSM 2039
- (C) ACCESSION NUMBER: M22535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

```
ATGTCTAAAG TTACAGGTAA AGTTTCCCAA ATTATTGGCC CAGTTATAGA       50
TGTGGAGTTC CAAGCAGGGG TAGATCTTCC AAAAATTTAT GATTCATTAG      100
AAATTAAAAA AGCAGATGGA TCAATTTTGG TTTTGGAAGT ACAATCACAC      150
ATTGGTGAGA ACACAGTAAG AACTATATCT ATGGATTCTT CTGATGGTTT      200
AAGTCGTGGA GCAGAGGTTA ATGCAACAGG AAGCGCTATA CAAATGCCAG      250
TTGGAGATGA CGTTTACGGA CGTTTATTTA ACGTAATTGG AGACGCTATT      300
GATGGTCTTG GGAATTTACC AAAATCTGGT AAAGATGGTT TGCCAATACA      350
CAGAGAGGCA CCAAAATTTG AAGACTTATC TACTTCTACA GAAGTATTAT      400
TTACAGGTAT TAAAGTAATT GACCTTATTG AGCCTTATGC AAAAGGTGGT      450
AAGATTGGTT TATTTGGAGG TGCCGGAGTA GGTAAAACAG TATTAATTCA      500
GGAATTAATT AACAACATTG CAAAAGGTCA CGGTGGACTT TCTGTATTTG      550
CTGGTGTAGG TGAGCGTACT CGTGAGGGTA ACGATTTACT ACGTGAGATG      600
TTAGAGTCTG GTATTATTAA ATACGGAGAT GACTTTATGC ACTCTATGGA      650
AGAAGGTGGT TGGGATTTAT CTAAAGTTGA TAAATCTGTA ATGAAAGATT      700
CTAAAGCAAC CTTTGTATTT GGACAAATGA ATGAGCCACC AGGAGCACGT      750
GCACGTGTTG CATTATCTGG TTTAACTATT GCAGAATATT TCCGTGATGG      800
AGCAGGTGAA GGTCAAGGTA AAGATGTACT TTTCTTTGTG GATAACATTT      850
TCCGTTTTAC ACAAGCTGGT TCTGAGGTAT CTGCATTACT TGGTCGTATG      900
CCATCTGCGG TAGGTTACCA ACCAACATTA GCAACAGAAA TGGGTGCTAT      950
GCAAGAGCGT ATTACATCAA CAAAAAGAGG TTCTATTACA TCTGTACAGG     1000
```

CGGTTTACGT ACCTGCGGAT GATTTAACGG ATCCAGCACC GGCAACTACC 1050
TTTGCTCACT TAGATGCAAC AACGGTATTG TCTCGTAAAA TTGCAGAGTT 1100
AGGTATTTAC CCAGCGGTAG ATCCATTAGA TTCTACTTCT AGAATCTTAG 1150
CTCCAGAAAT TTTAGGAAAA GATCACTACT CTTGTGCACA ACGTGTAAAA 1200
GAGTTGTTAC AACGTTATAA AGAATTACAA GATATTATTG CTATCCTTGG 1250
TATGGAAGAA TTATCTGAGG AAGATAAAAT GGCAGTTGGT AGAGCAAGAC 1300
GTGTACAACG TTTCTTATCT CAGCCTTTCC ACGTAGCAGA GCAATTTACA 1350
GGTCTTAAAG GTGTTTTAGT AGATATCAAG GATACTATTA AAGGATTTAA 1400
TATGATTATG GATGGTGAAT TAGATCACTT ACCAGAATCT GCATTTAACC 1450
TTAAAGGTAC TATTGAAGAA GCTATAGAAG CAGGAGAAAA AATGCTTGCT 1500
GAAGCATAA 1509

2) INFORMATION FOR SEQ ID NO: 673

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Ehrlichia risticii*
(B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

CCTAAAATAT ATGATGCATT ATATGTAAAA CTAGATAATG AAAATTTGTG 50
TTTAGAAGTT TCACAAATTA TTGGAGATAA TGTTGTTAGA TGTATTGCAA 100
TGGGAGCTAC TTATGGATTA AATCGTGGTT TAGAAGTAGT TTGTTCAGGA 150
AATCCAATTC AGGTTCCTGT AGGTGAACAA GTTTTAGGTA GAATGTTTAA 200
TGTTGTTGGT AAAACAATTG ACAATCTTGA ATCTTTAGAT GATAAAAATA 250
TAAAAATGAT GCCAATTCAT CGAAATCCAC CATCATTTGA AGAGCAATCC 300
AATGAAATTG AAATTTTTGA AACAGGCATT AAAGTTATTG ATTTATTAAT 350
TCCATATGCT AAAGGTGGTA AGATTGGATT ATTTGGTGGA GCAGGGGTTG 400
GGAAAACGGT TCTTGTTCAA GAATTAATTC ACAATATCGC AAAAGGTCAT 450
GGTGGTCTAT CTGTTTTTGC TGGAGTTGGT GAAAGAACTC GTGAAGGTAA 500
TGACTTGTAT TATGAAATGA TTGAAGGTGG AGTTATAGAT AAAACAGCCT 550
TAGTGTTTGG GCAAATGAAT GAACCTCCTG GCGCAAGAAT GCGCGTAGCA 600
TTAACTGCTT TAACAATGGC TGAATATTTC CGTGATGTTC AAAACCAAGA 650
TGTTTTGTTA TTTATTGATA ATATCTTTAG ATTTACACAA GCTGGTAGTG 700
AAGTTTCAGC ATTATTAGGA AGAATGCCAT CTGCTGTTGG TTATCAACCA 750
ACTTTGGCAT ATGAAATGGG ATTGTTACAA GAAAGAATCA CTTCCACTAA 800
AAGTGGTTCT ATAACATCT 819

2) INFORMATION FOR SEQ ID NO: 674

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 840 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Vibrio cholerae*
(B) STRAIN: ATCC 25870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

```
AGAGCGAAGT ACCAAGTGTT TACGATGCTC TGAATGTTGT GGATTCCAAA      50
GAACGTCTGG TTCTGGAAGT TCAACAGCAG CTAGGCGGTG GCGTGATTCG     100
CGCTATCGTT ATGGGTAGCT CGGATGGTTT ACGTCGTGGA ATGACAGTAC     150
AAAACACTGG CGCTCCAATT TCAGTACCAG TAGGTACTAA AACCCTAGGT     200
CGTATCATGA ACGTGCTTGG TGATGCGATT GACGAACGTG GCGACATTGG     250
CGCAGAAGAG GTGTACTCGA TTCACCGTCC TGCTCCAAGC TACGAAGAAC     300
AGTCTAGTGC AACTGAACTT TTGGAAACGG GTGTTAAGGT TATCGACCTG     350
ATCTGTCCGT TTGCGAAAGG CGGTAAAATC GGTCTGTTCG GTGGTGCGGG     400
TGTAGGTAAG ACCGTTAACA TGATGGAACT TATCAACAAC ATCGCGCTAC     450
AGCACTCAGG TTTGTCAGTA TTTGCTGGGG TAGGTGAGCG TACTCGTGAG     500
GGTAACGACT TCTACCACGA AATGCAGGAA GCGGGCGTTG TAAACGTTGA     550
ACAACCAGAA CTGTCGAAAG TAGCGATGGT TTACGGTCAG ATGAACGAGC     600
CACCAGGCAA CCGTCTGCGT GTAGCACTGA CTGGTCTGAC TATGGCGGAA     650
AAGTTCCGTG ATGAAGGCCG TGACGTACTG CTGTTTATCG ACAACATCTA     700
CCGTTACACC CTAGCGGGAA CGGAAGTATC TGCTCTGCTT GGCCGTATGC     750
CTTCAGCGGT AGGTTACCAA CCAACACTGG CTGAAGAGAT GGGTGTTCTG     800
CAAGAACGTA TCACGTCAAC CAAAAAAGGT TCTATCACCT               840
```

2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Vibrio cholerae*
(B) STRAIN: ATCC 25870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

```
CGGCGGTATC CTAGTTGTAG CGGCAACTGA CGGTCCAATG CCACAAACTC      50
GTGAGCACAT CCTGCTGGGT CGCCAAGTAG GTATTCCTTA CATCATCGTA     100
TTCATGAACA AGTGTGACAT GGTTGACGAT GAAGAGCTTC TAGAGCTGGT     150
AGAGATGGAA GTTCGTGAGC TGCTGTCTGA GTACGATTTC CCAGGTGATG     200
ACCTGCCAGT AATCCAAGGT TCAGCACTAG GCGCGCTAAA CGGCGAAGCA     250
CAGTGGGAAG CGAAGATTGT TGAGCTAGCA GAAGCACTGG ATACTTAYAT     300
TCCAGAGCCA GAGCGTGCAG TAGACATGGC ATTCCTGATG CCAATCGAAG     350
ACGTATTCTC AATCCAAGGT CGTGGTACAG TAGTAACTGG CCGTATCGAG     400
CGCGGCATCC TGAAAGTGGG TGACGAAGTA GCGATCGTTG GTATCAAAGA     450
GACAGTAAAA ACGACCTGTA CAGGTGTAGA GATGTTCCGT AAGCTGCTTG     500
ACGAAGGTCG TGCAGGTGAG AACGTAGGTG CACTRCTACG TGGTACTAAG     550
CGTGAAGAAG TAGAGCGTGG TCAAGTACTG GCGAAGCCAG GTTCAATCAC     600
ACCACACACT AAGTTCGAAT CAGAAGTATA CGTACTGTCA AAAGATGAAG     650
GTGGCCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC     700
CGTACAACTG ACGTAACAGG CAGCATTGAG CTACCAGARG GCGTAGAAAT     750
GGTAATGCCA GGCGACAACG TGAAGATGGT TGTAGACCTG ATTGCACCAA     800
TCGCGATGGA CGAAGGTCTA CGCTTCGC                             828
```

2) INFORMATION FOR SEQ ID NO: 676

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1298 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

```
CTTCTCGGAT GGCGTGCCGC CGGTGCTGAC GGCGCTGGAC GTGACGGAGG      50
AACTCGGGCG CGACGAGCCG CTGACGCTAG AGATCGTGCA ACACTTGGAC     100
GCGCACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TACTGAAGCT     150
GAAGTCGAAG GTCGTGTCGA CCGGCGGGAA CATCTCTGTG CCTGTGGGCC     200
GCGAGACGCT TGGCCGCATC TTCAACGTAC TGGGCGACGC GATTGACCAG     250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CGGAGGCGCC     300
GAAGCTGGCG GACCAGGCGG CGGAGGACAC GATCCTGACG ACCGGCATCA     350
AAGTGATCGA TCTGATCCTG CCGTACTGCA AGGGCGGCAA GATCGGTCTG     400
TTCGGCGGTG CCGGTGTGGG GAAGACTGTG ATCATCATGG AGCTGATCAA     450
CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTCGCC GGCGTTGGGG     500
AGCGCACCCG CGAGGGGACG GATCTGTACC TGGAGATGAT GCAATCGAAG     550
GTGATCGACC TGAAAGGTGA GTCGAAGTGT GTGCTTGTGT ACGGGCAGAT     600
GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA     650
TGGCCGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC     700
GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CAGCGCTGCT     750
GGGCCGCATC CCCGCCGCTG TGGGCTACCA ACCGACGCTT GCGGAGGATC     800
TCGGCATGTT GCAGGAGCGC ATCACGTCGA CGACGAAGGG GTCGATCACG     850
TCTGTGCAGG CGGTGTACGT GCCTGCGGAT GATATCACGG ATCCCGCGCC     900
GGCGACGACA TTCTCGCACC TGGACGCGAC GACGGTGCTG GACCGCGCGG     950
TGGCGGAGTC TGGCATCTAC CCCGCGGTCA ACCCACTGGA GTGCGCGTCG    1000
CGTATCATGG ACCCTGATGT GATCGACGTG GATCACTACA ACGTTGCGCA    1050
GGACATTGTT CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG    1100
CGGTGCTTGG TATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC    1150
CGTGCGCGCA AGGTGACCCG GTTCCTGTCA CAGCCGTTCC AGGTTGCGGA    1200
GGTGTTTACT GGCATGACAG GCCATTACGT ACAGCTGAGC GACACGGTGG    1250
AGTCGTTCTC CGGTTTGCTG ATGGGGTCGT ACGACCAGAT TCCGGAGA      1298
```

2) INFORMATION FOR SEQ ID NO: 677

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1083 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Babesia microtti*
(B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

```
CAAGCTCAAG TCTGAGCGTG AGAGAGGTAT TACTATTGAC ATTACTCTCT      50
GGAAATTTGA GACCCAGAAA TACGAGTACA CTGTCATAGA CGCACCTGGT     100
CATCGTGACT TTATCAAAAA TATGATTACT GGGACTTCAC AAGCCGACGT     150
TGCTATGCTT GTCGTTCCTG CTGAATCTGG CGGATTCGAG GCTGCTTTTT     200
CCAAAGAAGG TCAGACCCGT GAACACGCCT TACTAGCCTT CACACTTGGC     250
GTCAAACAGA TGATTGTTGC TATTAACAAA ATGGATTCTT GTCAGTACAA     300
GGAGGATCGT TATATGGAAA TTTTCAAGGA AGTACAGCAG TACTTGAAGA     350
AGGTGGGTTA CAAAGTTGAA AGCGTGCCGT TTGTTGCTAT TTCAGGATTC     400
CACGGTGACA ACATGGTTGA AAAATCTACT AACATGCCTT GGTATAAGGG     450
TAAGACCCTC GTAGAGGCAC TTGATCAAAT GGAGCCTCCA AAACGTCCGG     500
TCGAAAAACC TCTTAGATTG CCCCTGCAGT CAGTCTATAA AATTGGAGGT     550
ATTGGTACGG TACCAGTCGG AAGGGTCGAA ACAGGACAAC TGAAAGCAGG     600
AATGATCATT ACTTTTGCCC CCACTGGTTT GACCACTGAA TGTAAATCTG     650
TTGAAATGCA TCACGAGGTT GTGGAAGTGG CTAGCCCCGG TGATAACGTT     700
GGATTTAATG TCAAGAATGT GTCTGTTAAG GATATTAAGA GAGGAAATGT     750
GGCTTCGGAT TCGAAAAATG ACCCAGCCAA GGAAGCTACC TCTTTCTCTG     800
CACAAGTCAT TGTACTCAAT CACCCTGGTA CCATCAAGGC CGGTTACTCA     850
CCTGTGGTTG ATTGCCATAC TGCCCACATT GCTTGCAAAT TCGAATCTCT     900
AGACACTAGG ATTGACAAGC GTACTGGCAA GACTTTGGAA GAAAATCCTA     950
AGACTATTAA GAATGGTGAC GCTGCCATGG TGACTATGAA ACCAAATAAA    1000
CCCATGGTTG TGGAAACTTT CACCGACTAC GCCCCGTTGG GCCGGTTCGC    1050
CGTGCGTGAT ATGCGCCAAA CCGTTGCCGT CGG                      1083
```

2) INFORMATION FOR SEQ ID NO: 678

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptococcus neoformans*
(B) STRAIN: Lev-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

```
TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCT CACGGTGGTT      50
ACTCTGTCTT CACTGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG     100
TACCACGAAA TGAGGGAGAC TGGTGTTATC AACCTTGAGG GTGACTCCAA     150
GGTCGCTCTT GGTGAGTTCT TTTTTTTCTT CAGGCTAATT AGTCGATGAC     200
GTGGGCCCTG ACTAAAACTG TTTCTTCCAG TCTTCGGTCA GATGAACGAG     250
CCCCCTGGAG CCCGTGCCCG AGTTGCCCTT ACTGGTTTGA CCATTGCCGA     300
GTACTTCCGT GACGAGGAAG GCCAGGATGT GTTGCTTTTC ATTGACAACA     350
TTTTCCGATT CACCCAGGCC GGTTCCGAGG TGTCTGCCTT GCTCGGTCGT     400
ATCCCCTCTG CCGTCGGTTA CCAGCCCACT CTTTCCACCG ACATGGGTGG     450
TATGCAGGAG CGAATGTAGG TTGCATTCTC TGTGATTTTA CGGCAAGCCT     500
TGACTTTTTT TTTCTAGTAC CACCACCAAG AAGGGTTCCA TTACCTCCGT     550
C                                                         551
```

2) INFORMATION FOR SEQ ID NO: 679

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 552 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptococcus neoformans*
(B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT 50
ACTCCGTCTT CACCGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG 100
TACCACGAAA TGAGGGAGAC TGGTGTTATC AACCTTGAGG GTGACTCCAA 150
GGTCGCTCTT GGTGAGTTCT TTTTTTTGGG AGCTAATTAG TCGATGACGT 200
GGGCCCTGAC CAAAACCGTT TCTTTCAGTC TTCGGTCAGA TGAACGAGCC 250
CCCTGGAGCC CGTGCCCGAG TTGCTCTTAC TGGTTTGACC ATTGCCGAGT 300
ACTTCCGTGA CGAGGAAGGC CAGGATGTGT TGCTTTTCAT TGACAACATT 350
TTCCGATTCA CCCAGGCCGG TTCCGAGGTG TCTGCCTTGC TCGGTCGTAT 400
CCCCTCTGCC GTCGGTTACC AGCCCACTCT TTCCACCGAT ATGGGTGGTA 450
TGCAAGAGCG AATGTAAGTT GCATTTTTTG TGATTTTACG GCAAGTCTTG 500
ACTTACATTT TTTTCTAGCA CCACCACCAA GAAGGGTTCC ATTACCTCCG 550
TC 552

2) INFORMATION FOR SEQ ID NO: 680

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1018 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cunninghamella bertholletiae*
(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

TCTCCCTGCT ATTTTAAACG CTCTTGAAGT TAAGGATCAT GCTGGTGGTC 50
GTCTTGTTCT TGAAGTTGCT CAACACTTGG GTGAAAACAC TGTACGTACT 100
ATTGCTATGG ATGGTACTGA AGGTAAGTTT ATTTTTAGAT GATCATAAAT 150
AATTGATCAT AATGATAAAA AAAAAAGAAG AAGAAGAACA GGATGTATAT 200
AATGGTTAAT AAATAATATT TTCATATTGK ATATAACTAT TTAATCTGTT 250
TTTTTTTCTT CATGATTATA TATATATATG TMCTAATATC TAATATGAAC 300
CTTTTTTATA AAATTAATCA GGTCTTGTCC GTGGTCAAAA GGTTGTTGAT 350
ACTGGTGCTC CTATTACCAT TCCTGTTGGT AAGGAAGTTC TTGGTCGTAT 400
CATCAACGTT ATTGGTGAAC CCATTGATGA ACGTGGTCCT ATTAAGGCCA 450
AGTCTCACCG TGCTATTCAC GCTGAAGCTC CAGAATTCGT TGATCAATCT 500
CCTACTCCCG AAATTCTTGA AACTGGTATT AAGGTTGTCG ATTTATTAGC 550
TCCTTATGCT CGTGGTGGTA AGATTGGTCT TTTCGGTGGT GCTGGTGTAG 600
GTAAAACTGT CTTGATTCAA GAACTTATTA ACAACATTGC TAAAGCCCAT 650
GGTGGTTACT CTATTTTCTG TGGTGTTGGT GAACGTACTC GTGAAGGTAA 700

CGATTTATAC CACGAAATGA TGGAAACTGG TGTCATTAAA CTTGAAGGTG 750
ACTCCAAGTG TGCTCTTGTA TTCGGTCAAA TGAACGAACC TCCTGGTGCT 800
CGTGCCCGTG TTGCTTTAAC TGGTTTAACC ATTGCTGAAT ACTTCCGTGA 850
TGAAGAAGGT CAAGATGTGT TACTTTTCAT TGATAACATT TTCCGTTTCA 900
CTCAAGCTGG TTCTGAAGTA TCTGCCCTTT TAGGTCGTAT TCCATCTGCT 950
GTAGGTTACC AACCCACTTT ATCTACTGAT ATGGGTGGTA TGCAAGAACG 1000
TATTACTACT ACCAAGAA 1018

2) INFORMATION FOR SEQ ID NO: 681

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC 23

2) INFORMATION FOR SEQ ID NO: 682

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC 26

2) INFORMATION FOR SEQ ID NO: 683

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

GTIACIGGIT CISWIAWRTC ICCICC 26

2) INFORMATION FOR SEQ ID NO: 684

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3267 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida tropicalis*
(C) ACCESSION NUMBER: M64984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

ATGGCTGGTG CTTTAGAAAA CGCAAGAAAA GAAATTAAAC GTCTTTCATT 50
AGATGACACC AATGAATCCC AATATGGTCA AATCTATTCT GTTTCCGGTC 100
CGGTTGTTAT TGCCGAAAAC ATGATTGGAT GTGCCATGTA CGAATTGGTT 150
AAAGTTGGTC ATGATAATTT AGTTGGGGAA GTTATTAGAA TTAATGGTGA 200
TAAAGCAACC ATTCAAGTTT ATGAAGAAAC TGCAGGGGTC ACTGTTGGTG 250
ATCCAGTTTT AAGAACTGGT AAACCATTAT CTGTTGAATT AGGTCCTGGT 300
TTAATGGAAA CTATTTATGA TGGTATTCAA AGACCTTTAA AAGCCATTAA 350
AGATGAATCC CAATCTATTT ATATCCCAAG AGGTATTGAT GTTCCTGCTT 400
TATCAAGAAC TGTTCAATAT GATTTCACTC CAGGTCAATT GAAAGTTGGT 450
GATCATATCA CTGGTGGGGA CATTTTTGGT TCTATTTATG AAAACTCTTT 500
ATTGGATGAC CATAAGATTT TGTTACCTCC AAGAGCAAGA GGTACTATTA 550
CTTCTATTGC TGAAGCCGGT TCTTATAATG TTGAAGAACC AGTTTTGGAA 600
GTTGAATTTG ATGGTAAGAA ACATAAATAC TCTATGATGC ATACATGGCC 650
AGTTAGAGTT CCAAGACCAG TTGCTGAAAA ATTGACTGCT GATCATCCAT 700
TGTTGACCGG TCAAAGAGTC TTGGATTCTT TATTCCCATG TGTTCAAGGT 750
GGTACTACTT GTATCCCAGG GGCTTTTGGT TGTGGTAAAA CTGTTATTTC 800
TCAATCTTTG TCCAAATTCT CCAACTCTGA TGTTATTATC TATGTTGGTT 850
GTTTCACTAA AGGTACTCAA GTCATGATGG CTGATGGTGC CGACAAATCT 900
ATTGAATCTA TTGAAGTTGG TGACAAAGTC ATGGGTAAAG ATGGTATGCC 950
AAGAGAAGTT GTTGGCTTAC CAAGAGGTTA TGATGATATG TACAAGGTTC 1000
GTCAACTTTC TAGTACTAGA CGTAATGCTA AATCCGAAGG CTTGATGGAT 1050
TTCACTGTTT CTGCTGATCA TAAACTTATC TTGAAAACTA AACAAGATGT 1100
CAAGATTGCT ACACGTAAAA TTGGTGGCAA CACCTATACT GGTGTTACTT 1150
TCTATGTTTT GGAAAAGACT AAGACTGGTA TTGAATTAGT TAAAGCCAAG 1200
ACTAAAGTTT TCGGTCATCA TATCCATGGT CAAAATGGCG CTGAAGAAAA 1250
AGCTGCTACT TTTGCTGCTG GCATTGACTC TAAAGAATAC ATTGATTGGA 1300
TCATTGAAGC TAGAGATTAT GTACAAGTTG ATGAAATTGT CAAGACCAGC 1350
ACCACTCAAA TGATCAACCC AGTTCATTTT GAATCTGGTA AACTCGGTAA 1400
CTGGTTACAC GAACACAAGC AAAACAAATC ACTTGCTCCA CAATTGGGTT 1450
ACTTGTTGGG TACTTGGGCT GGTATTGGAA ATGTTAAATC TTCTGCTTTC 1500
ACCATGAACT CCAAAGATGA TGTTAAATTA GCTACAAGAA TTATGAACTA 1550
CTCTTCAAAA TTGGGCATGA CTTGTTCTTC TACTGAATCC GGTGAACTCA 1600
ATGTCGCTGA AAACGAAGAA GAATTTTTCA ATAACCTTGG TGCTGAAAAG 1650
GATGAAGCTG GTGATTTCAC TTTTGATGAA TTTACCGATG CTATGGATGA 1700
ATTGACTATC AATGTTCATG GTGCAGCTGC AAGCAAGAAG AACAATTTGT 1750
TGTGGAATGC TTTGAAATCT CTTGGTTTCA GAGCCAAGTC TACTGATATT 1800
GTCAAGAGTA TTCCTCAACA TATTGCTGTT GATGATATTG TTGTCAGAGA 1850
ATCTTTGATT GCCGGTTTAG TTGATGCTGC TGGTAATGTT GAAACCAAAT 1900
CCAATGGTTC TATTGAAGCT GTTGTTAGAA CTTCTTTCAG ACATGTCGCT 1950
AGAGGTCTTG TCAAGATTGC TCATTCTTTG GGTATTGAAT CATCTATTAA 2000
TATTAAAGAT ACTCACATTG ATGCTGCTGG TGTTAGACAA GAATTTGCTT 2050
GTATTGTCAA TTTGACTGGT GCTCCACTTG CTGGTGTTCT TTCTAAATGT 2100
GCACTTGCAA GAAACCAAAC TCCAGTTGTC AAATTTACCA GAGACCCAGT 2150
TTTGTTCAAC TTTGATTTGA TCAAATCTGC AAAAGAAAAC TATTATGGTA 2200
TTACTTTGGC TGAAGAAACT GATCATCAAT TCCTTTTATC CAACATGGCC 2250
TTGGTGCACA ACTGTGGTGA ACGTGGTAAT GAGATGGCTG AAGTTTTGAT 2300

GGAATTCCCA GAATTGTTTA CTGAAATTTC TGGTAGAAAA GAACCAATTA 2350
TGAAACGTAC CACTTTGGTT GCCAATACTT CTAATATGCC AGTCGCTGCC 2400
AGAGAAGCTT CTATTTATAC TGGTATTACA TTGGCTGAAT ATTTCAGAGA 2450
TCAAGGTAAG AATGTTTCTA TGATTGCTGA TTCTTCTTCA CGTTGGGCTG 2500
AAGCTTTGAG AGAAATTTCT GGTAGATTGG GTGAAATGCC TGCTGATCAA 2550
GGTTTCCCAG CTTATTTGGG TGCTAAATTG GCTTCTTTCT ATGAGCGTGC 2600
CGGTAAAGCC ACTGCTTTGG GTTCACCAGA TAGAGTTGGT TCAGTTTCTA 2650
TTGTTGCTGC TGTTTCTCCA GCTGGTGGTG ATTTCTCTGA TCCAGTTACT 2700
ACTTCTACTT TGGGTATTAC TCAAGTTTTC TGGGGGTTGG ATAAGAAATT 2750
GGCCCAAAGA AAACATTTCC CATCTATTAA CACCAGTGTT TCTTATTCTA 2800
AATACACCAA TGTTTTGAAC AAATACTATG ATTCCAACTA TCCAGAATTC 2850
CCACAATTGA GAGACAAAAT TAGAGAAATT TTATCTAATG CTGAAGAATT 2900
GGAACAAGTT GTTCAATTAG TTGGTAAATC TGCATTGTCT GATTCTGATA 2950
AGATTACTTT AGATGTTGCT ACCTTGATTA AAGAAGATTT CTTGCAACAA 3000
AATGGTTATT CTTCATATGA TGCATTCTGT CCAATTTGGA AGACTTTTGA 3050
TATGATGAGA GCATTTATTT CATATTATGA TGAAGCACAA AAAGCAATTG 3100
CCAATGGTGC TCAATGGTCT AAATTAGCTG AAAGTACTAG TGATGTTAAA 3150
CATGCTGTTT CTTCAGCTAA ATTCTTTGAA CCATCAAGAG GTCAAAAAGA 3200
AGGTGAAAAA GAATTTGGAG ATTTATTAAC CACTATCTCC GAAAGATTTG 3250
CTGAAGCTTC AGAATAA 3267

2) INFORMATION FOR SEQ ID NO: 685

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1782 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus hirae*
(B) STRAIN: ATCC 9790
(C) ACCESSION NUMBER: D17462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

TTGCAAATTG GAAAAATCAT AAAAGTCTCC GGTCCTCTCG TTATGGCAGA 50
AAATATGTCA GAAGCAAGTA TTCAAGACAT GTGTTTAGTG GGAGATTTAG 100
GAGTCATCGG CGAAATCATT GAGATGCGTC AAGATGTGGC GTCTATTCAA 150
GTATATGAAG AAACTTCAGG AATTGGTCCC GGAGAACCTG TTCGTTCCAC 200
TGGGGAAGCA CTATCTGTTG AGCTAGGACC AGGAATCATT TCACAAATGT 250
TTGACGGGAT TCAAAGACCA CTGGATACAT TTATGGAAGT GACTCAAAGT 300
AACTTCTTAG GACGTGGGGT CCAATTACCA GCTTTAGATC ATGAGAAACA 350
ATGGTGGTTT GAAGCGACAA TCGAAGAAGG AACAGAAGTA AGTGCTGGAG 400
ACATCATTGG GTACGTGGAT GAAACGAAGA TCATTCAGCA CAAAATCATG 450
GTCCCTAATG GTATCAAAGG AACTGTACAA AAAATTGAAT CTGGATCATT 500
TACGATCGAT GATCCGATTT GTGTGATCGA AACGGAACAA GGCTTAAAAG 550
AGCTGACGAT GATGCAAAAA TGGCCAGTAC GTCGTGGTCG ACCAATCAAA 600
CAAAAATTAA ATCCAGATGT ACCGATGATC ACCGGTCAAA GGGTCATTGA 650
CACGTTTTTC CCAGTAACTA AAGGAGGAGC GGCAGCCGTT CCAGGTCCGT 700
TTGGTGCAGG GAAGACAGTT GTGCAACACC AGATTGCTAA GTGGTCGGAC 750
GTAGATCTAG TGGTTTACGT TGGTTGTGGG GAACGAGGAA ATGAAATGAC 800
GGATGTCGTC AATGAATTTC CTGAACTGAT CGATCCAAAT ACAGGCGAGT 850
CTTTGATGGA ACGAACTGTG TTGATCGCTA ATACATCGAA CATGCCAGTA 900
GCTGCTCGAG AAGCTTCTAT TTATACGGGA ATCACGATTG CCGAGTACTT 950
CCGTGACATG GGGTATGATG TAGCAATCAT GGCAGATTCC ACTTCTCGTT 1000

GGGCAGAAGC ACTGCGTGAA ATGAGCGGAC GTTTAGAAGA AATGCCTGGT 1050
GATGAAGGTT ATCCCGCTTA TCTGGGCTCT CGTCTAGCTG AATACTATGA 1100
ACGTTCAGGA CGTGTCATTG CTCTAGGCTC TGACCAACGT GAGGGCAGTA 1150
TCACTGCCAT CAGTGCGGTT TCTCCTTCTG GTGGAGATAT CTCTGAACCA 1200
GTGACTCAAA ATACCTTACG TGTGGTGAAG GTTTTCTGGG GATTAGATTC 1250
TAGTCTTGCT CAAAAAAGAC ATTTTCCATC GATTAACTGG ATCCAAAGTT 1300
ACTCATTATA TTCAACAGAA GTTGGCAGAT ATATGGATCA AATCTTACAA 1350
CAGGATTGGT CTGATATGGT AACTGAAGGC ATGCGGATCT TGCAAGAAGA 1400
AGAACAATTA AATGAAATCG TGCGCTTGGT AGGGATCGAT TCGCTTTCTG 1450
ATAACGATCG CTTGACCCTT GAAGTAGCAA AATCGATTCG AGAAGACTAT 1500
TTACAACAAA ATGCTTTTGA TGATGTAGAT ACGTTTACTT CAAGAGAAAA 1550
ACAATTCAAC ATGTTGAAAG TTATTTTGAC TTTTGGGAAA GAAGCTCGAA 1600
AAGCCTTATC GTTGGGAGCG TACTTCAATG AAATCATGGA AGGTACAGTA 1650
GCGGTCAGAG AACGCATTAG TCGGAGCAAG TATATTCCAG AAGAAGAGTT 1700
AGCCAAAATT AGTAGTATAA ATGAAGAAAT CAAAGAAACG ATCCAATTGA 1750
TTGTTTCAGA AGGAGGGATG ACCGATGATT AA 1782

2) INFORMATION FOR SEQ ID NO: 686

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1781 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydia pneumoniae*
(B) STRAIN: CWL 029
(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

CAGGGACATG TTATAGAAGC TTATGGAAAC TTGTTACGTG TACGCTTTGA 50
CGGATATGTT AGACAAGGTG AAGTTGCATA TGTCAACGTA GATAATACCT 100
GGTTAAAAGC AGAAGTGATT GAAGTTGCTG ATCAAGAAGT CAAGGTTCAG 150
GTATTTGAAG ATACACAAGG CGCGTGTCGA GGAGCTCTTG TTACGTTTTC 200
AGGACATCTT TTAGAAGCCG AGTTAGGGCC TGGCTTGCTT CAGGGCATTT 250
TCGATGGACT TCAAAATCGT CTTGAGGTGC TAGCTGAAGA TAGTTCTTTC 300
TTGCAGAGAG GCAAGCATGT TAATGCTATT TCTGATCATA ATTTATGGAA 350
TTATACTCCC GTAGCTTCTG TTGGGGATAC TTTAAGACGA GGAGATCTTC 400
TAGGAACAGT ACCTGAAGGA CGATTTACTC ATAAGATTAT GGTTCCTTTT 450
TCTTGCTTTC AAGAGGTTAC CCTGACTTGG GTAATTTCTG AAGGAACCTA 500
TAATGCTCAT ACTGTGGTCG CAAAAGCTCG AGATGCTCAG GGTAAAGAAT 550
GTGCCTTTAC TATGGTGCAA AGATGGCCGA TCAAACAAGC TTTTATTGAA 600
GGAGAGAAGA TCCCTGCGCA TAAGATTATG GATGTGGGTT TGCGAATCTT 650
AGATACGCAA ATTCCAGTAT TGAAGGGGGG AACTTTCTGT ACCCCAGGAC 700
CTTTTGGTGC AGGGAAAACA GTCTTACAAC ACCATCTTTC TAAGTACGCT 750
GCTGTAGATA TTGTGATTTT GTGTGCGTGC GGAGAGCGTG CTGGTGAAGT 800
TGTTGAGGTA TTACAAGAGT TCCCTCATCT TATCGACCCC CATACCGGAA 850
AGTCTTTAAT GCACAGAACA TGTATTATTT GTAACACATC ATCCATGCCT 900
GTGGCTGCCC GAGAGTCTTC GATCTATTTA GGAGTGACGA TTGCAGAATA 950
CTATCGCCAG ATGGGACTAG ATATTCTGCT TTTAGCTGAT TCTACATCCC 1000
GATGGGCACA AGCCCTTAGA GAGATTTCGG GACGTCTTGA AGAAATCCCT 1050
GGAGAGGAAG CATTTCCTGC ATACCTGTCT TCTAGAATAG CTGCTTTTTA 1100
TGAGCGAGGA GGAGCTATCA CCACGAAAGA TGGTTCTGAA GGATCTTTAA 1150
CTATATGTGG TGCGGTGTCT CCTGCAGGAG GAAACTTTGA AGAACCAGTC 1200

ACTCAATCTA CATTAGCTGT AGTCGGAGCG TTCTGTGGTC TTTCAAAAGC 1250
ACGAGCTGAC GCACGTAGGT ATCCTTCAAT AGACCCTTTG ATTTCTTGGT 1300
CAAAATATTT GAACCAGGTA GGACAAATTT TAGAAGAGAA GGTTTCAGGC 1350
TGGGGTGGTG CTGTGAAAAA AGCAGCACAG TTTCTAGAGA AAGGTTCAGA 1400
AATCGGCAAG CGTATGGAAG TTGTCAGTGA AGAAGGGGTT TCTATGGAAG 1450
ACATGGAAAT CTACTTAAAG GCAGAACTTT ATGATTTTTG TkATCTCCAG 1500
CAGAACGCAT TCGATCCTGT GGACTGTTAT TGTCCTTTTG AGAGACAGAT 1550
AGAGTTATTT TCATTAATCA GTCGTATTTT TGATGCTAAA TTTGTTTTTG 1600
ATAGTCCTGA TGATGCAAGA AGCTTTTTCC TTGAGCTGCA GAGCAAGATT 1650
AAGACATTAA ATGGCCTGAA ATTTCTTTCA GAGGAATATC ATGAGAGTAA 1700
AGAGGTCATA GTTAGACTGT TGGAAAAAAC AATGGTACAA ATGGCGTAAG 1750
GATATGCAAA CAATCTACAC AAAAATAACT G 1781

2) INFORMATION FOR SEQ ID NO: 687

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1758 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Halobacterium salinarum*
(C) ACCESSION NUMBER: S56356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

ATGAGTCAAG CTGAAGCAAT CACTGACACC GGCGAAATCG AGAGCGTGAG 50
CGGTCCGGTC GTGACCGCCA CGGGCCTCGA CGCGCAGATG AACGACGTCG 100
TCTACGTGGG CGACGAGGGT CTGATGGGCG AGGTCATCGA GATCGAAGGC 150
GACGTAACCA CCATCCAGGT CTACGAGGAG ACGTCCGGCA TCGGGCCGGG 200
CCAGCCCGTC GACAACACGG GCGAACCGCT CACCGTGGAC CTGGGCCCGG 250
GGATGCTGGA CTCCATCTAC GATGGTGTGC AGCGTCCACT GGACGTCCTC 300
GAAGACGAGA TGGGGGCGTT CCTCGATCGC GGTGTTGACG CACCCGGCAT 350
CGACCTCGAC ACCGACTGGG AGTTCGAGCC CACCGTCGAG GCGGGCGACG 400
AGGTCGCGGC CGGCGATGTC GTCGGCACCG TCGACGAAAC GGTCAGCATC 450
GAACACAAGG TTCTGGTGCC CCCCCGCAGT GACGGCGGCG AAGTCGTCGC 500
CGTCGAATCC GGCACGTTCA CCGTCGACGA CACGGTCGTC GAGTTGGACA 550
CCGGCGAGGA GATCCAGATG CACCAGGAGT GGCCGGTCCG CCGCCAGCGC 600
CCCACCGTCG ACAAGCAGAC GCCGACGGAG CCGCTGGTGT CCGGCCAGCG 650
CATCCTCGAC GGCCTGTTCC CGATCGCGAA AGGCGGGACG GCCGCGATCC 700
CGGGGCCGTT CGGGTCCGGG AAGACGGTCA CCCAGCAGTC CCTCGCGAAG 750
TTCGCCGACG CGGACATCGT TGTCTACATC GGCTGTGGTG AGCGCGGCAA 800
CGAGATGACG GAAGTCATCG AGGACTTCCC GGAGCTGCCC GACCCCCAGA 850
CCGGGAACCC GCTGATGGCC CGCACCACGC TCATCGCGAA CACGTCGAAC 900
ATGCCGGTTG CCGGGCGTGA GTCCTGCATT TACACGGGAA TCACCATCGC 950
GGAGTACTAC CGCGACATGG GCTACGACGT GGCGCTGATG GCCGACTCCA 1000
CCTCGCGGTG GGCGGAGGCC ATGCGGGAGA TCTCCTCGCG ACTCGAGGAG 1050
ATGCCCGGCG AGGAGGGGTA TCCCGCGTAC CTGGCCGCCC GCCTCTCGGA 1100
GTTCTACGAG CGCGCCGGCT ACTTCGAGAA CTTCAACGGG ACCGAGGGCT 1150
CCATCTCGGT CATCGGTGCG GTGTCGCCGC CCGGCGGGGA CTTCTCCGAG 1200
CCGGTCACCC AGAACACGCT GCGCATCGTG AAGACGTTCT GGGCGCTTGA 1250
CTCGGACCTC GCCGAGCGCC GGCACTTCCC GGCGATCAAC TGGGACGAGT 1300
CCTACAGCCT CTACAAGGAC CAACTCGACC CGTGGTTCAC GGACAACGTC 1350
GTCGACGACT GGGCCGAGCA GCGCCAGTCG GCGGTCGACA TCCTCGACGA 1400
GGAATCCGAA CTCGAAGAGA TCGTGCAGCT CGTCGGGAAG GACGCGCTGC 1450

```
CCGAGGACCA GCAGCTCACG CTGGAAGTCG CGCGGTACAT CCGCGAGGCG    1500
TGGCTCCAGC AGAACGCGCT CCACGACGTG GATCGCTACT GCCCGCCCGA    1550
GAAGACGTAC GCCATCCTCT CCGGCATCAA GACGCTTCAC GAGGAGTCCT    1600
TTGAGGCGTT GGACGCCGGT GTGCCAGTCG AGGAGATCAC GTCGATCGAC    1650
GCCGCGCCGC GCCTGAATCG TCTCGGCACG ACGCCCGACG ACGAGCACGA    1700
GGCGGAGGTC GCGGAGATCA AACAGCAGAT TACCGAGCAG CTTCGGGAGC    1750
TCTACTGA                                                 1758
```

2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human
(C) ACCESSION NUMBER: L09234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

```
GAATTCCGGC AGCTGACTAG TCTTGTGATT GGGGTCCTGG GCTGATAAAA      50
TCATTCCAAA TGACGAGCAC ATTGATAAAG ACGTCCGATG AGGACCGGGA     100
GTCCAAATTC GGCTTTGTTT TTGCCGTATC TGGACCTGTG GTGACAGCTG     150
AACGAATGGC CGGTTCTGCT ATGTACGAAC TGGTGCGTGT CGGTTATTAT     200
GAACTGGTCG GAGAGATCAT CCGGTTGGAG GGTGACATGG CAACAATCCA     250
AGTATACGAA GACACCTCAG GTGTGACAGT AGGCGATCCC GTGCTGCGCA     300
CAGGCAAGCC GCTGTCCGTG GAACTGGGAC CCGGAATCAT GGGCAGCATC     350
TTCGACGGTA TCCAGCGACC GCTGAAGGAT ATCAATGAAC TGTCAAATAG     400
TATCTACATC CCGAAAGGTG TCAATGTGCC TGCCCTGAGT CGCACTGCAC     450
AGTGGGACTT CAGTCCCGTC AGTGTCAAGG TTGGAAGCCA CATTACTGGT     500
GGTGACCTGT ACGGTTTGGT CCACGAAAAT ACTCTGGTGA AACACAAGTT     550
GCTGCTGCCG CCCCGTGCCA AGGGAACTGT CACGTACATT GCAGAACCTG     600
GAAACTACAC AGTTGATGAT GTTGTCCTGG AGACAGAATT TGACGGCGAG     650
CGATCAAAGT TCACCATGCT GCAAGTGTGG CCTGTACGTC AGCCCAGGCC     700
TGTTACAGAA AAGTTGCCAG CTAACTACCC CCTCCTTACT GGCCAGCGTG     750
TGCTCGACTC CCTATTCCCG TGTGTCCAGG GTGGAACAAC AGCTATTCCT     800
GGGGCCTTCG GATGTGGCAA GACTGTAATA TCACAGTCTT TGTCAAAATA     850
CTCAAACTCC GATGTAATTA TCTATGTAGG TTGTGGTGAG CGAGGTAATG     900
AAATGTCAGA AGTACTCAGG GATTTCCCGC AGTTGTCGTT GGAGATTGAT     950
GGTGTGACTG AATCAATCAT GAAGAGAACA GCCCTGGTCG CAAACACATC    1000
AAACATGCCT GTGGCTGCTC GAGAAGCATC TATCTACACA GGTATTACAC    1050
TGTCAGAATA CTTCAGGGAC ATGGGTTACA ATGTATCCAT GATGGCTGAC    1100
TCAACTTCAC GATGGGCCGA AGCTCTTCGA GAAATCTCAG GTCGATTGGC    1150
TGAAATGCCT GCCGACAGCG GTTATCCCGC CTACCTAGGT GCACGACTTG    1200
CCAGTTTCTA CGAGCGTGCC GGCCGTGTGA AGTGCTTGGG TAACCCAGAC    1250
AGGGAGGGCT CCGTGAGTAT AGTGGGCGCC GTGTCGCCGC CCGGTGGAGA    1300
CTTCTCAGAT CCCGTGACGA CGGCCACACT AGGTATCGTC CAGGTGTTCT    1350
GGGGTCTCGA CAAGAAACTT GCCCAGCGAA AGCACTTCCC ATCCATCAAC    1400
TGGCTCATCT CGTACAGTAA ATACATGCGT GCTCTGGATG ACTTCTACGA    1450
CAAGAATTTC CCAGAGTTTG TCCCACTGCG TACAAAGGTG AAGGAGATTT    1500
TGCAGGAGGA AGAAGACCTG TCTGAAATTG TGCAGTTGGT CGGTAAAGCT    1550
TCATTGGCAG AAACTGACAA GATCACACTT GAGGTTGCCA AACTATTAAA    1600
GGATGATTTC CTGCAACAGA ACAGCTATTC ACCATATGAC CGTTTCTGCC    1650
CATTCTACAA GACAGTAGGA ATGCTGAAAA ATATGATTGC TTTCTACGAT    1700
```

ATGTCTCGGC ATGCAGTTGA ATCTACTGCT CAGAGCGAGA ACAAGATCAC 1750
TTGGAATGTT ATTAGAGATT CTATGGGCAA TATTCTGTAT CAGCTTTCCT 1800
CCATGAAATT CAAGGATCCA GTCAAGGATG GAGAAGCGAA GATCAAGGCA 1850
GACTTTGAGC AGCTTCATGA AGACATTCAG CAAGCCTTCA GGAACCTGGA 1900
GGATTAAAGT GGTAGCTGCC AGTGGTTCTC TCGGTGCAGT TGTCACATTT 1950
GGCAAGCTCT GTAGGGTTGC CGAGTGGCAT CGGTGCTAGA CACCTGAGCA 2000
TTCCTTTGCC ACATAAAGAC TAAAGCAGGT GGAATTTCAG TTGTAAAAAG 2050
CTGGTTCCAT TGGTGCTAAG ATTATGTTGT GCCCTTTTCT GCTTCTCACA 2100
TTCCAACAGA GGAATTTACT TCCAGTTTTC TTCCATTTTC CTCCTCATTT 2150
TAAGTGTCGG TACAGAGGCA ATAATCTGAT AACTCTGTAC CGTCACTTAC 2200
AAGCAGGGAG AATTTGTAAT TATTACAAAT CCCATTATCT CTGTGCACCA 2250
CAGCCTTGTA AATTCATTTG TCCCAGGACT CCCTCTTGTG TGTACGTGAG 2300
ATTGCCGTCT GTATGTATGT ACACACCGTA CTGCAGTATT TGAAGTCAGT 2350
CAGAAGGTGA ATTACACCAC TTACTCATTG TGTCACGTAG CAAGTGTGCA 2400
AACTGCCATC CATTGTCCTA TTTATTCACA TAACTAGTTT TCTTTGCATT 2450
TCCAGTGTTG CAAATTGTGT TTAGAAAATT ATGCCATCGA GACTGGTCGA 2500
ACCTCACATT GTAACTCAGT ATTTACACAC ACGTTTACTT GCTACAGAAA 2550
TGTAGAAAAA ATAATTGTTG TATATTGAAA GTACAAGTGA CAAAGTTGCA 2600
TTTAAAATGG TGAATGTATT TTATATTTCT TTTGTAGACA CAAGAGTTAA 2650
TGCATTTTGC TTAATGGAGA TGTATGTAAA CCTAAAATAG CAGTTTGTGC 2700
ACAAATTATG TATATGTGAA ATGGAGATGG TTTCTAATTT GCTGATTGAT 2750
TGCCAGTATT AATTTAAACA ACTGTAGTTG TGGGATGTAG TGGGAAGATT 2800
TTTTTTTTCC TATAAAATTG GTGGATGTAT GTGTCGGAGA TTTTGATTGT 2850
ATGTGTAAAA TAGTGATCCC AGTAACTGTA AAGCTTTAGA ATACAGTTAC 2900
TGACTGTATA GTTGTACAGG TGTTGTTACT TTTAAGAATT TATTGACACA 2950
AAGGTGAAAG TCTATTATTG TATTGTAATG TTTAAAGCAT TTAAGGTTTA 3000
AAAATCCTAC TTCTGTGTAT AAATGTTACC ATTCCTCATA TAACATAACT 3050
GTGTAGAAAT ACAGTCAACT TCATGTTCAT TAGCATTTCA CTGTTGTCAC 3100
ATAAATTATG CCCGGAAT 3118

2) INFORMATION FOR SEQ ID NO: 689

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1836 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Plasmodium falciparum*
(B) STRAIN: 3D7
(C) ACCESSION NUMBER: L08200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

ATGACAAAAG TTGCTGTTGA AAAAGAGGAA CCAGGAGTTG TTTATAAGGT 50
GGCTGGTTCA TTAGTTATTG CTGAGAATAT GAGTGGAACT CGTATGTACG 100
AGTTAGCTAA AGTAGGATGG AATAAATTGG TTGGAGAAAT TATTAGATTA 150
GAAGGGAATT ATGCATATAT ACAAGTTTAT GAAGATACTT CAGGTTTATC 200
TGTAGGAGAC CCTGTTATAA AAACAGGAAA TGCTTTATCA GTCGAATTGG 250
GTCCTGGTAT TTTAGATAAT ATTTATGATG GTATTCAAAG ACCATTAGAA 300
AGAATAGCAA ATGTGTGTGG TGATGTATAT ATATATAAAG GTATTGATAT 350
GACATCTTTA GATCATGATA AACAATGGCA ATTTTATGCT GATAAGAAAT 400
TAAAATTAAA TGATATTGTT ACTGGTGGAG ATATCTTTGG ATTTGTTGAT 450
GAAAATAAAT TATTTAAAGA ACACAAAATT ATGGCTCCAC CTAATGCTAA 500
AGGGAGGCTT ACATATATTG CTCCAGATGG ATCATATACT TTAAAAGATA 550

AAATATTTGA ATTAGAATAT CAAGGAAAAA AATATACATA TGGTTTATCT 600
CATTTATGGC CTGTTCGTGA TCCTAGACCT GTTTTAGAAA AGGTAACAGG 650
GGATACTTTA TTATTAACAG GGCAAAGAGT TTTAGATTCG TTATTTCCAA 700
CAGTTCAAGG AGGTACTTGT GCTATTCCTG GTGCATTTGG TTGTGGAAAA 750
ACTTGTGTTT CTCAGGCCTT ATCAAAATAT TCTAATAGTG AAGTTATTAT 800
ATATGTAGGA TGTGGTGAAA GAGGTAATGA AATGGCTGAA ATTTTATCCG 850
ACTTTCCTGA ATTAACTACT AAAGTAGATA ATGAAGATGT AGGTATTATG 900
CAAAGAACGT GTTTAGTTGC TAATACTTCT AACATGCCTG TCGCTGCAAG 950
AGAAGCTAGT ATTTATACAG GTATTACTTT ATGTGAATAT TTCCGTGATA 1000
TGGGTTATAA TGCTACCATG ATGGCTGATA GTACAAGTAG ATGGGCAGAA 1050
GCCTTAAGAG AAATTTCAGG ACGTTTAGCT GAAATGCCTG CAGATAGTGG 1100
TTATCCAGCT TATTTAGGTG CTAGATTAGC TTCCTTTTAT GAACGTGCAG 1150
GAAAAGTCAA ATGTATTGGT TCTCCATCTC GTATAGGATC CATTACAATT 1200
GTGGGTGCTG TGTCTCCACC AGGTGGTGAT TTCTCTGACC CTGTAACTAC 1250
AGCAACCATG TCTATTGTTC AAGCATTTTG GGGGTTAGAT AAAAAACTAG 1300
CTCAAAGAAA ACATTTCCCT TCTGTTAATT GGTCTACATC CTTTTCAAAG 1350
TATGTCAGAC AATTAGAACA ATACTTTGAT AATTTTGATC AAGATTTCTT 1400
ATCTTTAAGA CAAAAAATTA GTGATATTTT ACAACAAGAA AGTGACTTGA 1450
ATGATATTGT TCAACTAGTA GGAAAGGATT CATTATCAGA AGACCAAAAA 1500
GTTGTTATGG AAGTAGCCAA AATTATTAGA GAAGATTTTC TTCAACAAAA 1550
TGCATTTAGC GATTATGATT ATATGTGCCC ATTACAAAAA ACAGTTGGTA 1600
TGATGAGAAT TATTTGCCAC TTTTATGCTC AATGCTTAAG AACATTACAA 1650
GAATATGACT CAAGAGAAAG AAAAATTGGT TGGGGATCTA TATATAATAC 1700
ATTAAGACCA ACTATAAATA AAATTACACA TATGAAATTT GAAAACCCAA 1750
AAAATTCAGA TGAATATTTC AAAAAGTATT TTAAGGCACT TGAAGAAGAA 1800
ATAACAGTAG GTTTAAGAAA CTTGATGGAA AAATGA 1836

2) INFORMATION FOR SEQ ID NO: 690

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3216 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Saccharomyces cerevisiae*
(B) STRAIN: X2180-1A
(C) ACCESSION NUMBER: J05409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

ATGGCTGGTG CAATTGAAAA CGCTCGTAAG GAAATAAAAA GAATCTCATT 50
AGAAGACCAT GCTGAATCTG AATATGGTGC CATCTATTCT GTCTCTGGTC 100
CGGTCGTCAT TGCTGAAAAT ATGATTGGTT GTGCCATGTA CGAATTGGTC 150
AAGGTCGGTC ACGATAACCT GGTGGGTGAA GTCATTAGAA TTGACGGTGA 200
CAAGGCCACC ATCCAAGTTT ACGAAGAAAC TGCAGGCCTT ACGGTCGGTG 250
ACCCTGTTTT GAGAACAGGT AAGCCTCTGT CGGTAGAATT GGGTCCTGGT 300
CTGATGGAAA CCATTTACGA TGGTATTCAA AGACCTTTGA AAGCCATTAA 350
GGAAGAATCG CAATCGATTT ATATCCCAAG AGGTATTGAC ACTCCAGCTT 400
TGGATAGGAC TATCAAGTGG CAATTTACTC CGGGAAAGTT TCAAGTCGGC 450
GATCATATTT CCGGTGGTGA TATTTACGGT TCCGTTTTTG AGAATTCGCT 500
AATTTCAAGC CATAAGATTC TTTTGCCACC AAGATCAAGA GGTACAATCA 550
CTTGGATTGC TCCAGCTGGT GAGTACACTT TGGATGAGAA GATTTTGGAA 600
GTTGAATTTG ATGGCAAGAA GTCTGATTTC ACTCTTTACC ATACTTGGCC 650
TGTTCGTGTT CCAAGACCAG TTACTGAAAA GTTATCTGCT GACTATCCTT 700

TGTTAACAGG TCAAAGAGTT TTGGATGCTT TGTTTCCTTG TGTTCAAGGT 750
GGTACGACAT GTATTCCAGG TGCTTTTGGT TGTGGTAAGA CCGTTATCTC 800
TCAATCTTTG TCCAAGTACT CCAATTCTGA CGCCATTATC TATGTCGGGT 850
GCTTTGCCAA GGGTACCAAT GTTTTAATGG CGGATGGGTC TATTGAATGT 900
ATTGAAAACA TTGAGGTTGG TAATAAGGTC ATGGGTAAAG ATGGCAGACC 950
TCGTGAGGTA ATTAAATTGC CCAGAGGAAG AGAAACTATG TACAGCGTCG 1000
TGCAGAAAAG TCAGCACAGA GCCCACAAAA GTGACTCAAG TCGTGAAGTG 1050
CCAGAATTAC TCAAGTTTAC GTGTAATGCG ACCCATGAGT TGGTTGTTAG 1100
AACACCTCGT AGTGTCCGCC GTTTGTCTCG TACCATTAAG GGTGTCGAAT 1150
ATTTTGAAGT TATTACTTTT GAGATGGGCC AAAAGAAAGC CCCCGACGGT 1200
AGAATTGTTG AGCTTGTCAA GGAAGTTTCA AAGAGCTACC CAATATCTGA 1250
GGGGCCTGAG AGAGCCAACG AATTAGTAGA ATCCTATAGA AAGGCTTCAA 1300
ATAAAGCTTA TTTTGAGTGG ACTATTGAGG CCAGAGATCT TTCTCTGTTG 1350
GGTTCCCATG TTCGTAAAGC TACCTACCAG ACTTACGCTC CAATTCTTTA 1400
TGAGAATGAC CACTTTTTCG ACTACATGCA AAAAAGTAAG TTTCATCTCA 1450
CCATTGAAGG TCCAAAAGTA CTTGCTTATT TACTTGGTTT ATGGATTGGT 1500
GATGGATTGT CTGACAGGGC AACTTTTTCG GTTGATTCCA GAGATACTTC 1550
TTTGATGGAA CGTGTTACTG AATATGCTGA AAAGTTGAAT TTGTGCGCCG 1600
AGTATAAGGA CAGAAAAGAA CCACAAGTTG CCAAAACTGT TAATTTGTAC 1650
TCTAAAGTTG TCAGAGGTAA TGGTATTCGC AATAATCTTA ATACTGAGAA 1700
TCCATTATGG GACGCTATTG TTGGCTTAGG ATTCTTGAAG GACGGTGTCA 1750
AAAATATTCC TTCTTTCTTG TCTACGGACA ATATCGGTAC TCGTGAAACA 1800
TTTCTTGCTG GTCTAATTGA TTCTGATGGC TATGTTACTG ATGAGCATGG 1850
TATTAAAGCA ACAATAAAGA CAATTCATAC TTCTGTCAGA GATGGTTTGG 1900
TTTCCCTTGC TCGTTCTTTA GGCTTAGTAG TCTCGGTTAA CGCAGAACCT 1950
GCTAAGGTTG ACATGAATGG CACCAAACAT AAAATTAGTT ATGCTATTTA 2000
TATGTCTGGT GGAGATGTTT TGCTTAACGT TCTTTCGAAG TGTGCCGGCT 2050
CTAAAAAATT CAGGCCTGCT CCCGCCGCTG CTTTTGCACG TGAGTGCCGC 2100
GGATTTTATT TCGAGTTACA AGAATTGAAG GAAGACGATT ATTATGGGAT 2150
TACTTTATCT GATGATTCTG ATCATCAGTT TTTGCTTGCC AACCAGGTTG 2200
TCGTCCATAA TTGCGGAGAA AGAGGTAATG AAATGGCAGA AGTCTTGATG 2250
GAATTCCCAG AGTTATATAC TGAAATGAGC GGTACTAAAG AACCAATTAT 2300
GAAGCGTACT ACTTTGGTCG CTAATACATC TAACATGCCG GTTGCAGCCA 2350
GAGAAGCTTC TATTTACACT GGTATCACTC TTGCAGAATA CTTCAGAGAT 2400
CAAGGTAAAA ATGTTTCTAT GATTGCAGAC TCTTCTTCAA GATGGGCTGA 2450
AGCTTTGAGA GAAATTTCTG GTCGTTTGGG TGAGATGCCT GCTGATCAAG 2500
GTTTCCCAGC TTATTTGGGT GCTAAGTTGG CCTCCTTTTA CGAAAGAGCC 2550
GGTAAAGCTG TTGCTTTAGG TTCCCCAGAT CGTACTGGTT CCGTTTCCAT 2600
CGTTGCTGCC GTTTCGCCAG CCGGTGGTGA TTTCTCAGAT CCTGTTACTA 2650
CTGCTACATT GGGTATCACT CAAGTCTTTT GGGGTTTAGA CAAGAAATTG 2700
GCTCAAAGAA AGCATTTCCC ATCTATCAAC ACATCTGTTT CTTACTCCAA 2750
ATACACTAAT GTCTTGAACA AGTTTTATGA TTCCAATTAC CCTGAATTTC 2800
CTGTTTTAAG AGATCGTATG AAGGAAATTC TATCAAACGC TGAAGAATTA 2850
GAACAAGTTG TTCAATTAGT TGGTAAATCG GCCTTGTCTG ATAGTGATAA 2900
GATTACTTTG GATGTTGCCA CTTTAATCAA GGAAGATTTC TTGCAACAAA 2950
ATGGTTACTC CACTTATGAT GCTTTCTGTC CAATTTGGAA GACATTTGAT 3000
ATGATGAGAG CCTTCATCTC GTATCATGAC GAAGCTCAAA AAGCTGTTGC 3050
TAATGGTGCC AACTGGTCAA AACTAGCTGA CTCTACTGGT GACGTTAAGC 3100
ATGCCGTTTC TTCATCTAAA TTTTTTGAAC CAAGCAGGGG TGAAAAGGAA 3150
GTCCATGGCG AATTCGAAAA ATTGTTGAGC ACTATGCAAG AAAGATTTGC 3200
TGAATCTACC GATTAA 3216

2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1860 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Schizosaccharomyces pombe*
(B) STRAIN: 972 h-
(C) ACCESSION NUMBER: S47814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

```
ATGGCGGGAG GAATTGAACT GGCCAAGAAG GCTATCAGGA GCCTCAAAAA      50
TTACGACGAG CATGAAAACC GATATGGATC TATTTTCAGC GTTTCTGGTC     100
CTGTCGTTGT TGCAGCCAAT ATGCTTGGAT GTTCGATGTA CGAACTCGTT     150
CGCGTTGGTC ATGAAGAACT AGTTGGTGAA GTAATTCGTA TCCATCAAGA     200
TAAATGTACT ATTCAAGTAT ACGAAGAGAC GTCCGGTCTC ACTGTTGGTG     250
ATCCTGTCCA ACGCACTGGA AAGCCATTAT CTGTTGAATT AGGTCCTGGT     300
TTAGCTGAGA CTATTTATGA TGGTATCCAA CGTCCGTTAA AGCAAATTTT     350
CGACAAATCT CAAAGTATTT ATATTCCTAG AGGTATTAAT ACAGAATCAC     400
TTAATCGTGA GCATAAGTGG GATTTCACAC CAAATAAGGA TTTACGCATT     450
GGCGATCATG TATCCGGTGG TGATGTTTTC GGTTCTGTAT TTGAAAACTC     500
TCTTTTCAAT GATCATAAAA TTATGTTACC CCCTAGAGCC CGTGGTACCG     550
TCACATATAT TGCTGAAGCT GGATCATACC ATGTTGATGA AAAACTTCTT     600
GAAGTCGAGT TTAATGGCAA GAAACATTCT TTTAGTATGT TGCATACTTG     650
GCCTGTCCGT GCTGCTCGTC CAGTTGCGGA CAACTTAACT GCTAATCAAC     700
CTTTATTGAC TGGTCAACGT GTTTTGGATG CGTTATACCC CTGTGTTCAA     750
GGTGGCACTA CTGCTATCCC CGGTGCCTTT GGTTGTGGTA AAACAGTTAT     800
TTCACAATCT CTTTCTAAGT ACTCTAATTC TGATTTGATT GTTTACGTCG     850
GTTGTGGTGA ACGTGGAAAC GAAATGGCAG AAGTGTTAAT GGATTTCCCA     900
GAACTAACAA TTGATATTAA TGGTAAACCA GAGCCCATTA TGAAGCGTAC     950
TACATTGGTA GCCAACACTT CTAACATGCC TGTCGCTGCT CGTGAAGCTT    1000
CCATTTATAC CGGTATTACA CTTGCTGAAT ATTATCGTGA TCAAGGTAAG    1050
AACGTTTCAA TGATGGCTGA TTCTACATCT CGTTGGGCTG AAGCTTTGCG    1100
TGAAATTTCT GGTCGTTTGG CTGAGATGCC TGCCGATTCT GGTTATCCCG    1150
CTTATTTGGG TGCCAAATTG GCTTCTTTTT ACGAACGTGC TGGTCGTGCT    1200
CGTTGCTTGG GAAGTCCTGA CCGTGAAGGA ACAGTTTCAA TTGTTGGAGC    1250
TGTTTCTCCT CCGGGTGGTG ATTTTTCTGA TCCTGTTACT AGTGCAACCT    1300
TGGGAATTGT TCAAGTCTTC TGGGGTTTGG ACAAGAAATT GGCCCAACGT    1350
AAACACTTTC CCTCAATCAA CACCTCTCTT TCCTATTCTA AATACATCAA    1400
TGCTTTGCAA CCTTGGTATG AGGAAAGAGT TCCAGGCTTT AATACTCTTC    1450
GTGATCAAAT CAAACAGATC ATTCAACAAG AAGATTCCAT GTTGGAAATT    1500
ATTCAGTTGG TTGGTAAGTC GGCTCTTTCT GAAACGGATA AAGTTACTTT    1550
GGACATAGCC GGTATTATTA AGAATGACTT CTTACAACAA AACGGTTATT    1600
CTGATTACGA TCGCTGTTGC CCTCTTTACA AGACTTATCA TATGATGCGA    1650
AACATGATTG CTTACTACAC AAAGGCTAAA AGTGCCGTTG AAACTGGTAG    1700
CGTTCCTTGG TCAAAGATTA AAGAAAGTAC TTCAGATATC TTTTATGAGT    1750
TAACCTCGAT GAAATTCGAA AACCCTAATG AAGGCGAGAA GGAAATAGTC    1800
GAACACTATG AAACTCTGCA CAAGAAGATT GAGGACAAGT TCACACTCT     1850
GACTGAGTAA                                                1860
```

2) INFORMATION FOR SEQ ID NO: 692

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trypanosoma congolense*
(B) STRAIN: IL3000
(C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

ATGACGAGCG ATAAAAACCC TTACAAAACA GAGCAGCGCA TGGGGGCCGT 50
GAAGGCCGTC TCCGGGCCAG TTGTCATTGC TGAAAACATG GGCGGTAGCG 100
CTATGTATGA GCTTGTGCAG GTAGGTTCCT TCCGGTTAGT GGGCGAGATC 150
ATTCGTCTAG AGGGCGATAC CGCCACTATT CAGGTCTATG AGGAAACAGG 200
TGGCCTCACT GTCGGAGACC CGGTGTACTG TACGGGTAAG CCTCTTTCGC 250
TTGAGCTTGG ACCTGGAATC ATGTCTGAAA TATTTGACGG TATCCAGCGG 300
CCTCTTGACA CCATCTACCG CATGGTGGAA AACGTGTTTA TCCCCAGGGG 350
CGTTCAGGTG AAGTCACTCA ATGACCAGAA ACAGTGGGAC TTTAAGCCAT 400
GCCTGAAGGT TGGAGATCTT GTGTCTGGTG GTGATATCAT TGGCTCAGTG 450
GTGGAGAACT CTCTCATGTA CAATCACAGC ATTATGATTC CGCCCAATGT 500
GCGGGGCCGT GTTACTTCCA TTGTTCCTTC AGGAAATTAC ACCCTCCAAG 550
ATGACATTAT TGAATTGGAA TATAATGGGA CAGTGAAATC ACTAAAACTT 600
ATGCATCGCT GGCCAGTACG GACCCCGCGT CCTGTGGCGT CAAAAGAATC 650
CGGCAATCAT CCGCTTCTCA CCGGACAGCG TGTGCTCGAT GCTCTCTTTC 700
CATCCGTCCA GGGTGGAACA TGCGCCATCC CTGGCGCGTT TGGATGCGGA 750
AAGACGGTTA TCAGTCAGGC TCTTTCGAAG TTCTCCAACA GCGACGCTGT 800
TATCTATGTC GGCTGCGGCG AGCGTGGGAA TGAGATGGCA GAGGTGCTCA 850
TGGACTTCCC CACACTCACC ACCGTTATTG ATGGTCGTGA GGAGTCCATC 900
ATGAAGCGTA CCTGCCTGGT GGCAAACACC TCAAATATGC CTGTCGCTGC 950
TCGTGAGGCG TCTATTTACA CTGGCATCAC TTTAGCTGAG TATTATCGTG 1000
ATATGGGCAA GCACATTGCT ATGATGGCCG ACTCTACCTC TCGATGGGCT 1050
GAGGCTCTCC GTGAGATCTC TGGGCGTCTC GCTGAAATGC CCGCTGATGG 1100
TGGTTACCCT GCGTACCTCA GTGCGCGTCT TGCTTCCTTC TACGAGCGTG 1150
CGGGGCGCGT GACATGCATC GGTGGGCCAA AACGCGAGGG CTCAGTAACC 1200
ATCGTTGGTG CCGTTTCTCC TCCTGGAGGT GACTTTTCTG ACCCAGTGAC 1250
GTCCGCTACG CTTGGTATTG TGCAAGTCTT TTGGGGTCTT GAGAAGCGTC 1300
TTGCGCAACG TAAACACTTT CCTTCTGTTA ATTGGCTCAT TTCCTATTCA 1350
AAATACCTTA ATGCTTTGGA GCCCTTCTTC AACACGCTTG ACCCTGACTA 1400
CATGCGCCTG CGGTCAGTTG CTGCGGAGAT CCTTCAGCGT GAGGAAGAGT 1450
TGCAAGAAAT TGTTCAACTT GTCGGTAAGG ACTCACTTTC GGAGTCTGAC 1500
AAAATTATTC TAGAAACGGC TAAGGTTATT CGTGAAGAGT TTCTCCAGCA 1550
GAATGCCTTT ACGCCGTACG ACAAGTATTG CCCGCCGTAC AAGACCTGCT 1600
GGATGCTACG TAACATTGTC GCGTTCTACG AGGAGAGCCA GCGCGTTGTA 1650
GCTGAGTCCG CTGGGGAACT TAAGATTACG TGGAACTACA TTCGTGAAAT 1700
GATTCCTCAT ATTTACACGG GTTTAACTGA GATGAAGTTC CGTGATCCTC 1750
AGGAGGGTGA GGAGGCCAAC GTAGAATTCT ACAGAAAACA AAATGAGGAA 1800
ATTGTCAGCG CATTCGCCTC GCTGCTGCAA TAA 1833

2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1758 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Thermus thermophilus*
(B) STRAIN: HB8
(C) ACCESSION NUMBER: D63799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

```
ATGATCCAAG GGGTGATCCA GAAGATCGCG GGCCCGGCGG TGATCGCCAA       50
GGGCATGCTC GGGGCCCGCA TGTACGACAT CTGCAAGGTG GGCGAAGAGG      100
GCCTCGTGGG CGAGATCATC CGCCTGGACG GGGACACGGC CTTCGTCCAG      150
GTCTACGAGG ACACCTCGGG CCTAAAGGTG GGGGAGCCCG TGGTCTCCAC      200
GGGCCTTCCC TTGGCGGTGG AGCTCGGCCC CGGGATGCTG AACGGCATCT      250
ACGACGGCAT CCAGCGCCCC CTGGAGCGCA TCCGGGAGAA GACGGGGATC      300
TACATCACCC GGGGCGTGGT GGTCCACGCC CTGGACCGGG AGAAGAAGTG      350
GGCCTGGACG CCCATGGTCA AGCCCGGGGA CGAGGTGCGG GGGGGTATGG      400
TCCTGGGCAC GGTGCCCGAG TTCGGCTTCA CCCACAAGAT CCTGGTACCC      450
CCGGACGTGC GGGGCCGGGT CAAGGAGGTG AAGCCCGCCG GGGAGTACAC      500
CGTGGAGGAG CCGGTGGTGG TCCTCGAGGA CGGCACCGAG CTCAAGATGT      550
ACCACACCTG GCCCGTTCGC CGGGCGAGGC CCGTGCAAAG GAAGCTTGAC      600
CCCAACACCC CCTTCCTCAC GGGGATGCGC ATCCTGGACG TCCTCTTCCC      650
CGTGGCCATG GGGGGCACCG CCGCCATCCC TGGGCCCTTC GGCAGCGGCA      700
AGACCGTGAC CCAGCAGTCC CTGGCCAAGT GGTCCAACGC CGACGTGGTG      750
GTCTACGTGG GCTGCGGGGA GCGGGGGAAC GAGATGACCG ACGTGCTCGT      800
GGAGTTCCCC GAGCTCACCG ACCCCAAGAC GGGTGGGCCC TTGATGCACC      850
GCACCGTCCT CATCGCCAAC ACCTCCAACA TGCCCGTGGC CGCCCGCGAG      900
GCCAGCATCT ACGTGGGCGT GACCATCGCC GAGTACTTCC GCGACCAGGG      950
CTTCTCCGTG GCCCTCATGG CCGACTCCAC GAGCCGCTGG GCCGAGGCTT     1000
TGCGCGAGAT CTCTAGCCGC CTCGAGGAGA TGCCCGCCGA GGAGGGCTAC     1050
CCGCCCTACC TCGCCGCCAG GCTCGCCGCC TTCTACGAGC GGGCGGGCAA     1100
GGTCATCACC CTGGGCGGCG AGGAGGGGGC GGTGACCATC GTGGGGGCCG     1150
TCTCCCCGCC GGGCGGCGAC ATGTCCGAGC CCGTGACCCA GTCCACCTTG     1200
AGGATCGTGG GGGCCTTCTG GCGGCTTGAC GCCTCCCTGG CCTTCCGCCG     1250
CCACTTCCCC GCCATCAACT GGAACGGCTC CTACAGCCTC TTCACCTCCG     1300
CCCTTGACCC CTGGTACCGG GAGAACGTGG CCGAGGACTA CCCCGAGCTC     1350
CGCGACGCCA TCTCCGAGCT TTTGCAGCGG GAGGCGGGCC TCCAGGAGAT     1400
CGTCCAGCTC GTGGGGCCGG ACGCCCTCCA GGACGCCGAG CGCCTCGTCA     1450
TTGAGGTGGG CCGGATCATC CGCGAGGACT TCCTGCAGCA GAACGCCTAC     1500
CACGAGGTGG ACGCCTACTG CTCCATGAAG AAGGCCTACG GGATCATGAA     1550
GATGATCCTC GCCTTCTACA AGGAGGCGGA GGCGGCCATC AAGCGGGGGG     1600
TTTCCATAGA CGAGATCCTG CAGCTCCCCG TTCTGGAGCG CATCGGCCGC     1650
GCCCGCTACG TGAGCGAGGA GGAGTTCCCC GCCTACTTTG AGGAGGCCAT     1700
GAAGGAGATC CAGGGGGCCT TCAAGGCTGG CCTAAAGGGG GAGAGATGGA     1750
CCTTCTGA                                                  1758
```

2) INFORMATION FOR SEQ ID NO: 694

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

```
CGGCGCIATC  YTSGTTGTTG  C                                    21
```

2) INFORMATION FOR SEQ ID NO: 695

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

GTTTCACGTG ATGACGTACA 20

2) INFORMATION FOR SEQ ID NO: 696

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

ATIGGICAYR TIGAYCAYGG IAARAC 26

2) INFORMATION FOR SEQ ID NO: 697

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

CCIACIGTIC KICCRCCYTC RCG 23

2) INFORMATION FOR SEQ ID NO: 698

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

```
GTGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTTA ACGTTGGTAC      50
TATCGGCCAC GTTGACCACG GTAAAACTAC TCTGACCGCT GCAATCACCA     100
CCGTACTGGC TAAAACCTAC GGCGGTGCTG CTCGTGCATT CGACCAGATC     150
GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACTTCTCA     200
CGTTGAATAC GACACCCCGA CCCGTCACTA CGCACACGTA GACTGCCCGG     250
GGCACGCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC     300
GGCGCGATCC TGGTAGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG     350
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT     400
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAACTGGTT     450
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA     500
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG     550
AGTGGGAAGC GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCTTATATT     600
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA     650
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC     700
GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG     750
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA     800
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC     850
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG     900
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG     950
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC    1000
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG    1050
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT    1100
CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG    1150
TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA                    1185
```

2) INFORMATION FOR SEQ ID NO: 699

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

GTIACIGGYT CYTYRARRTT ICCICC 26

2) INFORMATION FOR SEQ ID NO: 700

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

TIRTIGAYGT CGARTTCCCT CARG 24

2) INFORMATION FOR SEQ ID NO: 701

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTCACGA TCATCGATGC G 21

2) INFORMATION FOR SEQ ID NO: 702

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG 20

2) INFORMATION FOR SEQ ID NO: 703

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT 20

2) INFORMATION FOR SEQ ID NO: 704

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

AGTGCTCCAA TTAATGTTGG 20

2) INFORMATION FOR SEQ ID NO: 705

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

GTACAGTTCC AATACCTGAA 20

2) INFORMATION FOR SEQ ID NO: 706

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

TGAAATCTTC ACATCCAACA 20

2) INFORMATION FOR SEQ ID NO: 707

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTC AGTACCTTCT GGTAA 25

2) INFORMATION FOR SEQ ID NO: 708

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

TCRTCCATIC CIARIATIGC IATIAT 26

2) INFORMATION FOR SEQ ID NO: 709

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1656 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Borrelia burgdorferi*
(C) ACCESSION NUMBER: extracted from AE001122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

ATGAATGAAG TTTTATTTGT AAAGACTGCT GGTAGGAATT TAAAAGCAGA 50
AGTAATTCGT ATTAGGGGCA ATGAAGTTGA TGCACAGGTT TTTGAATTGA 100
CAAAAGGGAT ATCTGTTGGA GACCTAGTTG AATTTACAGA CAAACTTTTA 150
ACAGTTGAAC TCGGACCAGG GCTTTTAACT CAAGTATATG ATGGGCTTCA 200
AAATCCTTTG CCTGAATTGG CTATTCAATG TGGATTTTTT TTAGAAAGGG 250
GAGTATATTT AAGGCCCTTG AATAAAGATA AAAAGTGGAA TTTTAAAAAA 300
ACCTCCAAAG TTGGAGATAT CGTTATTGCA GGAGATTTTT TAGGTTTTGT 350
AATTGAGGGA ACTGTTCACC ATCAAATAAT GATTCCATTT TATAAAAGGG 400
ATTCTTATAA AATTGTGGAG ATTGTAAGTG ATGGCGACTA TTCGATTGAT 450
GAGCAAATTG CTGTAATTGA AGATGATTCT GGTATGAGGC ATAATATTAC 500
AATGTCTTTT CATTGGCCTG TTAAAGTTCC TATTACTAAT TATAAGGAAC 550
GCCTTATTCC TAGTGAACCT ATGTTGACTC AAACTAGAAT TATAGATACA 600
TTTTTCCCAG TTGCCAAAGG TGGAACTTTT TGCATTCCGG GTCCTTTTGG 650
AGCAGGAAAA ACGGTTCTTC AGCAGGTTAC AAGTCGAAAT GCTGATGTTG 700
ATGTAGTGAT TATTGCAGCT TGTGGTGAGC GAGCAGGAGA AGTGGTAGAA 750
ACTCTTAAAG AATTTCCCGA ATTAATGGAT CCAAAAACCG GCAAATCTTT 800
AATGGACAGG ACTTGTATTA TTTGTAATAC ATCTTCAATG CCAGTTGCAG 850
CTAGAGAAGC TTCTGTTTAT ACTGCTATTA CTATTGGTGA GTATTACAGG 900
CAAATGGGCC TTGATATTCT TCTTTTGGCA GATTCAACTT CAAGATGGGC 950
TCAAGCAATG AGAGAAATGT CTGGACGCCT TGAGGAAATT CCTGGCGAGG 1000
AGGCTTTTCC GGCATATCTT GAGTCTGTTA TTGCTTCCTT TTATGAAAGG 1050
GCAGGTATTG TAGTTCTTAA TAATGGGGAT ATTGGATCTG TAACAGTTGG 1100
TGGCTCTGTA AGTCCTGCTG GTGGTAATTT TGAAGAGCCA GTTACTCAAG 1150
CAACTTTAAA AGTTGTAGGA GCATTTCACG GGCTTACAAG AGAAAGGTCT 1200
GATGCTAGGA AATTTCCAGC TATTAGTCCT CTTGAATCTT GGAGTAAATA 1250
TAAAGGCGTT ATTGATCAAA AAAAGACTGA ATATGCAAGA TCTTTTTTGG 1300
TGAAAGGTAA TGAAATTAAT CAAATGATGA AAGTTGTTGG AGAAGAAGGC 1350
ATAAGTAACG ATGATTTTTT AATTTATTTA AAATCCGAGC TACTTGATTC 1400
GTGCTATTTG CAGCAAAATT CATTTGATTC TATTGATGCT GCTGTTAGTT 1450
CAGAGCGTCA AAATTATATG TTTGATATAG TTTATAACAT TCTTAAAACT 1500
AACTTTGAGT TTTCTGATAA ACTTCAAGCA AGAGATTTTA TAAATGAGTT 1550
AAGGCAAAAT CTTTTAGACA TGAATCTTTC TTCTTTTAAG GATCATAAGT 1600

TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAAGGTA 1650
ATTTAG 1656

2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Treponema pallidum*
(B) STRAIN: Nichols
(C) ACCESSION NUMBER: extracted from AE000520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

GTGATCAAAG ACGATGTGGT TACAGGCCGT GTAGTGAGGG TGTCTGGTCC 50
CATTGTGTAT GCCGAGGGCC TCTCTGCGTG CAGCGTATAC GATGTTGTCG 100
ACGTAGGGGA AGCATCGCTC ATCGGAGAAA TTATCCGGTT GGATGAGAGC 150
AAGGCGGTCG TGCAAGTATA CGAGGATGAC ACAGGTATGC GAGTCGGGGA 200
GAAGGTGACA AGCTTGCGTC GACCACTCTC AGTCCGCTTA GGGCCTGGAT 250
TAATCGGCAC CATTTATGAC GGTATTCAGC GCCCACTTGA GCGCCTCTTC 300
CAAGAAGACG GCGCCTTCTT GCGTCCTGGT GCGCGTTCAC AACCGCTTGA 350
TGGCTCCGTA CGCTGGGATT TTCGTCCTCA TTGTAACGAG CGCGGTGAGG 400
CCCTGTGCGC GGGGATTCCG ATTGCACCTG GGTCAGTGTT AGGGACCGTG 450
CAGGAGACTC CTTCTGTTGT GCACACTATC ATGGTTCCTC CTGACATCCG 500
GGGGAGCGTG CTATCTTCGT TCAAGGGCGC AGGTGCTTAC ACAATAGATG 550
AAGAAATTGG ACGCACTGAT CTTGGTGAGC CGCTTTTTCT ATCCCAGTAC 600
TGGCCAGTGC GTCGTGCGCG TCCTTTCAGC AAAAAACTTG CAGTGTGTGA 650
GCCACTAGTT ACTGGACAGC GGGCGATTGA TGTTTTCTTC CCCCTATCAA 700
AGGGAGGAAC GGCGGCTATT CCAGGGGGAT TTGGAACTGG GAAGACAATG 750
ACGCAGCATG CCGTTGCCAA GTGGTGTGAT GCAGATATTA TCGTGTACAT 800
CGGCTGCGGA GAGCGGGGCA ACGAGATGAC AGACGTGCTC TCTGAATTTC 850
CCAAACTCAT CGATCCGCGC ACAGGACGCT CTCTTATGGA GCGGACGATT 900
TTGATCGCAA ATACGTCCAA TATGCCTGTG TCCGCACGCG AGGTGTCGCT 950
GTATTCAGGG ATTACCCTTG CGGAATACTA CCGTGATATG GGTATGCATG 1000
TGGCCATCAT GGCTGATTCT ACCAGCCGCT GGGCGGAGGC GCTGCGTGAA 1050
TTGTCTGGGC GCATGGAAGA AATGCCTGCG GAGGAGGGAT TCCCTGCGTA 1100
CCTTCCGACG CGTCTTGCAG AATTTTATGA GCGCGCAGGA CGCGTGGAAA 1150
CCTGTGTGGC GCGCGAGGGC TCTGTGAGCA TCATTGGTGC TGTTTCTCCC 1200
CTGGGTGGAG ATTTCTCTGA GCCGGTGACG CAGCACACAA AGCGCTTCAT 1250
CCGTTGCTTT TGGGCCTTGG ATCGTGAACT TGCACACGCG CGTCATTACC 1300
CTGCCATTGG GTGGATAGAT TCATACTCTG AATATGCGCA GGAAGTAAGT 1350
GCATGGTGGA GTAAGTATGA CCCGCGCGCA GGCGCGTTGC GCGCCGCAGC 1400
CTTGGATTTG CTGAGAAAGG AACAGCGGTT ACAGCAAATT GTCAGGCTTG 1450
TCGGTCCTGA TGCGCTGCCT GGAGAAGATC GTCTGGTGCT AATGGTGTGT 1500
GAAATGATCA AAGGTGGCTT TCTGCAGCAG AACGCTTTTG ATCCGACGGA 1550
TGTGTTCTCC TGTCCCGAAA AGCAGGTGCA GATCTTGCGT ACCATAGTGG 1600
ATTTTCACGA ACGTGCCGTG GTGCTGCTGC GTGCAGGTAT TTCGCTTTCT 1650
GCGCTGTCCC AGCTTTCGTG CCGGGAGCTC ATCGTACGTA TGAAAACTAC 1700
GTACGGGAAT GAGGATGTAC ACAAGATGCA GAAAGTGTAC GACACGATGT 1750
GCACTGAGTT TGACCAACTG AGTGTGTGTG CTGCCGCGCG CACACAAGGG 1800
GGGGAGAAAG TCGAATGA 1818

2) INFORMATION FOR SEQ ID NO: 711

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1779 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydia trachomatis*
(B) STRAIN: MoPn

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

```
CAGGGCTATG TCGTAGAAGC TTACGGAAAT TTATTGCGGG TGCATTTTGA      50
TGGGCATGTG CGTCAAGGAG AAGTGGCCTA TGTCAGCGTG GATGATACTT     100
GGTTGAAAGC GGAAATTATA GAAGTTGTGG GAGATGAGGT TAAAGTCCAA     150
GTTTTTGAGG AAACTCAAGG AATTTCTCGA GGCGCTTTGG TAACTTTTTC     200
CGGGCATTTA TTAGAAGCGG AACTTGGGCC CGGTCTATTG CAAGGTATTT     250
TTGACGGACT TCAGAATCGC TTAGAGGTAT TGGCAGATAC AAGCTTGTTC     300
TTGAAAAGAG GGGAGTATGT TAATGCCATT TGTCGGGAAA CTGTATGGGC     350
TTATACGCAA AAGGCTTCTG TCGGGGATGT TCTATCTCGG GGAGATGTGC     400
TTGGTACAGT AAAGGAAGGG CGGTTTGATC ATAAAATCAT GGTTCCTTTC     450
TCTTGTTTTG AGGAAGTGAC TATCACTTGG GTCATTTCTT CAGGAGATTA     500
CACTGTTGAT ACCGTTATTG CTAAAGGACG TACTGCTTCA GGAGCCGAGC     550
TTGAATTTAC AATGGTTCAG AAATGGCCCA TTAAACAGGC TTTTTTAGAA     600
GGGGAAAAGG TACCGTCTCA TGAAATTATG GATGTTGGGT TACGAGTATT     650
AGATACTCAG ATCCCCGTCT TAAAGGGAGG AACTTTTTGT ACTCCAGGGC     700
CTTTTGGTGC AGGAAAGACC GTTTTACAGC ACCATTTATC TAAGTATGCA     750
GCTGTAGATA TCGTAGTTTT GTGTGCTTGT GGAGAGCGAG CTGGAGAGGT     800
TGTAGAAATT CTTCAGGAGT TCCCGCATTT GACAGATCCT CATACGGGGC     850
AGTCTTTGAT GCATAGGACC TGTATTATTT GTAATACATC TTCCATGCCT     900
GTAGCAGCTA GAGAGTCCTC CATTTATTTG GGTATTACTA TAGCAGAATA     950
TTACCGTCAA ATGGGGTTGC ATGTTTTGTT ATTGGCTGAC TCGACATCTA    1000
GATGGGCTCA AGCTTTAAGG GAAATTTCAG GGCGATTAGA AGAAATCCCT    1050
GGAGAAGAAG CTTTCCCAGC CTATTTGGCG TCTCGAATAG CAGCTTTTTA    1100
TGAGCGAGGC GGGGCTGTGA AAATGAAAGA TGGATCGGAA GGCTCCTTGA    1150
CTATCTGTGG AGCGGTTTCT CCCGCAGGAG GAAATTTTGA AGAGCCTGTT    1200
ACACAAGCAA CTTTATCTGT TGTTGGGGCT TTCTGTGGGC TTTCTAAGGC    1250
TAGAGCAGAT GCTAGACGGT ATCCTTCTAT TGATCCGATG ATTTCATGGT    1300
CTAAGTACTT GGATTCTGTG GCGGAGATTT TAGAGAAAAA AGTTCCAGGA    1350
TGGGGAGATT CCGTTAAAAA AGCTTCTCGT TTCTTAGAAG AAGGAGCAGA    1400
AATTGGTAAG CGAATAGAAG TTGTTGGGGA AGAAGGGATT TCTATGGAAG    1450
ATATAGAAAT CTTTTTGAAA TCAGAGTTGT ATGATTTCTG TTACTTACAG    1500
CAAAACGCTT TCGATGCAGA GGACTGTTAT TGTCCTTTTG ATCGTCAAAT    1550
AGAGCTTTTT TCTTTAATGA GTCATATTTT TAGCTCTAGA TTCTGTTTTG    1600
ATTGTCCAGA TAATGCTCGG AGTTTCTTTT TAGAGCTTCA AAGTAAAATT    1650
AAAACGCTGA ATGGTCAAAA ATTCCTTTCT GAAGACTATC AGAAGGGGCT    1700
AGAAGTGATC TATAAACTAT TAGAAAGCAA AATGGTGCAG ACGGCGTAGG    1750
TATGCAAACA ATATATACAA GAATTACGG                           1779
```

2) INFORMATION FOR SEQ ID NO: 712

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 965 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

```
GTGCAAATTG GAAAAATTGT CAAAGTTTCA GGTCCTTTGA TTTTAGCTGA      50
AAACATGTCA GATGCTAGTA TCCAAGACAT TTGTCATGTA GGAGATTTAG     100
GCGTTATCGG AGAGATTATT GAAATGCGAG GCGACGTCGC TTCGATTCAA     150
GTATATGAAG AAACAACAGG CATTGGACCA GGAGAACCAG TTATTTCAAC     200
AGGAGAACCA TTATCTGTTG AATTAGCCCC AGGTTTAATT GCCGAAATGT     250
TTGATGGTAT TCAACGACCA TTGGATACAT TTCAAGAAGT AACCCACAGT     300
AACTTTTTAG GCCGTGGCGT TAAAATTGAT GCGTTAGATC GTGAGAAAAA     350
ATGGACGTTT GAACCAACTG TGGCAGTTGG TGAAGAAGTG TCGGCAGGTG     400
ACATCGTCGG TGTGGTTCAA GAAACACCGA TTATTCAACA TAAAATTATG     450
GTGCCTTTCG GCGTTTCAGG AACGATTGCC GAAATTAAAG CAGGTGACTT     500
TGCCATTGAT GAAACAGTTT ACTCAGTGGA AACGGCTAAA GGAACGGAAA     550
GTTTTAGCAT GATGCAAAAA TGGCCCGTTC GGCGGGGACG TCCCATTTTA     600
GAAAAACTAA GTCCCAAAGT ACCGATGGTG ACCGGACAAC GCGTAATTGA     650
TACCTTTTTC CCAATTACGA AAGGCGGAGC GGCAGCAGTT CCAGGACCAT     700
TTGGCGCTGG AAAAACAGTC GTTCAGCACC AAATTGCTAA GTGGGCCGAT     750
GTCGACTTAG TCGTTTACGT TGGTTGTGGG GAACGCGGGA ATGAAATGAC     800
AGATGTTTTA AATGAATTTC CAGAATTAAT TGACCCAACA ACTGGTGAGT     850
CTTTGATGAA TCGGACGATT TTAATTGCGA ATACGTCAAA TATGCCGGTA     900
GCGGCACGGG AAGCCTCGAT TTATACAGGG ATTACCATTG CAGAATATTT     950
CCGTGATATG GGTTA                                          965
```

2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1737 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Methanosarcina barkeri*
(C) ACCESSION NUMBER: extracted from J04836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

```
GTGGAAGTAA AAGGTGAAAT TTATCGTGTG TCTGGGCCTG TCGTCACCGC      50
CATCGGCTTG CAGGCAAAAA TGTATGACCT GGTCAAAGTC GGTAATGAAG     100
GTTTAATGGG TGAAGTCATT CAGATATTAG GGCCCAAGAC CATCATCCAG     150
GTATATGAAG AGACCGCAGG TATCAAGCCA GGGGAACCCT GTGTATCTAC     200
AGGGTCGTCT CTGTCCGTAG AACTTGGTCC GGGTCTTCTT TCCAGTATTT     250
ATGACGGGGT TCAAAGGCCT CTGCACGTCC TGCTTGAAAA AATGGGTAGC     300
TTCATCCAGA GAGGTGTCAG CGCAGATGGG CTTGATCATA AGAAACTCTG     350
GGATTTCAAA CCCATTGTCA AGAAGGGCGA TTCCGTAAAA GGTGGAGACG     400
```

TAATTGGTGT TGTACAGGAA ACCGTGAATA TTGAACATAA GATCATGGTG 450
CCTCCTGATA TCTCAGGTAC AATTTCCGAC ATAAAGAGCG GAAACTTTAC 500
GGTAGTAGAC ACAATCTGTA CTCTGACTGA TGGGACCGAA TTGCAGATGA 550
TGCAGAGGTG GCCTGTTCGA AGACCCAGAC CTGTGAAGGC AAAACTTACT 600
CCAACCAGGC CTCTGGTTAC AGGAATGAGA ATCCTTGATG GGCTTTTCCC 650
TGTGGCAAAA GGCGGAACAG CTGCAATCCC CGGACCTTTC GGATCGGGAA 700
AGACCGTAAC TCAGCAGTCG CTTGCAAAAT GGAGTGATAC CGAAATTGTG 750
GTCTACATCG GTTGTGGTGA GCGTGGAAAC GAAATGGCAG ATGTTCTGAG 800
CGAATTCCCT GAACTCGAAG ATCCGCAGAC CGGGCGCCCA CTTATGGAGC 850
GTACTGTTCT TATCGCTAAC ACTTCAAACA TGCCTGTGGC CGCAAGAGAA 900
GCATCTGTGT ATACCGGAAT CACCATTGCA GAATACTACC GTGACATGGG 950
ATTAGATGTA TCCCTTATGG CAGACTCCAC CTCAAGGTGG GCAGAAGCCA 1000
TGAGAGAAAT CTCTTCCCGT CTGGAAGAAA TGCCTGGTGA AGAAGGTTAC 1050
CCAGCATACC TGTCTGCAAG ACTGGCCGAA TTCTACGAGC GTGCCGGGGT 1100
TGCGGAGAGT CTTTGCGGCG AAACAGGTTC CATTACTGTT ATTGGAGCAG 1150
TATCTCCACC TGGCGGTGAC TTCTCAGAGC CTGTTACACA GAATACCCTG 1200
CGTATCGTAA AAGTGTTCTG GGCTCTCGAT GCCAAACTAT CTCAGAGGCG 1250
TCACTTCCCG GCCATCAACT GGCTGAACAG TTACAGTCTG TATAAGGACA 1300
GTCTTAATGA CTGGTTTGCA GATAATGTGG CTCCTGATTA TGTGCCTTTG 1350
AGGGAAAGAG CAATGGAAAT GCTCCAGACA GAATCTGAAC TGCAGGAAAT 1400
CGTGCAGCTT GTAGGTTCCG ATGCTCTGCC AGACGACCAG CAGCTTCTGC 1450
TTGAAATCAC CCGTATGCTT AGGGAAATTT TCCTGCAGCA GAATGCATTC 1500
CACCCAGTAG ATGCATACAG CCCGTTCGAT CAGCAGTACA AGATCCTTAA 1550
GGCAATCATG AAATGGGGAG ACGCTGCGAT GGATGCCTTG AAATCAGGTG 1600
TTCCCGTAAC TGAAATTATC AAGCTTGAAT CCAAAAATGT GCTTGCTAAG 1650
GTCAAGTACG AAGAGAAGTT TGATGAGTCT ATGAATGCTG TCCTGGCACA 1700
GATGGATAAA GAGTTTGCAT CCCTGAGAGG TAGGTAA 1737

2) INFORMATION FOR SEQ ID NO: 714

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1785 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Methanosarcina jannaschii*
(C) ACCESSION NUMBER: extracted from U67477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

ATGAAAAGAG AGGTTGAGAA TATGCCAGTT GTTGGTAAGA TTATTAAAAT 50
CGCAGGGCCT GTTGTAGTTG CAGAGGGAAT GAAAGGAGCT CAGATGTATG 100
AGGTCGTTAA AGTAGGAGAA GAGAAATTGA CTGGAGAAAT CATTCAGTTG 150
CACGATGATA AAGCAGTTAT TCAGGTTTAT GAAGAAACAT CTGGAATTAA 200
ACCAGGAGAG CCAGTTGTTG GTACTGGAGC TCCATTGTCT GTTGAATTAG 250
GGCCAGGGAT GTTAAGAGCT ATGTATGATG GTATTCAGAG GCCTTTAACA 300
GCAATTGAAG AGAAAACAGG TTCAATCTTT ATCCCAAGAG GAGTTGATGT 350
CCCTGCATTA CCAAGAGATA TAAAATGGGA ATTTAAACCA GTGGTAAATG 400
AAGGAGATTA TGTTGAAGAA GGAGACATAA TTGGAACTGT TGATGAAACT 450
CCTTCAATAG TTCATAAAAT CTTAGTTCCA ATTGGTGTTA AAGGAAAAAT 500
TGTTGAAATA AAAGAGGGTA AATTTACAGT TGAAGAGACA GTTGCAGTTG 550
TAGAAACAGA AAATGGAGAA AGGAAAGAAA TTACAATGAT GCAAAAATGG 600
CCAGTAAGAA AACCAAGACC ATATAAAGAG AAACTACCTC CAGAAATTCC 650
ATTAATTACA GGGCAAAGAG TTGAAGACAC TTTCTTTACA TTAGCAAAAG 700

GAGGAACAGC AGCAATTCCA GGTCCATTCG GTTCAGGAAA AACGGTTACT 750
CAGCATCAGT TGGCAAAGTG GTCTGACGCT GATGTCGTTG TTTATATCGG 800
ATGTGGAGAA AGAGGAAACG AGATGACAGA GGTTATTGAA GAGTTCCCAC 850
ACTTAGAAGA TATTAGAACT GGAAACAAAT TAATGGATAG AACTGTATTA 900
ATAGCCAACA CATCAAACAT GCCTGTCGCT GCAAGGGAAG CATCTGTCTA 950
TACAGGAATT ACAATTGCAG AGTACTTCAG AGATATGGGT TATGGAGTTT 1000
TATTAACAGC AGATTCAACA TCAAGATGGG CAGAGGCAAT GAGAGAAATT 1050
TCAGGTAGAT TGGAAGAAAT GCCAGGGGAA GAAGGGTATC CAGCATACTT 1100
AGCTTCAAGA TTGGCTCAGT TCTATGAAAG AGCTGGAAGA GTTATAACCT 1150
TAGGGAAAGA TAACAGACAA GGATTCGTTT GTATCGTTGG AGCTGTTTCA 1200
CCACCAGGAG GGGACTTCTC AGAACCAGTT ACATCAAACA CACTAAGGAT 1250
AGTTAAGGTA TTCTGGGCGT TAGATGCAAA CTTGGCAAGA AGAAGACACT 1300
TCCCAGCTAT CAACTGGTTG CAGAGTTATT CATTATACAT TGATGATGTT 1350
ACAGAGTGGT GGAACACAAA TACTGGTCCA GATTGGAGAC AATTAAGAGA 1400
TGAAGCAATG AGCTTATTAC AAAAAGAGGC AGAGTTGCAA GAGATTGTTC 1450
AGTTAGTTGG GCCTGATGCA TTGCCAGATA GGGAGAGAGT TATTTTAGAA 1500
GTTGCAAGAA TGTTGAGGGA GGATTTCTTA CAGCAAGATG CGTTTGATGA 1550
GGTAGATACC TACTGTCCTC CAATGAAACA GTACTTAATG TTAAAGATAA 1600
TTATGACATT CTACCAAGAA GCATTGAAGG CAGTTGAAAG AGGAGTTGAA 1650
CCAGCTAAGA TTTTAGGAGT TTCAGTTAAG CAAGATATTG CAAGAATGAA 1700
ATACATCCCA CACGATGAGT TTATAAATGT TAAATCAAAA GAAATAATGG 1750
AGAAAATTAA GAATGAATTA GGTTCATTAA ACTAA 1785

2) INFORMATION FOR SEQ ID NO: 715

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1354 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Porphyromonas gingivalis*
(B) STRAIN: W83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

TGAGCGAGGT GATCAAGGTG ATCGGCAAAA ATGCTTATGT GCAGGTTTTC 50
GAAAGTACTC GCGGTATGCA CGTAGGAGAT GAGGCAGAGT TTACCGGCAG 100
TATGCTTGAG GTAACGCTCG GCCCCGGTAT GCTTTCGAAG AACTACGACG 150
GTCTGCAACA CGACTTGGAC AAGATGGACG GGATCTTCCT CAAACGAGGC 200
GATTATACTC CCGCTCTCGA TGACGACAAG CTGTGGGACT TCAAGCCTTT 250
GGCCAATGTG AACGACAATG TGATCGCAGG CTCATGGCTC GGAGAGGTGA 300
CGGAAAATTT CCAACCGCAC AAGATCATGG TACCTTTCGT TTTCGAAGGC 350
AATTACAAGG TGAAGAGTCT GGCCAAAGCC GGTTCGTACA AAGTGAACGA 400
TGTGATCGCT GTGGTAACGG ATCAGGACGG GAAAGACCAC AATGTAACCA 450
TGGTGCAGAA ATGGCCGGTG AAACGTGCTA TCACTTGCTA TCGCGAGAAG 500
CCGCGTCCTT TCAAACTGCT CGAAACGGGT ATCCGTATCA TCGACACTTT 550
CAACCCCATC GTAGAGGGTG GTACGGGATT TATCCCCGGT CCTTTCGGTA 600
CGGGAAAGAC GGTGCTCCAG CATGCTATCT CGAAGCAGGC GGAAGCCGAT 650
ATCGTGATCA TTGCAGCCTG TGGCGAGCGT GCAAACGAGG TTGTGGAGAT 700
CTTTGCGGAA TTCCCCCACC TGAATGACCC CCACACGGGA CGTAAATTGA 750
TGGAACGTAC CATTATTATT GCTAATACGT CGAATATGCC TGTGGCTTCG 800
CGTGAGGCAT CCGTATATAC GGCCATGACG ATAGCCGAGT ACTATCGCTC 850
CATGGGCCTT CGCGTGCTGA TGATGGCAGA CTCCACTTCG CGTTGGGCAC 900
AGGCTCTGCG TGAGATGTCT AACCGTCTGG AAGAGCTTCC CGGACCGGAT 950

GCTTTCCCGA TGGACTTGTC AGCTATCGTA GCCAACTTCT ACGCTCGTGC 1000
AGGATACGTT TACCTGAACA ACGGTTCGGC CGGTTCGGTA ACGTTCATCG 1050
GTACGGTATC TCCCGCCGGT GGTAACCTCA AAGAGCCTGT GACGGAAAAC 1100
ACCAAGAAAG TGGCTCGCTG CTTCTATGCT TTGGAGCAGA ATCGTGCCGA 1150
CCGCAAACGT TATCCGGCTG TAAACCCCAT CGATAGTTAC TCGAAGTACA 1200
TCGAATATCC CGAATTCGAG AGCTATATAT CGAACCACAT CAGTTTACTC 1250
ATTATATTCA ACAGAAGTTG GCAGATATAT GGATCAAATC TTACAGCAGA 1300
CTGGACTACT AAGGTGAATG AGCTGAAGAT GCGCTTGCAT CAGGGTAAAG 1350
AAAT 1354

2) INFORMATION FOR SEQ ID NO: 716

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1788 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: Type 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

TTTGACTCAA GGGAAGATTA TAAAAGTATC GGGACCTCTA GTTATTGCAT 50
CAGGTATGCA GGAGGCTAAT ATTCAAGATA TTTGCCGTGT AGGTAAGCTA 100
GGGTTAATCG GTGAAATTAT TGAAATGAGA AGAGATCAGG CATCTATCCA 150
AGTCTATGAA GAAACATCTG GTCTTGGTCC GGGAGAACCT GTTGTTACAA 200
CTGGAGAACC TCTCTCGGTT GAATTAGGGC CAGGATTGAT TTCTCAAATG 250
TTTGATGGCA TACAACGCCC ATTAGATCGA TTTAAATTGG CTACTCATAA 300
TGATTTTCTA GTTCGTGGGG TAGAAGTTCC AAGTTTGGAT AGAGATATTA 350
AGTGGCATTT TGATTCCACT ATAGCAATTG GTCAAAAAGT GAGTACGGGT 400
GATATTCTTG GAACTGTCAA GGAAACCGAG GTAGTTAATC ATAAAATTAT 450
GGTTCCTTAT GGAGTATCTG GAGAAGTCGT TTCTATTGCA TCTGGCGATT 500
TTACAATTGA TGAAGTTGTA TATGAAATAA AAAAATTGGA CGGTAGTTTC 550
TATAAAGGAA CGCTTATGCA AAAATGGCCT GTCCGCAAGG CGCGTCCTGT 600
TTCTAAACGT TTAATTCCAG AAGAACCATT AATCACAGGT CAACGAGTTA 650
TTGATGCATT CTTTCCAGTA ACCAAAGGGG GAGCTGCAGC AGTTCCTGGA 700
CCGTTTGGAG CAGGAAAGAC AGTTGTACAA CACCAAGTAG CTAAATTTGC 750
CAATGTTGAT ATTGTTATTT ATGTCGGTTG TGGAGAACGT GGAAATGAAA 800
TGACGGATGT ACTGAATGAG TTTCCTGAGT TGATTGACCC TAATACCGGA 850
CAATCAATTA TGCAACGGAC AGTTCTGATT GCTAATACTT CAAATATGCC 900
TGTTGCTGCT CGTGAGGCTT CAATTTATAC AGGAATTACC ATGGCTGAGT 950
ATTTTCGTGA TATGGGCTAC TCTGTCGCCA TTATGGCTGA TTCAACTTCA 1000
CGTTGGGCAG AAGCGCTACG TGAAATGTCA GGACGTCTAG AAGAAATGCC 1050
TGGTGATGAG GGTTATCCTG CTTATCTGGG AAGTCGTATC GCTGAATATT 1100
ATGAAAGAGC AGGACGTTCT CAGGTTCTAG GGCTTCCAGA ACGTGAAGGA 1150
ACGATTACTG CTATTGGAGC TGTATCGCCA CCTGGTGGAG ATATTTCAGA 1200
ACCAGTTACT CAAAACACTT TACGGATTGT GAAAGTTTTT TGGGGGCTTG 1250
ATGCTCCGTT GGCACAGCGA CGTCATTTTC CTGCAATTAA CTGGCTTACA 1300
TCTTATTCAC TATATAAAGA CAGTGTGGGC ACTTATATAG ATGGTAAAGA 1350
GAAGACAGAT TGGAATAGTA AAATAACTCG TGCGATGAAC TACTTACAAC 1400
GGGAATCTAG TTTAGAGGAA ATTGTTCGTC TTGTTGGAAT TGATTCTCTG 1450
TCTGATAATG AACGACTAAC GATGGAAATT GCTAAACAAA TTCGAGAAGA 1500
TTATTTGCAA CAGAACGCTT TTGATTCGGT AGATACATTC ACTTCGTTTG 1550
CAAAACAAGA AGCAATGCTA AGTAATATTC TCACTTTTGC TGATCAGGCA 1600

AATCATGCTT TAGAGTTGGG TTCTTACTTT ACAGAGATTA TGGAAGGTAC 1650
CGTGGCAGTT CGAGACCGTA TGGCGAGAAG TAAATATGTT TCAGAAGATA 1700
GATTAGATGA AATCAAAATT ATATCAAATG AGATTACACA TCAAATTCAT 1750
TTGATATTAG AAACAGGAGG TCTATAAATG AGTGTTAT 1788

2) INFORMATION FOR SEQ ID NO: 717

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Burkholderia mallei*
(B) STRAIN: GB8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT GTGCTCGGCC GCTGACGGCC CGATGCCGCA AACGCGTGAG 50
CACATCCTGC TGGCGCGTCA GGTCGGTGTG CCGTACATCA TCGTGTTCCT 100
GAACAAGTGC GACATGGTGG ACGACGCGGA GCTGCTCGAG CTGGTCGAAA 150
TGGAAGTGCG CGAACTGCTG TCGAAGTACG ACTTCCCGGG CGACGACACG 200
CCGATCATCA AGGGTTCGGC GAAGCTGGCG CTGGAAGGCG ACAAGGGCGA 250
GCTGGGCGAA GTGGCGATCA TGAACCTGGC CGACGCGCTG GACACGTACA 300
TCCCGACGCC GGAGCGTGCG GTCGACGGCG CGTTCCTGAT GCCGGTGGAA 350
GACGTGTTCT CGATCTCGGG CCGTGGTACG GTGGTGACGG GTCGTGTCGA 400
GCGCGGCGTG ATCAAGGTTG GCGAGGAAAT CGAAATCGTC GGTATCAAGG 450
CGACGGCGAA GACGACCTGC ACGGGCGTGG AAATGTTCCG CAAGCTGCTG 500
GACCAGGGTC AGGCGGGCGA CAACGTCGGT ATCCTGCTGC GCGGCACAAA 550
GCGTGAAGAC GTGGAGCGCG GCCAGGTTCT GGCGAAGCCG GGTTCGATCA 600
CGCCGCACAC GCACTTCACG GCAGAAGTGT ACGTGCTGAG CAAGGACGAA 650
GGCGGCCGCC ACACGCCGTT CTTCAACAAC TACCGTCCGC AGTTCTACTT 700
CCGTACGACG GACGTGACGG GCTCGATCGA GCTGCCGAAG GACAAGGAAA 750
TGGTGATGCC GGGCGACAAC GTGTCGATCA CGGTGAAGCT GATCGCGCCG 800
ATCGCGATGG AAGAAGGTCT GCG 823

2) INFORMATION FOR SEQ ID NO: 718

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Burkholderia pseudomallei*
(B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

GCGATCCTGG TGTGCTCGGC CGCTGACGGC CCGATGCCGC AAACGCGTGA 50

GCACATCCTG CTGGCGCGTC AGGTCGGTGT GCCGTACATC ATCGTGTTCC 100
TGAACAAGTG CGACATGGTG GACGACGCGG AGCTGCTCGA GCTGGTCGAA 150
ATGGAAGTGC GCGAACTGCT GTCGAAGTAC GACTTCCCGG GCGACGACAC 200
GCCGATCATC AAGGGTTCGG CGAAGCTGGC GCTGGAAGGC GACAAGGGCG 250
AGCTGGGCGA AGTGGCGATC ATGAACCTGG CCGACGCGCT GGACACGTAC 300
ATCCCGACGC CGGAGCGTGC GGTCGATGGC GCGTTCCTGA TGCCGGTGGA 350
AGACGTGTTC TCGATCTCGG GCCGTGGTAC GGTGGTGACG GGTCGTGTCG 400
AGCGCGGCGT GATCAAGGTT GGCGAGGAAA TCGAAATCGT CGGTATCAAG 450
GCGACGGCGA AGACGACCTG CACGGGCGTG GAAATGTTCC GCAAGCTGCT 500
GGATCAGGGT CAGGCGGGCG ACAACGTCGG TATCCTGCTG CGCGGCACGA 550
AGCGTGAAGA CGTGGAGCGC GGCCAGGTTC TGGCGAAGCC GGGTTCGATC 600
ACGCCGCACA CGCACTTCAC GGCTGAAGTG TACGTGCTGA GCAAGGACGA 650
AGGCGGCCGC CACACGCCGT TCTTCAACAA CTACCGTCCG CAGTTCTACT 700
TCCGTACGAC GGACGTGACG GGCTCGATCG AGCTGCCGAA GGACAAGGAA 750
ATGGTGATGC CGGGCGACAA CGTGTCGATC ACGGTGAAGC TGATCGCGCC 800
GATCGCGATG GAAGAAGGTC TGCG 824

2) INFORMATION FOR SEQ ID NO: 719

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 800 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium beijerincki* (deposited as *Clostridium butyricum*)
(B) STRAIN: ATCC 8260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

TGTATCAGCA GCAGATGGTC CAATGCCACA AACAAGAGAA CATATACTAC 50
TAGGATCAAG AGTTGGTATC CAATATATCG TAGTATTCTT AAATAAAGCA 100
GATATGGTAG ACGATCCAGA ATTATTAGAA TTAGTAGAAA TGGAAGTAAG 150
AGAATTATTA AGCGAATATG ACTTCCCAGG AGACGATATT CCAGTAATAA 200
CAGGATCAGC ATTAAAAGCA TTAGAAAATC CAACAGATGA AGAAGCAATT 250
AAGCCAATCA TGGATTTAAT GGAAGCAGTA GATAGCTATA TCCCAACTCC 300
AGAAAGAGCA ACAGATAAGC CATTCTTAAT GCCAATCGAA GATGTATTCA 350
CAATTACAGG AAGAGGAACA GTTGCAACAG GAAGAGTTGA AGCTGGAGTA 400
CTTCATGTAG GAGATGAAGT AGAAATCGTT GGATTAACAG AAGAAAAGAA 450
GAAAGTTGTA GTAACTGGAA TCGAAATGTT CAGAAAGTTA TTGGATGAAG 500
CACAAGCTGG AGATAACATC GGAGCATTAT TAAGAGGAGT TCAAAGAACT 550
GATATTGAAA GAGGTCAAGT TTTATCAAAA CCAAATTCAG TACACCCTCA 600
CACTAAATTT GTAGGTCAAG TATACGTACT TAAAAAAGAA GAAGGTGGAA 650
GACATACTCC ATTCTTTGAT GGATACAGAC CACAATTCTA TTTCAGAACA 700
ACAGACGTTA CAGGRTCAAT CAAGTTACCA GATGGAATGG AAATGGTAAT 750
GCCTGGAGAT CACATTGATA TGAATGTTGA ATTAATCACT CCAATCGCAA 800

2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium innocuum*
(B) STRAIN: ATCC 14501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

GGTGCTATCC TGGTTGTTGC TGCATCTGAT GGTCCTATGC CTCAGACTCG 50
TGAGCACATC CTGCTTGCTC GTCAGGTAGG TGTTCCTTAC ATCGTTGTAT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAACTGAT CGACCTTGTT 150
GAAATGGAAG TACGTGAGCT GTTAAGCGAG TACGGATTCG ACGGAGATAA 200
CGCTCCGGTT ATCCGTGGTT CTGCACTGAA GGCTCTGGAA GGTGACGACA 250
AATACGTTGG CGCTATCAAA GAACTGATGG ATGCAGTTGA TGAATTCATC 300
CCAGATCCAA CTCGTGAAAC TGACAAACCA TTCCTGATGT CTGTAGAAGA 350
CGTTATGACA ATCACAGGAC GTGGTACAGT TGCTACAGGA CGTGTTGAGC 400
GTGGGGTAGT AAAACTGGGA GAAGAAGTTG AAATCGTTGG TATCAAGGAT 450
ACTCAGAAAA CTGTTGTTAC CGGACTGGAA ATGTTCCGTA AGCAGCTGGA 500
CTTCGCAGAA TCCGGAGACA ACATCGGTGC TCTGCTGCGT GGTATCAACC 550
GTGACCAGAT TCAGCGTGGA CAGGTTCTTG CTAAACCAGG ATCCGTACAT 600
CCACACACAA AGTTCAAGGC TCAGGTTTAT GTATTAACAA AAGAAGAAGG 650
TGGACGTCAC ACTCCATTCG TTTCTAACTA CCGTCCTCAG TTCTACTTCC 700
GTACAACTGA CGTAACTGGT GTTATTACAT TACCGGAAGG AACTGAAATG 750
GTTATGCCTG GTGACAACGT TGAAATGAAC GTTGAGCTGA TTGCTCCAA 799

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 789 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

TTGTATCAGC AGCAGATGGT CCAATGCCAC AAACAAGAGA ACACATCCTA 50
TTAGCATCAA GAGTAGGAGT TAACCACATA GTAGTATTCT TAAACAAAGC 100
AGACCAAGTA GATGATCCAG AATTACTAGA ATTAGTAGAA ATGGAAGTAA 150
GAGAATTATT AAGCGAATAC GGATTTGACG GAGACGAATG TCCAGTAGTA 200
GTAGGATCAG CATTAAAAGC AATCGAAGAA GGGGATGACC AATGCATCCT 250
AGACTTAATG AAAGCTGTAG ATGAATATAT CCCAACTCCA GAAAGAGCAA 300
CAGATCAACC ATTCTTAATG CCTGTAGAAG ATGTATTTAC AATTACAGGA 350
AGAGGAACAG TTGCAACAGG AAGAGTTGAA AGAGGAGTAC TACACGTAGG 400
AGATGAAGTA CAAATCGTAG GAATGAAAGA AGAAATCGGA AAGACAACAA 450
TCACAGGAGT AGAAATGTTC AGAAAGATGT TAGATGAAGC AATGGCTGGA 500
GATAACATCG GAGCATTATT AAGAGGAGTA CAAAGAGACG AAATCGAAAG 550
AGGTCAAGTA CTAGCAAAAC CAGGTTCAGT AACACCTCAC AAAAAATTCG 600
TAGGTCAAGT TTACGTATTA AAGAAAGAAG AAGGTGGAAG ACACACTCCA 650
TTCTTTAACG GATACAGACC ACAATTCTAC TTCAGAACAA CAGACGTAAC 700

AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGGAGACC 750
ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA 789

2) INFORMATION FOR SEQ ID NO: 722

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 798 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium septicum*
(B) STRAIN: ATCC 12464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

GTTCAGCAGC AGACGGTCCA ATGCCACAAA CAAGAGAACA TATACTACTA 50
GCATCAAGAG TTGGTGTTGA CTATATCGTA GTATTCTTAA ACAAGGCAGA 100
TATGGTAGAT GACGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTAGAG 150
AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCC AGTAATCAAG 200
GGATCAGCTT TAGTAGCATT AGAAAACCCA ACAGATGAAA AATCAATCGC 250
TCCAATCTTA GAATTAATGG AAGCAGTAGA TAGCTACATT CCAACACCAG 300
AAAGAGCAAC AGATAAGCCA TTCTTAATGC CAGTAGAAGA TGTATTCACA 350
ATAACTGGTA GAGGAACAGT TGCAACAGGA AGAGTTGAAA GAGGAGTTCT 400
TCATGTAGGA GACGAAGTAG AAATCGTTGG ATTATCAGAA GAAAGCAGAA 450
AAGTAGTAGT AACAGGAATA GAAATGTTCA GAAAGTTACT AGACGAAGCA 500
CAAGCTGGAG ATAATGTTGG AGTACTTTTA AGAGGTGTTC AAAGAACAGA 550
TATCGAAAGA GGTCAAGTAT TAGCAAAGAC TGGATCAGTT AAGCCACACA 600
GCAAGTTCGT AGGTCAAGTA TACGTACTTA AGAAAGAAGA AGGTGGAAGA 650
CATACTCCAT TCTTCGATGG ATACAGACCA CAATTCTACT TCAGAACAAC 700
AGACGTTACT GGATCAATCA AATTACCAGA CGGAATGGAA ATGGTTATGC 750
CAGGAGACCA CATTGATATG AACGTTGAAT TAATCACTCA AGTAGCAA 798

2) INFORMATION FOR SEQ ID NO: 723

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 799 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium tertium*
(B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

GTTCAGCAGC AGATGGTCCA ATGCCTCAAA CAAGAGAACA CATACTACTA 50
GCTTCAAGAG TTGGTGTTGA CTACATAGTT GTTTTCTTAA ACAAGGCAGA 100
TATGGTAGAT GACGAAGAAT TATTAGAATT AGTTGAAATG GAAGTAAGAG 150
AATTATTATC AGAATACAAC TTCCCAGGAG ATGATATTCC AGTAATAAAG 200

GGTTCAGCTT TACAAGCATT AGAAAACCCA ACAGATGAAA AAGCAATCGC 250
TCCAATCCTT GAGTTAATGG AAGCTGTAGA TAGCTACATT CCAACTCCAG 300
AAAGAGCAAC AGATAAGCCA TTCTTAATGC CAGTAGAAGA TGTATTCACA 350
ATCACTGGTA GAGGAACAGT TGCTACAGGA AGAGTTGAAA GAGGAGTTCT 400
TCACGTAGGA GACGAAGTAG AAATCGTTGG ATTATCAGAA GACAGCAGAA 450
AAGTAGTAGT AACAGGAATA GAAATGTTCA GAAAGTTACT AGACGAAGCG 500
CAAGCTGGAG ACAACGTAGG AGTTCTTTTA AGAGGAGTTC AAAGAACTGA 550
CATCGAAAGA GGTCAAGTTT TAGCAAAAGT TGGATCAGTT AAGCCACACA 600
AGAAATTTGT AGGTCAAGTA TACGTACTTA AAAAAGAAGA AGGTGGAAGA 650
CATACTCCAT TCTTCGATGG ATACAGACCA CAATTCTACT TCAGAACAAC 700
AGAYGTTACT GGTTCAATCA AGTTACCAGA TGGAATGGAA ATGGTTATGC 750
CAGGAGACCA CATTGATATG AACGTTGAAT TAATCACTCA AGTAGCTAT 799

2) INFORMATION FOR SEQ ID NO: 724

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 801 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium tetani*
(B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

TAGTAAGTGC AGCAGATGGT CCAATGCCAC AAACAAGAGA ACACATACTA 50
TTAGCATCCA GAGTTGGAGT TGAGCACATA GTAGTATTCT TAAATAAAGC 100
AGACCAAGTA GATGACGCAG AGTTAATCGA ATTAGTAGAA ATGGAAGTAA 150
GGGAATTAAT GAACGAATAC GGATTCCCAG GAGATGACGC ACCAGTAGTA 200
GTAGGATCCG CATTAAAAGC ATTAGAAAAT CCAGAAGATG ATGCAGCAAC 250
ACAATGCATA ATGGACTTAA TGGCAGCAGT AGATGAATAT ATACCAACAC 300
CAGAAAGAGC AACAGATAAG CCATTCTTAA TGCCAGTAGA AGATATCTTC 350
ACAATCACAG GAAGAGGAAC AGTTGCAACA GGAAGAGTAG AAAGAGGAAT 400
TCTAAAAGTA GGAGACGAAA TAGAAATCGT AGGATTAAGT GATGAAAGCA 450
AGAAATCAGT AATCACAGGA ATAGAAATGT TCAGAAAACT ATTAGATGAA 500
GCACAAGCAG GAGATAACAT CGGAGCATTA TTAAGAGGTG TTCAAAGAGA 550
TGAAATCCAA AGAGGTCAAG TATTAGCAGC AACAGGATCA GTAAAACCAC 600
ATAAGAGTTT TACAGGTCAA GTATATGTAT TAAAGAAAGA AGAAGGAGGA 650
AGACACACTC CATTCTTTAA CGGATACAGA CCACAATTCT ACTTTAGAAC 700
AACAGACGTA ACAGGTTCAA TCGCACTACC AGAAGGAGTA GAAATGGTAA 750
TGCCAGGAGA CCACATAGAC ATGAAGGTAG AATTAATAAC AAGAGTAGCA 800
A 801

2) INFORMATION FOR SEQ ID NO: 725

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 633 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus malodoratus*
(B) STRAIN: ATCC 43197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

```
TATGCCTCAA ACTCGTGAAC ACATCTTGTT ATCTCGTAAC GTTGGTGTTC      50
CTTACATCGT TGTATTCTTA AACAAAATGG ATATGGTTGA TGATGAAGAA     100
TTACTAGAAT TAGTTGAAAT GGAAGTTCGT GACTTATTGT CAGAATACGA     150
CTTCCCAGGC GACGACACTC CAGTTATCGC TGGTTCAGCT TTGAAAGCTT     200
TAGAAGGCGA TGCTTCATAC GAAGAAAAAA TCTTAGAATT AATGGCTGCT     250
GTTGATGAAT ATATCCCAAC ACCAGTTCGT GATACTGACA AACCATTCAT     300
GATGCCAGTC GAAGATGTAT TCTCAATCAC TGGTCGTGGA ACTGTTGCAA     350
CTGGTCGTGT TGAACGTGGA CAAGTTCGCG TTGGTGACGA AGTTGAAATC     400
GTTGGTATTG CTGAAGCAAC TGCTAAAACA ACTGTTACAG GTGTTGAAAT     450
GTTCCGTAAA TTGTTAGATT ACGCTGAAGC AGGCGATAAC ATTGGTGCAT     500
TGTTACGTGG TGTTGCACGT GAAGACATCC AACGTGGACA AGTATTGGCT     550
AAACCAGCTT CAATCACTCC ACATACAAAA TTCTCTGCAG AAGTTTACGT     600
TTTAACTAAA GAAGAAGGCG GACGTCATAC TCC                       633
```

2) INFORMATION FOR SEQ ID NO: 726

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 623 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus sulfureus*
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

```
CACGTGAACA CATCTTGTTA TCTCGTAACG TAGGTGTTCC TTACATCGTT      50
GTATTCTTAA ACAAAATGGA TATGGTTGAT GACGAAGAAT TATTAGAATT     100
AGTAGAAATG GAAGTTCGTG ACTTATTATC AGAATACGAT TTCCCAGGCG     150
ATGACACTCC AGTTGTTGCA GGTTCTGCTT TGAAAGCTTT AGAAGGCGAC     200
GCTTCTTACG AAGAAAAAAT CATGGAATTA ATGGCTGCAG TTGACGAGTA     250
CATCCCAACT CCAACTCGTG ACACTGACAA ACCATTCATG ATGCCAGTTG     300
AGGATGTATT CTCAATCACT GGACGTGGTA CTGTTGCTAC AGGTCGTGTT     350
GAACGTGGAC AAGTTCGCGT TGGTGACGTT GTAGATATCG TTGGTATCGC     400
TGACGAAACT GCTCAAACAA CTGTAACAGG TGTTGAAATG TTCCGTAAAT     450
TATTAGACTA CGCTGAAGCA GGCGATAACA TCGGTGCTTT ATTACGTGGT     500
GTTGCTCGTG AAGACATCCA ACGTGGACAA GTTTTAGCTA AACCAGCTTC     550
AATCACTCCA CATACAAAAT TCTCTGCTGA AGTATACGTA TTAAGCAAAG     600
AAGAAGGTGG ACGTCATACT CCA                                  623
```

2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 646 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lactococcus garvieae*
(B) STRAIN: ATCC 49156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

CGGTCCTATG CCTCAAACTC GTGAACACAT CTTGTTATCA CGTAACGTTG 50
GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT GGTTGATGAC 100
GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA 150
ATATGACTTC CCAGGCGACG ATGTTCCTGT AATCGCTGGT TCTGCTTTGA 200
AAGCTCTTGA AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG 250
GCTGCAGTTG ACGAATACGT TCCAACTCCA GAACGTGATA CTGACAAACC 300
ATTCATGATG CCAGTCGAAG ACGTATTCTC AATCACTGGA CGTGGTACTG 350
TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG TGATGAAGTA 400
GAAATCGTTG GTATTGCTGA CGAAACTGCT AAAACAACTG TAACAGGTGT 450
TGAAATGTTC CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG 500
GTGCATTGCT ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA 550
TTGGCTAAAG CTGGTACAAT CACACCTCAT ACAAAATTCA AAGCTGAAGT 600
TTATGTTTTG ACAAAAGAAG AAGGTGGACG TCACACTCCA TTCTTC 646

2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycoplasma pirum*
(B) STRAIN: ATCC 25960D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

GAGCAATTTT AGTTGTTTCT GCAACTGATG GTCCAATGCC TCAAACTCGT 50
GAACATATCT TATTAGCACG CCAAGTTGGT GTTCCTAAAA TGGTTGTTTT 100
CTTAAACAAA TGTGATGTTG CTTCTGATCC AGAAATGCAA GAATTAGTTG 150
CTGAAGAAGT AAAAGACTTA TTAAAATCTT ATGGTTTTGA TGGTGACAAT 200
ACTCCAATTA TTCGTGGTTC AGCATTAGAA GCATTAAATG GTAAACCTGA 250
ATGAGAAGAA AAAATTAAAG AATTAATGAA GGCAGTGGAT GACACTATTC 300
CTGATCCAGT TCGTGATACT GAAAAGCCAT TCTTGTTACC AATTGAAGAC 350
GTAATGACAA TTACAGGTCG TGGTACTGTT GTTACAGGTC GTGTAGAACG 400
TGGTACTCTA AAATTAAATG ATGAAGTTGA AATTGTTGGT TTAGGTGAAA 450
CATTTAAATC TGTTGTAACA GGTATTGAAA TGTTCCGTAA AGAATTAGAT 500
GAAGCTCGTG CTGGTGACAA TGCTGGTATT TTACTTCGTG GTGTTGACCG 550
TGGTCAAGTA CAACGTGGTC AAGTTCTTGC TAAACCAGGT TCTATTACTC 600
CTCATACTAA ATTTAAAGCT GAAATTTATG CTTTGAAAAA AGAAGAAGGT 650
GGTCGTCATA CTGCTTTCTT AAACGGTTAT CGTCCTCAAT TCTATTTCAG 700
AACAACTGAT GTTACAGGTT CTATTAAATT AAAAGATGGA ACTGAAATGG 750
TTATGCCTGG TGACAATACT GAAATCACTG TAGAATTAAT TTCACCAATT 800
GCTTGTAAAA AGGAAGTAAG TTT 823

2) INFORMATION FOR SEQ ID NO: 729

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycoplasma salivarium*
(B) STRAIN: ATCC 23064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

GGAGCAATCT TAGTTGTTGC TGCAACTGAT GGTGCGATGC CTCAAACTCG 50
TGAACACGTT TTACTTGCAA AACAAGTTGG TGTTCCTAAA ATCGTTGTTT 100
TCTTAAACAA AATCGATATG TTCAAGCCAG AAGAAAGAGC CGAAATGGTT 150
GAAATGGTTG AAATGGACAT TCGTGACTTA TTAAACAAAT ACGACTTTGA 200
TGGTGACAAT ACTCCTATTA TTGCTGGTTC AGCATTAAAA GCATTACAAG 250
GTGATCCAGA ATATGAAAAG AATATTCTAG AACTTATGGA TGCAGTAGAC 300
ACATACATTG ATGAACCTAC TCGTGATAAA GATAAACCAT TCTTAATGGC 350
TGTAGAAGAC GTATTTACAA TTACTGGTCG TGGAACTGTT GCTACTGGTA 400
GAGTAGAACG TGGTACATTA CATCTAAATG ATGAAGTTGA AATCGTTGGT 450
CTACGTCCAA CAATTAAAAC TGTTGTTACT GGAATTGAAA TGTTCCGTAA 500
AAATTTAAAA GAAGCTCAAG CTGGAGATAA TGCAGGACTT TTACTACGTG 550
GAATTGATAG AGATCAAGTA GAACGTGGAC AAGTTTTGGC CAAACCAAAA 600
AGTATTATTC CTCACACAGA ATTTGAAGCT GCTGTGTATG TTCTAAAAGC 650
TGAAGAAGGT GGACGTCACA CTCCATTCTT TGAACACTAT AAACCACAAT 700
TTTACTTTCG TACAACCGAC GTTACTGGTG GAATTAAATT CAAACCTGGA 750
CGTGAAATGG TTATGCCTGG CGAAAATGTT GAATTTACAG TTACTTTAAT 800
TGCTCCTATT GCAGTTGAAG AAGGAA 826

2) INFORMATION FOR SEQ ID NO: 730

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria polysaccharea*
(B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

TGGTATGTTC CGCAGCYGAY GGYCCTATGC CTCAAACTCG CGAACACATC 50
CTGYTGGCTC GCCAAGTAGG YGTACCTTAC ATCATCGTRT TCATGAACAA 100
ATGCGACATG GTTGACGATG CCGAGCTGTT GGAACTGGTT GAAATGGAAA 150
TCCGYGACCT GYTGTCMAGC TACGACTTCC CMGGCGACGA CTGCCCAATC 200
GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGYGAYGCTG GTTACGAAGA 250
GAAAATCTTC GAAYTGGCTG CTGCTTTGGA CAGCTACATC CCAACTCCTG 300

AGCGTGCTGT GGACAAACCK TTCYTGYTGC CTATCGAAGA CGTRTTCTCT 350
ATCTCTGGYC GYGGTACMGT AGTAACYGGY CGTGTAGAGC GCGGTRTCAT 400
CCACGTTGGT GACGAGATYG AAATCGTAGG TCTGAAAGAA ACCCAAAAAA 450
CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGTCAA 500
GCWGGTGACA ACGTAGGCGT ATTGYTGCGT GGTACCAARC GTGAAGACGT 550
AGAGCGTGGT CAAGTATTGG CYAAACCAGG YACCATYACT CCSCACACCA 600
AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG TGGTCGYCAC 650
ACTCCATTCT TCGCYAACTA CCGYCCMCAA TTCTACTTCC GTACYACTGA 700
CGTAACYGGT GCAGTTACTT TGGAAGAAGG TGTAGAAATG GTAATGCCAG 750
GTGAGAACGT AACCATTACY GTAGAACTGA TTGCGCCTAT CGCTAGGAAG 800
AAGGTCTGCG 810

2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Enteritidis
(B) STRAIN: ATCC 13076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC GTGAGCACAT 50
CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG TTCCTGAACA 100
AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT TGAAATGGAA 150
GTTCGYGAAC TGCTGTCTCA GTACGACTTC CCGGGCGACG ACACTCCGAT 200
CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA GAGTGGGAAG 250
CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT CCCGGAACCA 300
GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG ACGTATTCTC 350
CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA CGCGGTATCA 400
TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA GACTCAGAAG 450
TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG ACGAAGGCCG 500
TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA CGTGAAGAAA 550
TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA GCCGCACACC 600
AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG GCGGCCGTCA 650
CACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG 700
ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT GGTAATGCCG 750
GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA TCGCAATGGA 800
CGACGGTCTG CGT 813

2) INFORMATION FOR SEQ ID NO: 732

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA